

Searches run against the **Published_Applications AA** database on any Compugen machine between Feb 18 – Mar 16, 2004 had incomplete results.

The incomplete results were due to problem with the program that moves new applications into the Published_Applications_AA database. This problem was detected and corrected on Mar 17, 2004.

We have determined that a search was done for you on case in the Published_Applications_AA database between Feb 18 – Mar 16, 2004. This search has been rerun. The new results are attached.

STIC Database tracking # ¹¹⁴⁵²²
114627 original search completed 2/18/04

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 77.9211 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFWNRMMKWKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	10	US-09-847-940B-19
2	148	100.0	28	11	US-09-847-946A-19
3	134	90.5	28	10	US-09-847-940B-18
4	134	90.5	28	11	US-09-847-946A-18
5	101	68.2	26	15	US-10-097-175-101
6	100	67.6	36	9	US-09-731-023A-12
7	100	67.6	36	12	US-10-358-365-12
8	98	66.2	17	15	US-10-329-915-1
9	95	64.2	21	8	US-08-610-220A-11
10	95	64.2	21	9	US-09-150-623-11
11	95	64.2	30	15	US-10-188-947-11
12	94.5	63.9	269	12	US-10-116-275-190
13	94	63.5	34	15	US-10-161-499-79
14	94	63.5	36	9	US-09-731-023A-11
15	94	63.5	36	12	US-10-358-365-11

16	63.5	64	15	US-10-118-079-44	Sequence 44, Appl
17	63.5	217	15	US-10-097-340-129	Sequence 129, Appl
18	63.5	233	12	US-10-420-940-4	Sequence 4, Appl
19	63.5	295	15	US-10-118-079-4	Sequence 4, Appl
20	62.8	22	12	US-10-369-226-50	Sequence 50, Appl
21	62.8	28	9	US-09-214-371-9	Sequence 9, Appl
22	62.8	115	9	US-09-925-299-1169	Sequence 1169, Appl
23	62.8	115	11	US-09-925-299-1169	Sequence 1169, Appl
24	62.8	257	15	US-10-118-079-6	Sequence 6, Appl
25	62.8	16	8	US-08-610-220A-9	Sequence 9, Appl
26	62.2	16	9	US-09-214-371-43	Sequence 43, Appl
27	62.2	16	9	US-09-780-070-38	Sequence 38, Appl
28	62.2	16	9	US-09-150-623-9	Sequence 9, Appl
29	62.2	16	9	US-09-731-023A-10	Sequence 10, Appl
30	62.2	16	9	US-09-854-204-1	Sequence 1, Appl
31	62.2	16	10	US-09-900-147-8	Sequence 8, Appl
32	62.2	16	10	US-09-792-480-29	Sequence 29, Appl
33	62.2	16	10	US-09-785-802A-2	Sequence 2, Appl
34	62.2	16	10	US-09-785-802A-5	Sequence 5, Appl
35	62.2	16	10	US-09-902-432-32	Sequence 32, Appl
36	62.2	16	10	US-09-953-031A-10	Sequence 10, Appl
37	62.2	16	10	US-09-981-286A-3	Sequence 3, Appl
38	62.2	16	11	US-09-962-967A-6	Sequence 6, Appl
39	62.2	16	11	US-09-913-414-6	Sequence 54, Appl
40	62.2	16	11	US-09-775-052-54	Sequence 54, Appl
41	62.2	16	11	US-09-295-189-4	Sequence 4, Appl
42	62.2	16	11	US-09-965-876A-1	Sequence 1, Appl
43	62.2	16	12	US-10-017-672-11	Sequence 11, Appl
44	62.2	16	12	US-10-201-389A-14	Sequence 14, Appl
45	62.2	16	12	US-10-161-051-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-19
; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19

Query Match 100.0%; Score 148; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKWFWNRMMKWKKTALDASALQTE 28
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Db 1 DROIKWFWNRMMKWKKTALDASALQTE 28

RESULT 2
US-09-847-946A-19
; Sequence 19, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-19
Query Match 100.0%; Score 148; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRQIKWFQNRMRKWKKTALDASALQTE 28
Db 1 DRQIKWFQNRMRKWKKTALDASALQTE 28

RESULT 3
US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides

US-09-847-940B-18
Query Match 90.5%; Score 134; DB 10; Length 28;
Best Local Similarity 92.9%; Pred. No. 6e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 DRQIKWFQNRMRKWKKTALDASALQTE 28
Db 1 DRQIKWFQNRMRKWKKTALDWSWLQTE 28

RESULT 4
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US2003005499A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-18
Query Match 90.5%; Score 134; DB 11; Length 28;
Best Local Similarity 92.9%; Pred. No. 6e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 DRQIKWFQNRMRKWKKTALDASALQTE 28
Db 1 DRQIKWFQNRMRKWKKTALDWSWLQTE 28

RESULT 5
US-10-097-175-101
; Sequence 101, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VIBHA B.
; APPLICANT: FINDEIS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides

US-10-097-175-101
Query Match 68.2%; Score 101; DB 15; Length 26;
Best Local Similarity 73.9%; Pred. No. 2.4e-07;
Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 2 RQIKWFQNRMRKWKKTALDASA 24
Db 1 RQIKWFQNRMRKWKKTIESSS 23

RESULT 6
US-09-731-023A-12
; Sequence 12, Application US/09731023A
; Patent No. US2002007283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-cav-X fusion peptide
US-09-731-023A-12

Query Match 67.6%; Score 100; DB 9; Length 36;
Best Local Similarity 69.2%; Pred. No. 4.5e-07;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ROIKIWFQNRMRKWKKTALDASALQT 27
Db 1 ROIKIWFQNRMRKWKKGIDKAFPTT 26

RESULT 7
US-10-358-365-12
; Sequence 12, Application US/10358365
; Publication No. US20030165510A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/10/358,365
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 09/731,023
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-cav-X fusion peptide
US-10-358-365-12

Query Match 67.6%; Score 100; DB 12; Length 36;
Best Local Similarity 69.2%; Pred. No. 4.5e-07;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ROIKIWFQNRMRKWKKTALDASALQT 27
Db 1 ROIKIWFQNRMRKWKKGIDKAFPTT 26

RESULT 8
US-10-229-915-1
; Sequence 1, Application US/10229915
; Publication No. US20030083262A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: PPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/316,328
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-1

Query Match 66.2%; Score 98; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRKWKK 17
Db 1 DROIKIWFQNRMRKWKK 17

RESULT 9
US-08-610-220A-11
; Sequence 11, Application US/08610220A
; Publication No. US20030099638A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610,220A
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-610-220A-11

Query Match 64.2%; Score 95; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ROIKIWFQNRMRKWKKTA 19
Db 1 ROIKIWFQNRMRKWKKQA 18

RESULT 10
US-09-150-623-11
; Sequence 11, Application US/09150623
; Patent No. US20020044931A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL

Job time : 77.9766 secs

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RESULT 14
US-09-731-023A-11
; Sequence 11, Application US/09731023A
; Patent No. US2002007283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
; OTHER INFORMATION: peptide
US-09-731-023A-11

Query Match 63.5%; Score 94; DB 9; Length 36;
Best Local Similarity 65.4%; Pred. No. 3.le-06;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 RQIKWFFQNRRMKWKTKLDASALQT 27
Db 1 RQIKWFFQNRRMKWKKGDKIWKASFTT 26

RESULT 15
US-10-358-365-11
; Sequence 11, Application US/10358365
; Publication No. US20030165510A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/10/358,365
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 09/731,023
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/231,327
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
; OTHER INFORMATION: peptide
US-10-358-365-11

Query Match 63.5%; Score 94; DB 12; Length 36;
Best Local Similarity 65.4%; Pred. No. 3.le-06;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 RQIKWFFQNRRMKWKTKLDASALQT 27
Db 1 RQIKWFFQNRRMKWKKGDKIWKASFTT 26

Search completed: February 18, 2004, 15:42:02

Nb ant

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 106.289 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWQNRKMKKTKTALDASALQTE 28

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SIDSL/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	23	Mutated IKKbeta NE
2	148	100.0	28	23	NBD peptide SEQ ID
3	148	100.0	28	24	Human mutant NEMO
4	134	90.5	28	23	IKKbeta NEMO bindi
5	134	90.5	28	23	NBD peptide SEQ ID
6	134	90.5	28	24	Wild-type human NE
7	101	68.2	26	24	Androgen receptor
8	100	67.6	36	23	Antennapedia-caveo
9	98	66.2	20	21	Synthetic alpha sm

10	98	66.2	26	18	AAW11630	Anti-apoptotic pro
11	98	66.2	41	22	AB80924	Mixer SIM peptide.
12	98	66.2	41	22	AB80925	Mixer SIM mutant p
13	95	64.2	21	18	AAW45976	Cysteine protease
14	95	64.2	24	19	AAW82957	Oestrogen receptor
15	95	64.2	30	24	ABP58107	Mouse TIRAP-Antenn
16	95	64.2	36	21	AAW78416	Drosophila antenna
17	95	64.2	230	21	AAW58610	Protein regulating
18	94	63.5	27	18	AAW11629	Anti-apoptotic pro
19	94	63.5	27	18	AAW27444	Antennapedia inter
20	94	63.5	27	23	AB883151	Transduction domai
21	94	63.5	34	21	AAU79919	Human papillomavir
22	94	63.5	36	23	AAU79344	Antennapedia-caveo
23	94	63.5	42	23	ABP53779	Antennapedia helix
24	94	63.5	60	20	AAV42291	Drosophila antenna
25	94	63.5	60	20	AAV27403	D. melanogaster pa
26	94	63.5	60	20	AAV04364	Drosophila antenna
27	94	63.5	60	23	AB884470	S. cerevisiae Antp
28	94	63.5	61	22	AAE00811	D. melanogaster an
29	94	63.5	64	24	AAE32060	Antennapedia C3APL
30	94	63.5	128	24	ABP99729	Amino acid sequenc
31	94	63.5	217	22	AAE10922	Human HOXB7 varian
32	94	63.5	217	23	ABG96337	Human ovarian canc
33	94	63.5	295	24	AAE32047	Clostridium botuli
34	94	63.5	378	22	ABE72035	Drosophila melanog
35	94	63.5	417	22	ABE57755	Drosophila melanog
36	94	63.5	589	22	ABE58929	Drosophila melanog
37	93	62.8	22	20	AAW91049	Internalization se
38	93	62.8	22	21	AAE27063	Beta-catenin deriv
39	93	62.8	106	21	AAE21030	Human nucleic acid
40	93	62.8	115	21	AAE53629	Human colon cancer
41	93	62.8	220	22	AAW41487	Human polypeptide
42	93	62.8	236	22	AAW39701	Human polypeptide
43	93	62.8	243	19	AAW48885	Amino acid sequenc
44	93	62.8	257	24	AAE32048	Clostridium botuli
45	92.5	62.5	42	23	ABP53778	Antennapedia helix

ALIGNMENTS

RESULT 1

ABB08741

ID ABB08741 standard; peptide; 28 AA.

XX

XX ABB08741;

XX

XX 14-JUN-2002 (first entry)

XX

XX Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.

XX

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

XX autoimmune disease; transplant rejection; osteoporosis; cancer;

XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;

XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;

XX corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;

XX osteopathic; cytostatic; neurotropic; antiinflammatory; immunosuppressive;

XX antiarteriosclerotic; virucide; antiprotective; anti-HIV; human;

XX dermatological; antibacterial; antipsoriatic; antirheumatic;

XX antiarthritic; osteopathic; antiulcer; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

OS

XX Key Location/Qualifiers

XX Misc-difference 22 /note= "Wildtype Trp substituted by Ala"

XX

XX Misc-difference 24 /note= "Wildtype Trp substituted by Ala"

XX

XX WO200183547-A2.

XX

PD 08-NOV-2001.
 XX
 PF
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 DR
 XX
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 XX
 XX Claim 23; Fig 5; 82pp; English.
 PS
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyomyeloma, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 XX Sequence 28 AA;
 SQ
 Query Match 100.0%; Score 148; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRMRKWKKTALDASALQTE 28
 DB 1 DRQIKIWFQNRMRKWKKTALDASALQTE 28
 RESULT 2
 AM48524
 ID AM48524 standard; Peptide; 28 AA.
 XX
 AC AM48524;
 XX
 DT 20-MAR-2002 (first entry)

XX NBD peptide SEQ ID NO 19.
 DE
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 PT
 PS Example 5; Fig 5; 88pp; English.
 XX
 XX The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, The
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polyomyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 28 AA;
 SQ
 Query Match 100.0%; Score 148; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRMRKWKKTALDASALQTE 28
 DB 1 DRQIKIWFQNRMRKWKKTALDASALQTE 28
 RESULT 3

ABU08435
ID ABU08435 standard; peptide; 28 AA.
XX AC
XX ABU08435;
XX DT
XX 12-JUN-2003 (first entry)
XX DE
XX Human mutant NEMO binding site (NBD) peptide.
XX KW
XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX KW
XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
XX KW
XX nuclear factor-kappaB induction; inflammatory disorder;
XX KW
XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX KW
XX atherosclerosis; viral infection; Ataxia telangiectasia;
XX KW
XX transplantation detection; immunosuppressive; osteopathic;
XX KW
XX cytotatic; neutropic; neuroprotective; antiatherosclerotic; virucide;
XX KW
XX vasotropic; antirheumatic; antiarthritic; mutant; mutagen.
XX KW
XX Homo sapiens.
XX OS
XX Synthetic.
XX PN
XX US2002156000-A1.
XX XX
XX PD
XX 24-OCT-2002.
XX XX
XX 02-MAY-2001; 2001US-0847940.
XX XX
XX 02-MAY-2000; 2000US-201261P.
XX PR
XX 22-AUG-2000; 2000US-0643260.
XX XX
XX (MAYM/) MAY M J.
XX PA
XX (GHOS/) GHOSH S.
XX PI
XX May MJ, Ghosh S;
XX XX
XX WPI; 2003-209142/20.
XX XX
XX Novel antiinflammatory peptide compounds comprising NEMO binding
XX PT
XX domain, useful for modulating NF-kappaB induction in a cell and for
XX PT
XX treating NF-kappaB-mediated inflammation disorders e.g., asthma,
XX PT
XX psoriasis, vasculitis -
XX XX
XX Claim 22; Fig 5A; 47pp; English.
XX PS
XX The present invention relates to antiinflammatory compounds comprising
XX CC
XX NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX CC
XX found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
XX CC
XX (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX CC
XX are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
XX CC
XX in a cell, where the compounds are capable of blocking the interaction
XX CC
XX between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX CC
XX antiinflammatory compound further comprises at least one membrane
XX CC
XX translocation domain. The compounds are useful for treating
XX CC
XX inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX CC
XX Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX CC
XX telangiectasia, and for transplantation detection. The compounds of
XX CC
XX the invention block NF-kappaB induction by IKK but do not inhibit
XX CC
XX the basal activity of NF-kappaB. The present sequence represents
XX CC
XX a human mutant NBD peptide.
XX SQ
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 148; DB 24; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-15;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 DRQIKWFNRRMKWKKTALDASALQTE 28
XX |||||
XX Db 1 DRQIKWFNRRMKWKKTALDASALQTE 28
XX |||||
XX
XX RESULT 4
XX ABB08740

ABB08740 standard; peptide; 28 AA.
XX AC
XX ABB08740;
XX DT
XX 14-JUN-2002 (first entry)
XX DE
XX IKKbeta NEMO binding domain peptide SEQ ID NO 18.
XX KW
XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX KW
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX KW
XX autoimmune disease; transplant rejection; osteoporosis; cancer;
XX KW
XX Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
XX KW
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX KW
XX corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
XX KW
XX osteopathic; cytotatic; neutropic; neuroprotective; anti-HIV; human;
XX KW
XX antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
XX KW
XX dermatological; antibacterial; antipsoriatic; antirheumatic;
XX KW
XX antiarthritic; osteopathic; antiulcer.
XX OS
XX Homo sapiens.
XX PN
XX WO200183547-A2.
XX XX
XX 08-NOV-2001.
XX XX
XX 02-MAY-2001; 2001WO-US40654.
XX XX
XX 02-MAY-2000; 2000US-201261P.
XX PR
XX 22-AUG-2000; 2000US-0643260.
XX XX
XX (UYVA) UNIV VALE.
XX PA
XX May MJ, Ghosh S;
XX PI
XX WPI; 2002-179350/23.
XX DR
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
XX PT
XX inflammatory disorders, osteoporosis and cancer, comprises contacting a
XX PT
XX cell with an anti-inflammatory compound comprising at least one NEMO
XX PT
XX binding domain -
XX XX
XX Claim 23; Fig 5; 82pp; English.
XX PS
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
XX CC
XX comprising contacting a cell with an anti-inflammatory compound
XX CC
XX (ABB08740-ABB08742) comprising at least one NEMO binding domain
XX CC
XX (ABB77313). The compound has acts through selective inhibition of
XX CC
XX cytokine-mediated NF-kB activation by blocking the interaction of NEMO
XX CC
XX with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
XX CC
XX interaction results in inhibition of IKKbeta kinase activation and
XX CC
XX subsequent decreased phosphorylation of IkappaB. The compound may also
XX CC
XX act (directly or indirectly) by blocking the recruitment of leukocytes
XX CC
XX into sites of acute and chronic inflammation, by down-regulating the
XX CC
XX expression of E-selectin on leukocytes or by blocking osteoclast
XX CC
XX differentiation. The compound is useful in treating NF-kB mediated
XX CC
XX conditions, where the condition is an inflammatory disorder, an
XX CC
XX autoimmune disease, transplant rejection, osteoporosis, cancer,
XX CC
XX Alzheimer's disease, atherosclerosis, a viral infection or ataxia
XX CC
XX telangiectasia. The inflammatory disorder is asthma, allergies,
XX CC
XX urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
XX CC
XX rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
XX CC
XX bowel disease, chronic obstructive pulmonary disease, vasculitis and
XX CC
XX bursitis. The inflammatory disorder may also be dermatitis, eczema,
XX CC
XX psoriasis, osteoarthritis, psoriatic arthritis, lupus and
XX CC
XX spondylarthritis. Also for Crohn's disease, ulcerative colitis,
XX CC
XX polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
XX CC
XX cryoglobulinaemia or multiple sclerosis. For chronic viral infections
XX CC
XX caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
XX CC
XX diseases include HIV and influenza. The compound may also be useful for
XX CC
XX treating anaphylaxis, drug and food sensitivity, contact dermatitis,
XX CC
XX sunburn or aging. The compound may be used to replace corticosteroids in
XX CC
XX any application in which corticosteroids are used, including
XX CC
XX immunosuppression in transplants and cancer therapy. Also for identifying

CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.

XX Sequence 28 AA;
 SQ Query Match 90.5%; Score 134; DB 23; Length 28;
 Best Local Similarity 92.9%; Pred. No. 6.7e-13;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRMKWKKTALDASALQTE 28
 |||||
 Db 1 DRQIKWFQNRMRMKWKKTALDWSWLQTE 28

RESULT 5
 AAM48523
 ID AAM48523 standard; Peptide; 28 AA.

XX AC AAM48523;

XX DT 20-MAR-2002 (first entry)

XX DE NBD peptide SEQ ID NO 18.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WQ200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRACIS PHARM INC.

XX PA (UYUA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX Example 5; Fig 5; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 28 AA;

Query Match 90.5%; Score 134; DB 23; Length 28;

Best Local Similarity 92.9%; Pred. No. 6.7e-13;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMRMKWKKTALDASALQTE 28

Db 1 DRQIKWFQNRMRMKWKKTALDWSWLQTE 28

RESULT 6
 ABU08434

ID ABU08434 standard; peptide; 28 AA.

XX AC ABU08434;

XX DT 12-JUN-2003 (first entry)

XX DE Wild-type human NEMO binding site (NBD) peptide.

XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplant rejection; immunosuppressive; osteopathic;
 KW cytostatic; neutropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic.

XX OS Homo sapiens.

XX PN US2002156000-A1.

XX PD 24-OCT-2002.

XX PF 02-MAY-2001; 2001US-0847940.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (MAYM/) MAY M J.

XX PA (GHOS/) GHOSH S.

XX PI May MJ, Ghosh S;

XX DR WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -

XX Claim 35; Page 22; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The

CC antiinflammatory compound further comprises at least one membrane
CC translocation domain. The compounds are useful for treating
CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
CC telangiectasia, and for transplantation detection. The compounds of
CC the invention block NF-kappaB induction by IKK but do not inhibit
CC the basal activity of NF-kappaB. The present sequence represents
CC an antiinflammatory compound of the invention.

XX
SQ Sequence 28 AA;
Query Match 90.5%; Score 134; DB 24; Length 28;
Best Local Similarity 92.9%; Pred. No. 6.7e-13;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DQIKWFQNRKMKWKKTALDASALQTE 28
Db 1 DQIKWFQNRKMKWKKTALDWSWLQTE 28

RESULT 7
AAE31836
ID AAE31836 standard; peptide; 26 AA.
AC AAE31836;
XX
DT 07-MAR-2003 (first entry)
XX
DE Androgen receptor binding peptide #87.
XX
KW Androgen receptor; androgen-associated disorder; prostate cancer; acne;
KW benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome;
KW male pattern baldness; Stein-Leventhal syndrome; infertility; cytostatic;
KW X-linked spinal bulbar muscular atrophy; anti-seborrheic; dermatological;
KW depilatory; androgen receptor binding peptide.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 26 /note= "C-terminal amide"
FT
XX WO200272612-A2.
XX
PN
XX
PD 19-SEP-2002.
XX
XX 12-MAR-2002; 2002WO-US07487.
XX
XX 13-MAR-2001; 2001US-275240P.
PR 28-JAN-2002; 2002US-352399P.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX Joyal JL, Mueller J, Oza VB, Findeis MA,
XX WPI; 2003-067363/06.
XX
XX New peptide modulators of androgen receptor, useful for treating
XX androgen-associated disorder, e.g. prostate cancer, particularly
XX hormonally refractive prostate cancer, colon cancer, lung cancer, acne,
XX or hirsutism -
XX
XX Example; Page 30; 68pp; English.

XX The present invention relates to novel peptide modulators of androgen
XX receptor. The peptides of the invention are useful for treating androgen-
XX associated disorders such as prostate cancer, particularly hormonally
XX refractive prostate cancer, colon cancer, lung cancer, benign prostatic
XX hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal
XX syndrome, androgen insensitivity syndrome, infertility, endometrial
XX cancer and X-linked spinal bulbar muscular atrophy. The present sequence

CC is an androgen receptor binding peptide.
XX
SQ Sequence 26 AA;
Query Match 68.2%; Score 101; DB 24; Length 26;
Best Local Similarity 73.9%; Pred. No. 4.9e-08;
Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWFQNRKMKWKKTALDASA 24
Db 1 RQIKWFQNRKMKWKKTALTISSS 23

RESULT 8
AAU79345
ID AAU79345 standard; Peptide; 36 AA.
XX
AC AAU79345;
XX
DT 02-JUL-2002 (first entry)
XX
DE Antennapedia-caveolin-X fusion peptide.
XX
KW Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;
KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;
KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;
KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;
KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;
KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;
KW spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav;
KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
KW human; fruit fly; antennapedia internalisation signal.
XX
XX Drosophila melanogaster.
OS Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FT Misc-difference 1..16 /label= Antennapedia_internalisation_signal
FT /note= "Specifically claimed in claim 9"
FT Misc-difference 17..32
FT /label= Cav-X
FT /note= "Control peptide based on a human caveolin-1
FT scaffolding domain shown in AAU79340 residues
FT 82-101"
XX
XX WO200220768-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US42069.
XX
XX 08-SEP-2000; 2000US-231327P.
PR 07-DEC-2000; 2000US-0731023.
XX
XX (UYVA) UNIV VALE.
XX
XX Sessa WC;
XX
XX WPI; 2002-329877/36.
XX
XX New peptide having caveolin scaffolding domain, useful for modulating
XX activity of endothelial nitric oxide synthase and inhibiting
XX inflammation and tumour cell angiogenesis proliferation -
XX
XX Claim 16; Page 72; 73pp; English.

XX The invention describes an isolated caveolin scaffolding domain peptide
XX (I). A fusion peptide (II) containing (I) and at least a membrane
XX translocation sequence is useful for down regulating endothelial nitric
XX oxide synthase (eNOS) activity in a cell, resulting in blockage of
XX vasodilation. (II) is therefore useful for inhibiting inflammation and

CC tumour cell angiogenesis/proliferation in an animal; and for blocking the
 CC interaction of caveolin with a protein in vivo. (II) may be useful in
 CC treatment of inflammatory conditions such as osteoporosis, rheumatoid
 CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)
 CC are also useful for treating pathological processes associated with a
 CC pro-inflammatory response including allergies such as allergic rhinitis,
 CC uticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous
 CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,
 CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,
 CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and
 CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing
 CC corticosteroids useful for immunosuppression in transplant and cancer
 CC patients. When administered along with one or more antiinflammatory
 CC agent (I) and (II) are useful for inhibiting tumour growth or malignant
 CC neoplasm including cellular angiogenesis, proliferation, invasiveness,
 CC and metastasis in biological systems. This sequence represents a fusion
 CC peptide of the invention created from the fruit fly antennapedia
 CC internalisation signal and control sequence Cav-X, based on the human
 CC caveolin-1 scaffolding domain shown in AU79340, residues 82-101.
 XX
 SQ Sequence 36 AA;

Query Match 67.6%; Score 100; DB 23; Length 36;
 Best Local Similarity 69.2%; Pred. NO. 9.9e-08;
 Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRMMKWKKTALDASALQT 27
 DB 1 RQIKIWFQNRMMKWKKGIDKAFPTT 26

RESULT 9
 AABL3423
 ID AABL3423 standard; peptide; 20 AA.
 AC AABL3423;
 DT 23-NOV-2000 (first entry)
 DE Synthetic alpha smooth muscle actin inhibitor # 3.
 XX Alpha smooth muscle actin; alpha-SM; wound contraction;
 KW hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;
 KW lung fibrosis.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT
 XX WO200038733-A1.
 XX
 PD 06-JUL-2000..
 XX
 PF 15-DEC-1999; 99WO-EP09964.
 XX
 PR 24-DEC-1998; 98EP-0204396.
 XX
 PA (UNIO) UCB-BIOPRODUCTS SA.
 XX
 PI Gabbiani G, Scarso A;
 XX
 DR WPI; 2000-452308/39.
 XX
 PT A peptidic product for prevention and treatment of a disease related to
 PT alpha-SM actin expression comprises a tetrapeptide associated with a
 PT chemical entity that is able to introduce the tetrapeptide into the
 PT cell -
 XX
 PS Claim 7; Page 23; 31pp; English.
 XX
 CC The present invention relates to novel peptides comprising of a specific

CC tetrapeptide associated with an oligopeptide which allows the
 CC introduction of the tetrapeptide into the target cell. The present
 CC sequence is one such peptide. Residues 1 to 4 of the present sequence
 CC correspond to the specific tetrapeptide, while residues 5 to 20
 CC correspond to the oligopeptide. The specific tetrapeptide of the present
 CC sequence interferes with alpha smooth muscle (alpha-SM) actin
 CC organisation in stress fibers. The present sequence may be used in the
 CC prevention and/or treatment of a disease related to alpha-SM actin
 CC expression, e.g. wound contraction, hypertrophic scars, fibromatosis and
 CC Dupuytren disease and lung fibrosis.
 XX
 SQ Sequence 20 AA;

Query Match 66.2%; Score 98; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMMKWK 17
 DB 4 DRQIKIWFQNRMMKWK 20

RESULT 10
 AAW11630
 ID AAW11630 standard; peptide; 26 AA.
 XX
 AC AAW11630;
 XX

DT 16-OCT-1997 (first entry)

DE Anti-apoptotic protein blocking peptide FP2.

XX Cell permeable; apoptosis; blocking; inhibition; tumour growth;
 KW ex vivo purging; in vivo administration; Bcl-2.

XX Synthetic.

FH Key Location/Qualifiers
 FT Peptide 1..17 /label= sig_peptide

XX DE19526174-A1.

XX 23-JAN-1997.

XX 18-JUL-1995; 95DE-1026174.

XX 18-JUL-1995; 95DE-1026174.

XX (BRAC/) BRACH M.
 PA (HERR/) HERRMANN F.
 PA (KIEH/) KIEHNTOPF M.

XX Brach M, Herrmann F, Kiehnkopf M;

XX WPI; 1997-088160/09.

XX Peptide(s) that block anti-apoptotic proteins - useful for
 PT inhibiting tumour growth

XX Claim 6; Page 7; 7pp; German.

XX The present sequence is a cell permeable anti-apoptotic protein
 CC blocking peptide, which can be used to inhibit tumour growth, e.g.
 CC by ex vivo purging or (after stabilisation) in vivo
 CC administration. The peptide preferably blocks Bcl-2, and comprises
 CC a signal peptide mediating cell penetration and a functional
 CC sequence corresponding to a Bcl-2 domain.
 XX

SQ Sequence 26 AA;

Query Match 66.2%; Score 98; DB 18; Length 26;

Best Local Similarity 89.5%; Pred. No. 1.4e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DQIKIWFQNRKMKWKTA 19
:|||||
Db 1 ERQIKIWFQNRKMKWKAA 19

RESULT 11
AAB80924
ID AAB80924 standard; Protein; 41 AA.
XX
AC AAB80924;
XX
DT 04-JUN-2001 (first entry)
XX
DE Mixer SIM peptide.
XX
KW Smad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;
KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
KW Smad Interaction Motif; tissue repair; fibrotic condition;
KW immunosuppression; diabetic nephropathy; tumour.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Biotin.Aminohexanoic acid-R"
FT
FT
XX WO200114413-A2.
XX
XX 01-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-GB03265.
XX
XX 25-AUG-1999; 99GB-0020000.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
XX Germain SE, Hill CS, Howell MT;
XX
XX WPI; 2001-265836/27.
XX
XX Polypeptide capable of interacting with a Smad polypeptide, useful in
XX the treatment of cancer and for tissue remodelling or healing of a
XX PT wound, injury or surgery, comprises a Smad Interaction Motif and is
XX PT less than 32 amino acids in length -
XX
XX Claim 16; Page 140; 179pp; English.
XX
XX The present invention relates to peptides capable of interacting with a
XX Smad protein, comprising a Smad Interaction Motif (SIM; amino acid
XX sequence PP(T/N)K). The present sequence is one such Smad interacting
XX peptide. Smad proteins are a family of highly conserved, intracellular
XX proteins that signal cellular responses downstream of Transforming Growth
XX Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
XX is thought to be necessary for interaction with the MH2 domain of Smad2.
XX The peptides of the present invention are useful in the manufacture of a
XX medicament for the treatment of a patient in need of modulation of
XX activin or TGF-beta signalling; cancer; a patient in need of reducing
XX extracellular matrix deposition, encouraging tissue repair and/or
XX regeneration, tissue remodelling or healing of a wound, injury or
XX surgery, or reducing scar tissue formation arising from injury to the
XX brain; a patient with or at risk of end-stage organ failure, pathologic
XX extracellular matrix accumulation, a fibrotic condition, disease states
XX associated with immunosuppression (such as different forms of malignancy,
XX chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
XX growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy
XX or non-inflammatory renal disease) or renal fibrosis.

Query Match 66.2%; Score 98; DB 22; Length 41;

SQ Sequence 41 AA;

Best Local Similarity 85.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRKMKWKKTALD 21
:|||||
Db 1 RQIKIWFQNRKMKKKLMD 20

RESULT 12
AAB80925
ID AAB80925 standard; Protein; 41 AA.
XX
AC AAB80925;
XX
DT 04-JUN-2001 (first entry)
XX
DE Mixer SIM mutant peptide.
XX
KW Smad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;
KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
KW Smad Interaction Motif; tissue repair; fibrotic condition;
KW immunosuppression; diabetic nephropathy; tumour; mutuin.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Biotin.Aminohexanoic acid-R"
FT
FT
XX Misc-difference 25 /note= "Wild-type Pro replaced by Ala. Wild-type sequence
XX given in AAB80924."
XX FT
XX Misc-difference 26 /note= "Wild-type Pro replaced by Ala"
XX FT
XX WO200114413-A2.
XX
XX 01-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-GB03265.
XX
XX 25-AUG-1999; 99GB-0020000.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
XX Germain SE, Hill CS, Howell MT;
XX
XX WPI; 2001-265836/27.
XX
XX Polypeptide capable of interacting with a Smad polypeptide, useful in
XX the treatment of cancer and for tissue remodelling or healing of a
XX PT wound, injury or surgery, comprises a Smad Interaction Motif and is
XX PT less than 32 amino acids in length -
XX
XX Example 2; Page 123; 179pp; English.
XX
XX The present invention relates to peptides capable of interacting with a
XX Smad protein, comprising a Smad Interaction Motif (SIM; amino acid
XX sequence PP(T/N)K). The present sequence is one such Smad interacting
XX peptide. Smad proteins are a family of highly conserved, intracellular
XX proteins that signal cellular responses downstream of Transforming Growth
XX Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
XX is thought to be necessary for interaction with the MH2 domain of Smad2.
XX The peptides of the present invention are useful in the manufacture of a
XX medicament for the treatment of a patient in need of modulation of
XX activin or TGF-beta signalling; cancer; a patient in need of reducing
XX extracellular matrix deposition, encouraging tissue repair and/or
XX regeneration, tissue remodelling or healing of a wound, injury or
XX surgery, or reducing scar tissue formation arising from injury to the
XX brain; a patient with or at risk of end-stage organ failure, pathologic
XX extracellular matrix accumulation, a fibrotic condition, disease states
XX associated with immunosuppression (such as different forms of malignancy,
XX chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
XX growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy
XX or non-inflammatory renal disease) or renal fibrosis.

CC or non-inflammatory renal disease) or renal fibrosis.

SQ Sequence 41 AA;

Query Match 66.2%; Score 98; DB 22; Length 41;
Best Local Similarity 85.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWFOQRMRKWKKTALD 21
DB 1 RQIKWFOQRMRKWKKLMD 20

RESULT 13

AAW45976
ID AAW45976 standard; peptide; 21 AA.

XX AAW45976;

DT 01-JUL-1998 (first entry)

XX Cysteine protease inhibiting peptide for preventing cell death.

XX Neuronal cell death; neurodegenerative disorder; inhibition;
KW cysteine protease; cardiovascular; liver disease.

XX Synthetic.

Key Location/Qualifiers
FH Modified-site 1

FT /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"

PN WO9735876-Al.

PD 02-OCT-1997.

XX 04-MAR-1997; 97WO-US04158.

XX 04-MAR-1996; 96US-0610220.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Troy CM;

XX WPI; 1997-489561/45.

XX New cysteine protease inhibiting peptide(s) for preventing cell
PT death - in cases of neurodegenerative, cardiovascular and liver
PT diseases, and their peptidomimetics, and general method for
PT identifying enzyme inhibiting peptides

XX Claim 10; Page 68; 112pp; English.

CC This sequence represents a specifically claimed peptide of the formula:
V-(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5;
CC if n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more,
CC (AA1)n = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value
CC of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more,
CC (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'',
CC any or all of which may be absent, = agent able to direct the compound
CC to a specific cell. The peptides are inhibitors of cysteine proteases,
CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit
CC death of cells, particularly in humans, and can be used to treat
CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,
CC Parkinson's or Huntington's diseases, multiple sclerosis, muscular
CC dystrophy, stroke), cardiovascular disease and liver disorders.
CC The peptides should be more specific than pseudosubstrate inhibitors.

SQ Sequence 21 AA;

Query Match 64.2%; Score 95; DB 18; Length 21;
Best Local Similarity 94.4%; Pred. No. 3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKWFOQRMRKWKKTALD 19
DB 1 RQIKWFOQRMRKWKKQA 18

RESULT 14

AAW82957
ID AAW82957 standard; peptide; 24 AA.

XX AAW82957;

DT 04-FEB-1999 (first entry)

XX Oestrogen receptor activity inhibiting peptide #13.

XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;
KW breast cancer; estrogen; tumour; phosphotyrosyl peptide;
KW malonyltyrosyl peptide; steroid receptor co-activator-1.

XX Synthetic.

OS Homo sapiens.

Key Location/Qualifiers
FH Modified-site 19

FT /note= "phosphotyrosine"

XX WO9846250-Al.

XX 22-OCT-1998.

XX 14-APR-1998; 98WO-US07711.

XX 14-APR-1997; 97US-0043545.

XX (REGC) UNIV CALIFORNIA.

XX Pietras RJ;

XX WPI; 1998-594522/50.

XX New anti-oestrogen peptide compositions - comprise sequences based
PT on oestrogen receptor and steroid receptor co-activator-1 sequences,
PT used for treating cancers

XX Claim 11; Page 156; 182pp; English.

XX The present invention describes a composition comprising an isolated
CC oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The
CC peptides used in the composition comprise sequences of human oestrogen
CC receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1
CC (SCR-1). The peptide compositions, nucleic acids and vectors of the
CC present invention can reduce OR activity in a cell, reduced OR
CC polypeptide dimerisation in a cell and reduce the binding of SRC-1
CC polypeptide to an OR polypeptide dimer in a cell. They can be used for
CC killing cancer cells and treating cancers, particularly breast cancer.
CC The present sequence represents a specifically claimed anti-oestrogen
CC peptide.

SQ Sequence 24 AA;

Query Match 64.2%; Score 95; DB 19; Length 24;
Best Local Similarity 85.0%; Pred. No. 3.5e-07;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWFOQRMRKWKKTALD 21
DB 1 RQIKWFOQRMRKWKPLYD 20

RESULT 15

ABP58107
ID ABP58107 standard; Peptide; 30 AA.

XX ABP58107;
XX
XX DT 28-MAR-2003 (first entry)
XX DE Mouse TIRAP-Antennapedia fusion protein.
XX
XX Toll/interleukin-1 receptor adapter protein; TIRAP; mouse;
KW inhibitor; Antennapedia; antiinflammatory.
XX
XX OS Chimeric - Mus sp.
OS Chimeric - Drosophila sp.
XX
XX FH Key Location/Qualifiers
FT Peptide 1..16
FT /note= "Antennapedia peptide"
FT Peptide 17..30
FT /note= "mouse TIRAP inhibitor peptide"
XX
XX WO200290520-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002WO-US14915.
XX
XX 09-MAY-2001; 2001US-289738P.
PR 09-MAY-2001; 2001US-289815P.
PR 29-AUG-2001; 2001US-289866P.
PR 19-MAR-2002; 2002US-0101398.
XX
XX (UYA) UNIV YALE.
XX
XX Medzhitov R, Horng T, Barton G;
XX
XX WPI; 2003-120542/11.
XX
XX New toll/interleukin-1 receptor adapter protein (TIRAP) polynucleotides
PT and polypeptides, useful for treating a disease state associated with
PT TIRAP expression, e.g. inflammation, and for inducing and affecting
PT immune response -
XX
XX Disclosure; Page 74; 74pp; English.

XX The present sequence is that of a fusion protein comprising an
CC Antennapedia peptide and a mouse Toll/interleukin-1 receptor
CC adapter protein (TIRAP) inhibitor polypeptide (see ABP58106) of
CC the invention. Antennapedia, derived from Drosophila, is a
CC cellular membrane transport protein and can be used to deliver
CC the TIRAP inhibitor across the cell membrane so that it becomes
CC therapeutically active within the cell. TIRAP is a component of the
CC Toll-like receptor 4 (TLR4) signalling pathway. It mediates MyD88
CC independent signalling in response to TLR4 ligation, and controls
CC dendritic cell maturation. Characterisation of TIRAP has led to
CC the discovery of compounds that inhibit both the MyD88 independent
CC pathway as well as the MyD88 dependent pathway of TLR4 by
CC inhibiting TIRAP polypeptide mediated signalling. Compounds that
CC inhibit TIRAP activity are useful for preventing or reducing
CC inflammation and septic shock, and especially for assisting in the
CC prevention of graft rejection, which occurs, at least in part,
CC because of cellular necrosis induced inflammation. The invention
CC provides TIRAP inhibitor polynucleotides (see ABV76259-62) and
CC polypeptides (see ABP58105-08). The TIRAP inhibitors can inhibit
CC both the MyD88 independent response, e.g. activation of NF-kappaB
CC and MAP kinases, and the MyD88 dependent response in cells
CC expressing TLR4.
XX
XX SQ Sequence 30 AA;

Query Match 64.2%; Score 95; DB 24; Length 30;
Best Local Similarity 78.3%; Pred. No. 4.5e-07;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 RQIKWIFQNRMRMKKQLRDA 24

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 30.7632 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKIWFQNRMRKWKKTALDMSWLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	59.9	60	2	PC2399 antennapedia-like
2	97	59.9	60	2	PC2400 antennapedia-like
3	97	59.9	105	2	A27471 homeotic protein R
4	97	59.9	119	2	A03314 homeotic protein m
5	97	59.9	229	2	A28329 homeotic protein H
6	96	59.3	75	2	I51341 homeo box protein
7	95	58.6	66	2	S15336 homeotic protein H
8	95	58.6	81	2	B29585 homeotic protein H
9	95	58.6	96	2	A05266 homeotic protein H
10	95	58.6	97	2	C27176 homeotic protein H
11	95	58.6	224	2	S26400 homeotic protein H
12	95	58.6	224	2	A31324 homeotic protein H
13	94	58.0	33	2	S57235 antennapedia prote
14	94	58.0	42	2	I65241 homeotic protein H
15	94	58.0	45	2	PC1216 homeotic protein D
16	94	58.0	48	2	I51439 homeobox protein -
17	94	58.0	66	2	S15538 homeotic protein H
18	94	58.0	71	2	JC1161 homeotic protein 3
19	94	58.0	71	2	A60084 homeotic protein H
20	94	58.0	74	2	D34510 homeotic protein H
21	94	58.0	75	2	S58852 homeotic protein S
22	94	58.0	76	2	C43559 homeotic protein R
23	94	58.0	78	2	I51342 homeo box protein
24	94	58.0	81	2	S47605 homeotic protein H
25	94	58.0	82	2	S08302 homeotic protein H
26	94	58.0	83	2	S47603 homeotic protein H
27	94	58.0	83	2	S50066 homeotic protein H
28	94	58.0	86	2	A34510 homeotic protein H
29	94	58.0	86	2	JT0489 homeotic protein Z

30	94	58.0	86	2	S08303 homeotic protein H
31	94	58.0	87	2	S00589 homeotic protein H
32	94	58.0	88	2	A03317 homeotic protein M
33	94	58.0	96	2	S08639 homeotic protein Z
34	94	58.0	97	2	A24779 homeotic protein m
35	94	58.0	103	2	A32167 homeotic protein H
36	94	58.0	105	2	S47602 homeotic protein H
37	94	58.0	106	2	S36448 homeotic protein s
38	94	58.0	107	2	B61045 homeotic protein T
39	94	58.0	113	2	T10775 homeobox protein -
40	94	58.0	118	2	A24777 homeotic protein H
41	94	58.0	118	2	JT0273 homeotic protein H
42	94	58.0	118	2	B24777 homeotic protein M
43	94	58.0	138	2	S20087 homeotic protein b
44	94	58.0	148	2	PC4071 homeobox A5 protei
45	94	58.0	153	1	WJHU3C homeotic protein H

ALIGNMENTS

RESULT 1

PC2399

antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)
C;Species: Styela clava
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
C;Accession: PC2399

R;Ge, T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c

A;Reference number: PC2399; MUID:95011617; PMID:7926803

A;Accession: PC2399

A;Molecule type: DNA

A;Residues: 1-60 <GET>

A;Cross-references: GB:S73920; NID:G693714; PIDN:AAB33061.2; PID:G7387472
A;Note: The authors translated the codon ATT for residue 47 as Glu

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. NO. 1.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRMRKWK 17

Db 42 DRQIKIWFQNRMRKWK 58

RESULT 2

PC2400

antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)

C;Species: Styela plicata

C;Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997

C;Accession: PC2400

R;Ge, T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c

A;Reference number: PC2399; MUID:95011617; PMID:7926803

A;Accession: PC2400

A;Molecule type: DNA

A;Residues: 1-60 <GET>

A;Note: The authors translated the codon ATA for residue 47 as Glu

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;2-58/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. NO. 1.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRMRKWK 17

Db 42 DRQIKIWFQNRMRKWK 58

Db 42 DRQKIWFQNRMMKWK 58

RESULT 3

A27471 homeotic protein R5 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
 C:Accession: A27471
 R: Falzon, M.; Sanderson, N.; Chung, S.Y.
 Gene 54, 23-32, 1987

A:Title: Cloning and expression of rat homeo-box-containing sequences.
 A:Reference number: A91576; MUID:87277429; PMID:2886401

A:Accession: A27471

A:Molecule type: DNA

A:Residues: 1-105 <FAL>

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:6-62/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 105;
 Best Local Similarity 70.4%; Pred. No. 2.7e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMMKWKKTALDWSLQT 27

Db 46 ERQIKIWFQNRMMKWKKEHKSQAPT 72

RESULT 4

A03314 homeotic protein m6 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997
 C:Accession: A03314; S14043
 R: Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
 Nature 314, 713-718, 1985
 A:Title: Structural analysis of murine genes containing homeo box sequences and their e
 A:Reference number: A03314; MUID:85188311; PMID:2986010

A:Accession: A03314

A:Molecule type: DNA

A:Residues: 1-119 <COL>

R: Breier, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.

EMBO J. 5, 2209-2215, 1986

A:Title: Sequential expression of murine homeo box genes during F9 EC cell differentiat
 A:Reference number: S13785; MUID:87053860; PMID:2877873

A:Accession: S14043

A:Molecule type: DNA

A:Residues: 19-48, 'RI', 51-87 <BRE>

C:Genetics:

A:Gene: m6

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:20-76/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 119;
 Best Local Similarity 70.4%; Pred. No. 3.1e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMMKWKKTALDWSLQT 27

Db 60 ERQIKIWFQNRMMKWKKEHKSQAPT 86

RESULT 5

A28329 homeotic protein Hox A7 - mouse
 N:Alternate names: homeotic protein Hox 1.1; m6 homeotic protein
 C:Species: Mus musculus (house mouse)
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
 C:Accession: A28329; I49131
 R: Kessel, M.; Schulze, F.; Fibi, M.; Gruss, P.
 Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987

A:Title: Primary structure and nuclear localization of a murine homeodomain protein.
 A:Reference number: A28329; MUID:87260976; PMID:2885847

A:Accession: A28329

A:Molecule type: mRNA

A:Residues: 1-229 <KES>

A:Cross-references: GB:M17192; NID:G193906; PIDN:AAA37833.1; PID:G309313

R: Parikh, H.; Shah, S.; Hilt, D.; Peterkofsky, A.

Gene 154, 237-242, 1995

A:Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.

A:Reference number: I49131; MUID:95197009; PMID:7890170

A:Accession: I49131

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-42, 'CAG', 46-229 <RES>

A:Cross-references: EMBL:U15972; NID:G664757; PIDN:AAC52160.1; PID:G664758

C:Genetics:

A:Gene: Hoxa7

A:Introns: 126/1

C:Superfamily: homeotic protein Hox A7; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:130-186/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 229;
 Best Local Similarity 70.4%; Pred. No. 6.2e-06;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMMKWKKTALDWSLQT 27

Db 170 ERQIKIWFQNRMMKWKKEHKSQAPT 196

RESULT 6

I51341 homeo box protein - Atlantic salmon (fragment)
 C:Species: Salmo salar (Atlantic salmon)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
 C:Accession: I51341
 R: Fjose, A.; Molven, A.; Eiken, H.G.
 Gene 62, 141-152, 1988
 A:Title: Molecular cloning and characterization of homeobox-containing genes from Atlant
 A:Reference number: I51341; MUID:88226009; PMID:2897318

A:Accession: I51341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-75 <FJO>

A:Cross-references: GB:M18903; NID:G213797; PIDN:AAA49559.1; PID:G213798

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:2-58/Domain: homeobox homology <HOX>

Query Match 59.3%; Score 96; DB 2; Length 75;
 Best Local Similarity 78.3%; Pred. No. 2.6e-06;
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMMKWKKTALDWS 23

Db 42 ERQIKIWFQNRMMKWKKHQDES 64

RESULT 7

S15536 homeotic protein Hox A7 - human (fragment)
 N:Alternate names: homeotic protein Hox 1A
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
 C:Accession: S15536
 R: Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; St
 Genome 31, 745-756, 1989
 A:Title: Organization of human class I homeobox genes.
 A:Reference number: S15036; MUID:90215256; PMID:2576652
 A:Accession: S15536
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKIWFQNRMMKKKTA--LDWSWLQTE 28
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Db 187 ERQIKIWFQNRMMKKKESKLLSASQLSAE 216

RESULT 12

A13124
homeotic protein Hox 2.2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C:Accession: A31324
R:Schughart, K.; Utset, M.P.; Awgulewitsch, A.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
A:Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
A:Reference number: A31324; MUID:88289762; PMID:2899893
A:Accession: A31324
A:Molecule type: mRNA
A:Residues: 1-224 <SCH>
A:Cross-references: GB:J03782; NID:gl93929; PID:AAA37843.1; PID:G387203
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:147-203/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 224;

Best Local Similarity 66.7%; Pred. No. 1.1e-05; DB 2; Gaps 1;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKIWFQNRMMKKKTA--LDWSWLQTE 28
:|||||
Db 187 ERQIKIWFQNRMMKKKESKLLSASQLSAE 216

RESULT 13

S57235
antennapedia protein (clone p1105) - fruit fly (Drosophila pseudoobscura) (fragment)
C:Species: Drosophila pseudoobscura
C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999
C:Accession: S57235
R:Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.
Genetics 133, 319-330, 1993
A:Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.
A:Reference number: S57224
A:Accession: S57235
A:Molecule type: DNA
A:Residues: 1-33 <RAN>
A:Cross-references: EMBL:X77711
C:Genetics:
A:Gene: FlyBase:Antp
A:Cross-references: FlyBase:FBgn0012693
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 58.0%; Score 94; DB 2; Length 33;

Best Local Similarity 94.1%; Pred. No. 2e-06; DB 2; Gaps 0;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMMKKK 17
:|||||
Db 6 ERQIKIWFQNRMMKKK 22

RESULT 14

I65241
homeotic protein Hox-A - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
C:Accession: I65241
R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
Biochem. Genet. 32, 351-360, 1994
A:Title: Cloning of rat homeobox genes.

A:Reference number: I52340; MUID:95217128; PMID:7702549
A:Accession: I65241
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-42 <RES>
A:Cross-references: GB:S76290; NID:g913077
C:Genetics:
A:Gene: Hox-A; Hox-1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 58.0%; Score 94; DB 2; Length 42;

Best Local Similarity 94.1%; Pred. No. 2.6e-06; DB 2; Gaps 0;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMMKKK 17
:|||||
Db 24 ERQIKIWFQNRMMKKK 40

RESULT 15

PC1216
homeotic protein Dctbx1 - planarian (Dugesia tigrina) (fragment)
C:Species: Dugesia tigrina
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
C:Accession: PC1216
R:Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich, G.
Gene 121, 337-342, 1992
A:Title: Homeoboxes in flatworms.
A:Reference number: JC1386; MUID:93077050; PMID:1359988
A:Accession: PC1216
A:Molecule type: DNA
A:Residues: 1-45 <OLI>
A:Cross-references: EMBL:X66822
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-45/Domain: homeobox homology (fragment) <HOX>

Query Match 58.0%; Score 94; DB 2; Length 45;

Best Local Similarity 94.1%; Pred. No. 2.8e-06; DB 2; Gaps 0;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMMKKK 17
:|||||
Db 29 ERQIKIWFQNRMMKKK 45

Search completed: February 18, 2004, 14:38:53

Job time : 31.7632 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 77.9211 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWFQNRMMKKTALDWSLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	162	100.0	28	11	US-09-847-946A-18
3	134	82.7	28	10	US-09-847-940B-19
4	134	82.7	28	11	US-09-847-946A-19
5	105	64.8	18	11	US-09-847-946A-131
6	101	62.3	36	9	US-09-731-023A-12
7	101	62.3	36	12	US-10-358-365-12
8	98	60.5	17	15	US-10-229-915-1
9	97	59.9	34	15	US-10-161-499-79
10	96	59.3	26	15	US-10-097-175-101
11	95	58.6	21	8	US-08-610-220A-11
12	95	58.6	21	9	US-09-150-623-11
13	94	58.0	30	15	US-10-188-947-11
14	94	58.0	64	15	US-10-118-079-44
15	94	58.0	217	15	US-10-097-340-129

16	94	58.0	233	12	US-10-420-940-4	Sequence 4, Appli
17	94	58.0	269	12	US-10-116-275-190	Sequence 190, App
18	94	58.0	295	15	US-10-118-079-4	Sequence 4, Appli
19	93.5	57.7	36	9	US-09-731-023A-11	Sequence 11, Appl
20	93.5	57.7	36	12	US-10-358-365-11	Sequence 11, Appl
21	93	57.4	22	12	US-10-369-226-50	Sequence 50, Appl
22	93	57.4	28	9	US-09-214-371-9	Sequence 9, Appli
23	93	57.4	115	9	US-09-925-299-1169	Sequence 1169, Ap
24	93	57.4	115	11	US-09-925-299-1169	Sequence 1169, Ap
25	92	56.8	16	8	US-08-610-220A-9	Sequence 9, Appli
26	92	56.8	16	9	US-09-214-371-43	Sequence 43, Appl
27	92	56.8	16	9	US-09-780-070-38	Sequence 38, Appl
28	92	56.8	16	9	US-09-150-623-9	Sequence 9, Appli
29	92	56.8	16	9	US-09-731-023A-10	Sequence 10, Appl
30	92	56.8	16	9	US-09-854-204-1	Sequence 1, Appli
31	92	56.8	16	10	US-09-900-147-8	Sequence 8, Appli
32	92	56.8	16	10	US-09-792-480-29	Sequence 29, Appl
33	92	56.8	16	10	US-09-785-802A-2	Sequence 2, Appli
34	92	56.8	16	10	US-09-785-802A-5	Sequence 5, Appli
35	92	56.8	16	10	US-09-902-432-32	Sequence 32, Appl
36	92	56.8	16	10	US-09-953-031A-10	Sequence 10, Appl
37	92	56.8	16	10	US-09-981-286A-3	Sequence 3, Appli
38	92	56.8	16	11	US-09-962-967A-6	Sequence 6, Appli
39	92	56.8	16	11	US-09-912-414-6	Sequence 6, Appli
40	92	56.8	16	11	US-09-775-052-54	Sequence 54, Appl
41	92	56.8	16	11	US-09-295-189-4	Sequence 4, Appli
42	92	56.8	16	11	US-09-965-876A-1	Sequence 1, Appli
43	92	56.8	16	12	US-10-017-672-11	Sequence 11, Appl
44	92	56.8	16	12	US-10-201-389A-14	Sequence 14, Appl
45	92	56.8	16	12	US-10-161-051-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-18

Query Match 100.0%; Score 162; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. NO. 3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKWFQNRMMKKTALDWSLQTE 28
Db 1 DRQIKWFQNRMMKKTALDWSLQTE 28

RESULT 2
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

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; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18

Query Match      100.0%; Score 162; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKWFOQRNRMKWKKTALDWSWLQTE 28
Db 1 DROIKWFOQRNRMKWKKTALDWSWLQTE 28

RESULT 3
US-09-847-940B-19
; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides.
US-09-847-940B-19

Query Match      82.7%; Score 134; DB 10; Length 28;
Best Local Similarity 92.9%; Pred. No. 8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 DROIKWFOQRNRMKWKKTALDASALQTE 28

RESULT 4
US-09-847-946A-19
; Sequence 19, Application US/09847946A
; Patent No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

Query Match      82.7%; Score 134; DB 11; Length 28;
Best Local Similarity 92.9%; Pred. No. 8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 DROIKWFOQRNRMKWKKTALDASALQTE 28

RESULT 5
US-09-847-946A-131
; Sequence 131, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-131

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Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RRMKWKKTALDWSWLQTE 28
Db 1 RRMKWKKTALDWSWLQTE 18

RESULT 6
US-09-731-023A-12
; Sequence 12, Application US/09731023A
; Patent No. US20020077283A1
; GENERAL INFORMATION:
; APPLICANT: Sessa, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
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Query Match      60.5%; Score 98; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels
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Query Match 60.5%; Score 98; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels

Qy 1 DRQIKIWFFQNRMRMKWK 17
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Db 1 DRQIKIWFFQNRMRMKWK 17
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RESULT 9
US-10-161-499-79
; Sequence 79, Application US/10161499
; Publication No. US2003004427A1
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/10/161,499
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/347,504
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-499-79

Query Match 59.9%; Score 97; DB 15; Length 34;
Best Local Similarity 64.3%; Pred. NO. 3.3e-05;
Matches 18; Conservative 3; Mismatches 5; Indels

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RESULT 10
US-10-097-175-101
Sequence 101, Application US/10097175
Publication No. US20030045680A1
GENERAL INFORMATION:
APPLICANT: JOVAL, JOHN L.
APPLICANT: MUELLER, JOHN
APPLICANT: OZA, VIBHA B.
APPLICANT: FINDEIS, MARK A.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
FILE REFERENCE: PPI-110
CURRENT APPLICATION NUMBER: US/10/097,175
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,240
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/352,399
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101

Query Match          59.3%; Score 96; DB 15; Length 26;
Best Local Similarity 77.3%; Pred. No. 3.4e-05;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRRMKWKKTALDWS 23
Db 1 RQIKWIFQNRRMKWKKLTIES 22

RESULT 11
US-08-610-220A-11
; Sequence 11, Application US/08610220A
; Publication No. US20030099638A1
; GENERAL INFORMATION:
; APPLICANT: TROY, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-610-220A-11

Query Match          58.6%; Score 95; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 3.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRRMKWKKTA 19
Db 1 RQIKWIFQNRRMKWKQA 18

RESULT 12
US-09-150-623-11
; Sequence 11, Application US/09150623
; Patent No. US20020044931A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09150,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/610,220
; FILING DATE: MAR-04-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-150-623-11

Query Match          58.6%; Score 95; DB 9; Length 21;
Best Local Similarity 94.4%; Pred. No. 3.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRRMKWKKTA 19
Db 1 RQIKWIFQNRRMKWKQA 18

RESULT 13
US-10-188-947-11
; Sequence 11, Application US/10188947
; Publication No. US20030023993A1
; GENERAL INFORMATION:
; APPLICANT: MEDHITOV, Ruslan
; APPLICANT: HOENG, Tiffany
; APPLICANT: BARTON, Gregory
; TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
; FILE REFERENCE: 044574-5101US
; CURRENT APPLICATION NUMBER: US/10/188,947
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/289,738
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,815
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,866
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TIRAP/Antennapedia fusion protein
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: TIRAP/Antennapedia fusion protein
US-10-188-947-11
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Query Match 58.0%; Score 94; DB 15; Length 30;
Best Local Similarity 89.5%; Pred. NO. 6.8e-05;
Matches 17; Conservative 0; Mismatches 2; Indels

Qy 2 RQIKWIFQNRRMKWKKTAL 20
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Db 1 RQIKWIFQNRRMKWKKLQL 19

RESULT 14

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US-10-118-079-44
; Sequence 44, Application US/10118079
; Publication No. US20030103957A1
; GENERAL INFORMATION:
; APPLICANT: MCKERRACHER, LISA
; TITLE OF INVENTION: FUSION PROTEINS
; FILE REFERENCE: 06746-004-US-03
; CURRENT APPLICATION NUMBER: US/10/118,079
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: CA 2,367,636
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: CA 2,362,004
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: CA 2,342,970
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence
US-10-118-079-44

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Query Match 58.0%; Score 94; DB 15; Length 64;
Best Local Similarity 94.1%; Pred. No. 0.00013;
Matches 16; Conservative 1; Mismatches 0; Indels

Qy 1 DRQIKIWQNRMRMKWK 17
:|||||
Db 46 ERQIKIWQNRMRMKWK 62

RESULT 15

RES001 13
US-10-097-340-129
; Sequence 129, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 106.289 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-18
Perfect score: 162
Sequence: 1 DRQIKWFQNRKMKKTKTALDWSLQTE 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1992.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Result No.	Query Match	Length	DB ID	Description
1	162	100.0	28	23 AAB08740 IKKbeta NEMO bindi
2	162	100.0	28	23 AAM48523 NBD peptide SEQ ID
3	162	100.0	28	24 ABU08434 Wild-type human NE
4	134	82.7	28	23 ABB08741 Mutated IKKbeta NE
5	134	82.7	28	23 AAM48524 NBD peptide SEQ ID
6	134	82.7	28	24 ABU08435 Human mutant NEMO
7	105	64.8	18	23 AAM48628 Anti-inflammatory
8	105	64.8	18	23 AAM48629 Anti-inflammatory
9	101	62.3	36	23 AAU79345 Antennapedia-caveo

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

ABB08740

ID ABB08740 standard; peptide; 28 AA.

AC ABB08740;

XX

DT 14-JUN-2002 (first entry)

XX

DE IKKbeta NEMO binding domain peptide SEQ ID NO 18.

XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

KW autoimmune disease; transplant rejection; osteoporosis; cancer;

KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;

KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;

KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;

KW osteopathic; cytosolic; neutropenic; antineoplastic; anti-HIV; human;

KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;

KW dermatological; antibacterial; antipsoriatic; antitumor; antitubercular;

KW antiarthritic; osteopathic; antiulcer.

OS Homo sapiens.

XX

PN WO200183547-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US40654.

XX

PR 02-MAY-2000; 2000US-201261P.

XX

PR 22-AUG-2000; 2000US-0643260.

XX

PA (UYVA) UNIV YALE.
 XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 DR
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Claim 23; Fig 5; 82pp; English.
 PS
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.
 XX
 XX Sequence 28 AA;
 SQ
 Query Match 100.0%; Score 162; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DROIKIWFQNRMRKWKKTALDWSLQTE 28
 |||||
 DB 1 DROIKIWFQNRMRKWKKTALDWSLQTE 28
 |||||
 RESULT 2
 AAM48523
 ID AAM48523 standard; Peptide; 28 AA.
 XX
 AC AAM48523;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD peptide SEQ ID NO 18.
 DE
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 PS Example 5; Fig 5; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48643), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 28 AA;
 SQ
 Query Match 100.0%; Score 162; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DROIKIWFQNRMRKWKKTALDWSLQTE 28
 |||||
 DB 1 DROIKIWFQNRMRKWKKTALDWSLQTE 28
 |||||
 RESULT 3
 ABU08434
 ID ABU08434 standard; peptide; 28 AA.
 XX
 AC ABU08434;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 XX

DE Wild-type human NEMO binding site (NBD) peptide.
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 XX vasotropic; antirheumatic; antiarthritic.
 OS Homo sapiens.
 XX US2002156000-A1.
 XX 24-OCT-2002.
 XX
 XX 02-MAY-2001; 2001US-0847940.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (WAYM/) MAY M J.
 XX (GHOSH/) GHOSH S.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2003-209142/20.
 XX
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 XX domain, useful for modulating NF-kappaB induction in a cell and for
 XX treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 XX psoriasis, vasculitis -
 XX
 XX Claim 35; Page 22; 47pp; English.
 XX
 XX The present invention relates to antiinflammatory compounds comprising
 XX NEMO binding domain (NBD) peptides. The NEMO binding domains are
 XX found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 XX (IKKalpha) proteins. The antiinflammatory compounds of the invention
 XX are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 XX in a cell, where the compounds are capable of blocking the interaction
 XX between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 XX antiinflammatory compound further comprises at least one membrane
 XX translocation domain. The compounds are useful for treating
 XX inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 XX Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 XX telangiectasia, and for transplantation detection. The compounds of
 XX the invention block NF-kappaB induction by IKK but do not inhibit
 XX the basal activity of NF-kappaB. The present sequence represents
 XX an antiinflammatory compound of the invention.
 XX
 XX Sequence 28 AA;
 XX
 XX Query Match 100.0%; Score 162; DB 24; Length 28;
 XX Best Local Similarity 100.0%; Pred. No. 7.9e-15;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 DRQIKWFQNRKMKKTKALDWSWLQTE 28
 XX |||||||
 XX Db 1 DRQIKWFQNRKMKKTKALDWSWLQTE 28
 XX |||||||
 XX
 XX RESULT 4
 XX ABB08741
 XX ID ABB08741 standard; peptide; 28 AA.
 XX
 XX AC ABB08741;
 XX
 XX DT 14-JUN-2002 (first entry)
 XX
 XX DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.
 XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nontropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipruritic; antirheumatic;
 XX antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 22 /note= "Wildtype Trp substituted by Ala"
 XX Misc-difference 24 /note= "Wildtype Trp substituted by Ala"
 XX
 XX WO200183547-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 XX inflammatory disorders, osteoporosis and cancer, comprises contacting a
 XX cell with an anti-inflammatory compound comprising at least one NEMO
 XX binding domain -
 XX
 XX Claim 23; Fig 5; 82pp; English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 XX comprises contacting a cell with an anti-inflammatory compound
 XX (ABB08725-ABB08742) comprising at least one NEMO binding domain
 XX (ABB77313). The compound has acts through selective inhibition of
 XX cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 XX with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 XX interaction results in inhibition of IKKbeta kinase activation and
 XX subsequent decreased phosphorylation of IkappaB. The compound may also
 XX act (directly or indirectly) by blocking the recruitment of leukocytes
 XX into sites of acute and chronic inflammation, by down-regulating the
 XX expression of E-selectin on leukocytes or by blocking NF-kB mediated
 XX differentiation. The compound is useful in treating NF-kB mediated
 XX conditions, where the condition is an inflammatory disorder, an
 XX autoimmune disease, transplant rejection, osteoporosis, cancer,
 XX Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 XX telangiectasia. The inflammatory disorder is asthma, allergies,
 XX urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 XX rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 XX bowel disease, chronic obstructive pulmonary disease, vasculitis and
 XX bursitis. The inflammatory disorder may also be dermatitis, eczema,
 XX psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 XX spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 XX polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 XX cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 XX caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 XX diseases include HIV and influenza. The compound may also be useful for
 XX treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 XX sunburn or aging. The compound may be used to replace corticosteroids in
 XX any application in which corticosteroids are used, including
 XX immunosuppression in transplants and cancer therapy. Also for identifying
 XX antiinflammatory compounds and for diagnosis of an inflammatory disorder.

CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.

XX
 SQ Sequence 28 AA;
 Query Match 82.7%; Score 134; DB 23; Length 28;
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DRQIKIWFQNRMRMKWKKTALDWSWLQTE 28
 |||||
 Db 1 DRQIKIWFQNRMRMKWKKTALDASALQTE 28
 |||||

RESULT 5
 AAM48524
 ID AAM48524 standard; Peptide; 28 AA.

XX AAM48524;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD peptide SEQ ID NO 19.
 DE
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropenic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 XX WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX Example 5; Fig 5; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutropenic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 28 AA;

Query Match 82.7%; Score 134; DB 23; Length 28;
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DRQIKIWFQNRMRMKWKKTALDWSWLQTE 28
 |||||
 Db 1 DRQIKIWFQNRMRMKWKKTALDASALQTE 28
 |||||

RESULT 6
 ABU08435
 ID ABU08435 standard; peptide; 28 AA.

XX AC ABU08435;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human mutant NEMO binding site (NBD) peptide.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neutropenic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX
 PD 24-OCT-2002.

XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.
 XX (GHOS/) GHOSH S.

XX May MJ, Ghosh S;
 XX
 DR WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 CC Claim 22; Fig 5A; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The

CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. The present sequence represents
 CC a human mutant NBD peptide.

XX SQ Sequence 28 AA;
 Query Match 82.7%; Score 134; DB 24; Length 28;
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMKWKKKTALDWSWLQTE 28
 DB 1 DRQIKWIFQNRMKWKKKTALDASALQTE 28

RESULT 7
 AAM48628
 ID AAM48628 standard; Peptide; 18 AA.
 XX AAM48628;
 AC
 XX
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 131.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 12; Page 62; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytosclastic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 18 AA;
 Query Match 64.8%; Score 105; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RRMKWKKTALDWSWLQTE 28
 DB 1 RRMKWKKTALDWSWLQTE 18

RESULT 8
 AAM48629
 ID AAM48629 standard; Peptide; 18 AA.
 XX AAM48629;
 AC
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 132.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 12; Page 63; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

(AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, neotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia teangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.

XX Sequence 18 AA;
SQ

Query Match 64.8%; Score 105; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 RRMKWKKTALDWSWLOTE 28
|||||
DB 1 RRMKWKKTALDWSWLOTE 18

RESULT 9
AAU79345
ID AAU79345 standard; Peptide; 36 AA.
XX
AC AAU79345;
XX
DT 02-JUL-2002 (first entry)
XX
DE Antennapedia-caveolin-X fusion peptide.

XX Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;
KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;
KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;
KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;
KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;
KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;
KW spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav;
KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
KW human; fruit fly; antennapedia internalisation signal.

XX Drosophila melanogaster.
OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT Misc-difference 1..16
FT /label= Antennapedia internalisation signal
FT /note= "Specifically claimed in claim 9"
FT
FT Misc-difference 17..32
FT /label= Cav-X
FT /note= "Control peptide based on a human caveolin-1
FT scaffolding domain shown in AAU79340 residues
FT 82-101"
XX
XX WO200220768-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US42069.
XX
XX 08-SEP-2000; 2000US-231327P.

PR 07-DEC-2000; 2000US-0731023.
XX
XX (UYVA) UNIV YALE.
XX
XX Sessa WC;
XX
XX WPI; 2002-329877/36.
XX
XX New peptide having caveolin scaffolding domain, useful for modulating
PT activity of endothelial nitric oxide synthase and inhibiting
PT inflammation and tumour cell angiogenesis proliferation -
XX
XX Claim 16; Page 72; 73pp; English.
XX
XX The invention describes an isolated caveolin scaffolding domain peptide
CC (I). A fusion peptide (II) containing (I) and at least a membrane
CC translocation sequence is useful for down regulating endothelial nitric
CC oxide synthase (eNOS) activity in a cell, resulting in blockage of
CC vasodilation. (II) is therefore useful for inhibiting inflammation and
CC tumour cell angiogenesis/proliferation in an animal; and for blocking the
CC interaction of caveolin with a protein in vivo. (II) may be useful in
CC treatment of inflammatory conditions such as osteoporosis, rheumatoid
CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)
CC are also useful for treating pathological processes associated with a
CC pro-inflammatory response including allergies such as allergic rhinitis,
CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous
CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,
CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,
CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and
CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing
CC corticosteroids useful for immunosuppression in transplant and cancer
CC patients. When administered along with one or more antiinflammatory
CC agent (I) and (II) are useful for inhibiting tumour growth or malignant
CC neoplasm including cellular angiogenesis, proliferation, invasiveness,
CC and metastasis in biological systems. This sequence represents a fusion
CC peptide of the invention created from the fruit fly antennapedia
CC internalisation signal and control sequence Cav-X, based on the human
CC caveolin-1 scaffolding domain shown in AAU79340, residues 82-101.
XX
XX Sequence 36 AA;
SQ

Query Match 62.3%; Score 101; DB 23; Length 36;
Best Local Similarity 69.2%; Pred. No. 1.4e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRMKWKKTALDWSWLO 27
|||||
DB 1 ROIKIWFQNRMRMKWKKTALDWSWLO 26

RESULT 10
AAB80924
ID AAB80924 standard; Protein; 41 AA.
XX
XX AAB80924;
XX
XX 04-JUN-2001 (first entry)
XX
XX Mixer SIM peptide.
XX
XX Smad; Cytostatic; vulnery; cerebroprotective; immunosuppressive;
KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
KW Smad Interaction Motif; tissue repair; fibrotic condition;
KW immunosuppression; diabetic nephropathy; tumour.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FT Modified-site 1
FT /note= "Biotin.Aminohexanoic acid-R"
XX
XX WO200114413-A2.

PD 01-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-GB03265.
 XX
 PR 25-AUG-1999; 99GB-0020000.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX Germain SE, Hill CS, Howell MT;
 XX WPI; 2001-265836/27.
 DR
 XX Polypeptide capable of interacting with a Smad polypeptide, useful in
 PT the treatment of cancer and for tissue remodelling or healing of a
 PT wound, injury or surgery, comprises a Smad Interaction Motif and is
 PT less than 32 amino acids in length -
 XX
 XS Claim 16; Page 140; 179pp; English.
 XX
 XX The present invention relates to peptides capable of interacting with a
 CC Smad protein, comprising a Smad Interaction Motif (SIM; amino acid
 CC sequence PP(T/N)K). The present sequence is one such Smad interacting
 CC peptide. Smad proteins are a family of highly conserved, intracellular
 CC proteins that signal cellular responses downstream of Transforming Growth
 CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
 CC is thought to be necessary for interaction with the MH2 domain of Smad2.
 CC The peptides of the present invention are useful in the manufacture of a
 CC medicament for the treatment of a patient in need of modulation of a
 CC activin or TGF-beta signalling; cancer; a patient in need of reducing
 CC extracellular matrix deposition, encouraging tissue repair and/or
 CC regeneration, tissue remodelling or healing of a wound, injury or
 CC surgery, or reducing scar tissue formation arising from injury to the
 CC brain; a patient with or at risk of end-stage organ failure, pathologic
 CC extracellular matrix accumulation, a fibrotic condition, disease states
 CC associated with immunosuppression (such as different forms of malignancy,
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
 CC growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy
 CC or non-inflammatory renal disease) or renal fibrosis.
 XX
 SQ Sequence 41 AA;
 Query Match 61.7%; Score 100; DB 22; Length 41;
 Best Local Similarity 77.3%; Pred. No. 2.2e-06;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RQIKWIFQNRRMKWKKTALDWS 23
 DB 1 RQIKWIFQNRRMKWKKLMDFN 22
 RESULT 11
 AAB80925
 ID AAB80925 standard; Protein; 41 AA.
 AC AAB80925;
 XX
 XX 04-JUN-2001 (first entry)
 DT Mixer SIM mutant peptide.
 DE
 XX Smad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;
 KW Smad Interaction Motif; tissue repair; fibrotic condition;
 KW immunosuppression; diabetic nephropathy; tumour; mutein.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 PH Modified-site 1
 FT /note= "Biotin.Aminohexanoic acid-R"
 FT Misc-difference 25
 FT /note= "Wild-type Pro replaced by Ala. Wild-type sequence
 FT given in AAB80924."
 FT

FT Misc-difference 26
 FT /note= "Wild-type Pro replaced by Ala"
 XX
 PN WO200114413-A2.
 XX
 PD 01-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-GB03265.
 XX
 PR 25-AUG-1999; 99GB-0020000.
 XX
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 PA Germain SE, Hill CS, Howell MT;
 XX WPI; 2001-265836/27.
 DR
 XX Polypeptide capable of interacting with a Smad polypeptide, useful in
 PT the treatment of cancer and for tissue remodelling or healing of a
 PT wound, injury or surgery, comprises a Smad Interaction Motif and is
 PT less than 32 amino acids in length -
 XX
 XS Example 2; Page 123; 179pp; English.
 XX
 XX The present invention relates to peptides capable of interacting with a
 CC Smad protein, comprising a Smad Interaction Motif (SIM; amino acid
 CC sequence PP(T/N)K). The present sequence is one such Smad interacting
 CC peptide. Smad proteins are a family of highly conserved, intracellular
 CC proteins that signal cellular responses downstream of Transforming Growth
 CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM
 CC is thought to be necessary for interaction with the MH2 domain of Smad2.
 CC The peptides of the present invention are useful in the manufacture of a
 CC medicament for the treatment of a patient in need of modulation of a
 CC activin or TGF-beta signalling; cancer; a patient in need of reducing
 CC extracellular matrix deposition, encouraging tissue repair and/or
 CC regeneration, tissue remodelling or healing of a wound, injury or
 CC surgery, or reducing scar tissue formation arising from injury to the
 CC brain; a patient with or at risk of end-stage organ failure, pathologic
 CC extracellular matrix accumulation, a fibrotic condition, disease states
 CC associated with immunosuppression (such as different forms of malignancy,
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour
 CC growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy
 CC or non-inflammatory renal disease) or renal fibrosis.
 XX
 SQ Sequence 41 AA;
 Query Match 61.7%; Score 100; DB 22; Length 41;
 Best Local Similarity 77.3%; Pred. No. 2.2e-06;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RQIKWIFQNRRMKWKKTALDWS 23
 DB 1 RQIKWIFQNRRMKWKKLMDFN 22
 RESULT 12
 AAB13423
 ID AAB13423 standard; peptide; 20 AA.
 AC AAB13423;
 XX
 XX 23-NOV-2000 (first entry)
 DT Synthetic alpha smooth muscle actin inhibitor # 3.
 DE
 XX Alpha smooth muscle actin; alpha-SM; wound contraction;
 KW hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;
 KW lung fibrosis.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 PH Modified-site 1
 FT

/note= "N-terminal acetyl"

FT XX WO200038733-A1.
 PN XX
 XX XX
 PD XX 06-JUL-2000.
 XX XX
 PF XX 15-DEC-1999; 99WO-EP09964.
 XX XX
 PR XX 24-DEC-1998; 98EP-0204396.
 XX XX
 PA (UNIO) UCB-BIOPRODUCTS SA.
 XX XX
 PI Gabbiani G, Scarso A;
 DR WPI; 2000-452308/39.
 XX XX
 XX A peptidic product for prevention and treatment of a disease related to
 PT alpha-SM actin expression comprises a tetrapeptide associated with a
 PT chemical entity that is able to introduce the tetrapeptide into the
 PT cell -
 XX
 PS Claim 7; Page 23; 31pp; English.
 XX
 CC The present invention relates to novel peptides comprising of a specific
 CC tetrapeptide associated with an oligopeptide which allows the
 CC introduction of the tetrapeptide into the target cell. The present
 CC sequence is one such peptide. Residues 1 to 4 of the present sequence
 CC correspond to the specific tetrapeptide, while residues 5 to 20
 CC correspond to the oligopeptide. The specific tetrapeptide of the present
 CC sequence interferes with alpha smooth muscle (alpha-SM) actin
 CC organisation in stress fibers. The present sequence may be used in the
 CC prevention and/or treatment of a disease related to alpha-SM actin
 CC expression, e.g. wound contraction, hypertrophic scars, fibromatosis and
 CC fibrotic conditions. The present sequence may also be used to treat
 CC Dupuytren disease and lung fibrosis.
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 60.5%; Score 98; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRMRMKWK 17
 Db 4 DRQIKIWFQNRMRMKWK 20
 XX
 RESULT 13
 AAW11630
 ID AAW11630 standard; peptide; 26 AA.
 XX
 AC AAW11630;
 XX
 DT 16-OCT-1997 (first entry)
 XX
 DE Anti-apoptotic protein blocking peptide FP2.
 XX
 XX Cell permeable; apoptosis; blocking; inhibition; tumour growth;
 KW ex vivo purging; in vivo administration; Bcl-2.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= sig_peptide
 XX
 XX DE19526174-A1.
 XX
 XX 23-JAN-1997.
 XX
 XX 18-JUL-1995; 95DE-1026174.
 XX
 PR 18-JUL-1995; 95DE-1026174.

XX (BRAC/) BRACH M.
 PA (HERR/) HERMANN F.
 PA (KIEH/) KIEHNTOPF M.
 XX
 PI Brach M, Herrmann F, Kiehnkopf M;
 XX WPI; 1997-088160/09.
 DR
 XX Peptide(s) that block anti-apoptotic proteins - useful for
 PT inhibiting tumour growth
 PT
 XX Claim 6; Page 7; 7pp; German.
 XX
 CC The present sequence is a cell permeable anti-apoptotic protein
 CC blocking peptide, which can be used to inhibit tumour growth, e.g.
 CC by ex vivo purging or (after stabilisation) in vivo
 CC administration. The peptide preferably blocks Bcl-2, and comprises
 CC a signal peptide mediating cell penetration and a functional
 CC sequence corresponding to a Bcl-2 domain.
 XX
 SQ Sequence 26 AA;
 XX
 Query Match 60.5%; Score 98; DB 18; Length 26;
 Best Local Similarity 89.5%; Pred. No. 2.5e-06;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DRQIKIWFQNRMRMKWKTA 19
 Db 1 ERQIKIWFQNRMRMKWKA 19
 XX
 RESULT 14
 AAY79919
 ID AAY79919 standard; Peptide; 34 AA.
 XX
 AC AAY79919;
 XX
 DT 10-MAY-2000 (first entry)
 XX
 DE Human papillomavirus 16 E2 fusion peptide Ant-WP.
 XX
 KW Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
 KW E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
 KW preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
 KW epidermodysplasia verruciformis; anorectal carcinoma.
 XX
 OS Human papillomavirus.
 OS Synthetic.
 XX
 XX WO200001720-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US15144.
 XX
 PR 02-JUL-1998; 98US-0091661.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Howley P, Benson J, Kasukawa H;
 XX
 DR WPI; 2000-171001/15.
 XX
 PT Use of papillomavirus E2 protein peptidomimetics for treating
 PT papillomavirus-infected cells and papillomavirus-induced conditions in
 PT mammals by inhibiting E1-E2 interaction -
 XX
 PS Disclosure; Fig 13; 110pp; English.
 XX
 CC The present invention describes the use of a small organic compound (A)
 CC which competitively inhibits interaction of a papillomavirus (PV) E2
 CC protein with a PV E1 protein for treating a cell infected with PV or a

CC mammal with a PV-induced condition. (A) has antiviral, virucide,
 CC cytosatic, antiproliferative and dermatological activities. Methods
 CC from the present invention can be used to treat PV-induced conditions
 CC including growth of PV preneoplastic and neoplastic lesions, cutaneous
 CC lesions chosen from warts and other benign cutaneous lesions, plantar
 CC warts (verruca plantaris), common warts (verruca plana), Butcher's
 CC common warts, flat warts, genital warts (condyloma acuminatum) and
 CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,
 CC oesophageal and other upper airway papilloma or vaginal, cervical,
 CC vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be
 CC used to treat epithelial and internal fibropapillomas in animals.
 CC The present sequence represents a peptide sequence used in the
 CC exemplification of the present invention.

XX SQ Sequence 34 AA;

Query Match 59.9%; Score 97; DB 21; Length 34;
 Best Local Similarity 64.3%; Pred. No. 4.5e-06;
 Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWIFQNRMRMKWKKTALDWSLQTE 28
 Db 1 ERQIKWIFQNRMRMKWKKG--WKHRL 26

RESULT 15

AAE31836
 ID AAE31836 standard; peptide; 26 AA.

AC AAE31836;

XX 07-MAR-2003 (first entry)

XX Androgen receptor binding peptide #87.

XX Androgen receptor; androgen-associated disorder; prostate cancer; acne;
 KW benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome;
 KW male pattern baldness; Stein-Leventhal syndrome; infertility; cytostatic;
 KW X-linked spinal bulbar muscular atrophy; antiseborrheic; dermatological;
 KW depilatory; androgen receptor binding peptide.

XX Unidentified.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 26 /note= "C-terminal amide"

XX WO200272612-A2.

XX 19-SEP-2002.

XX 12-MAR-2002; 2002WO-US07487.

XX 12-MAR-2001; 2001US-275240P.

XX 28-JAN-2002; 2002US-352399P.

XX (PRAE-) PRAECIS PHARM INC.

XX Joyal JL, Mueller J, Oza VB, Findeis MA;

XX WPI; 2003-067363/06.

XX New peptide modulators of androgen receptor, useful for treating
 FT androgen-associated disorder, e.g. prostate cancer, particularly
 PT hormonally refractive prostate cancer, colon cancer, lung cancer, acne,
 PT or hirsutism

XX Example; Page 30; 68pp; English.

XX The present invention relates to novel peptide modulators of androgen
 CC receptor. The peptides of the invention are useful for treating androgen-

CC associated disorders such as prostate cancer, particularly hormonally
 CC refractive prostate cancer, colon cancer, lung cancer, benign prostatic
 CC hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal
 CC syndrome, androgen insensitivity syndrome, infertility, endometrial
 CC cancer and X-linked spinal bulbar muscular atrophy. The present sequence
 CC is an androgen receptor binding peptide.

XX SQ Sequence 26 AA;

Query Match 59.3%; Score 96; DB 24; Length 26;
 Best Local Similarity 77.3%; Pred. No. 4.6e-06;
 Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRMKWKKTALDWS 23
 Db 1 RQIKWIFQNRMRMKWKKTALDWS 22

Search completed: February 18, 2004, 14:26:27
 Job time : 107.289 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 32.9737 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKIWFQNRMRKWKKTALDMSWLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	59.9	34	4	US-09-347-504-79
2	95	58.6	24	4	US-09-419-826-34
3	94	58.0	27	4	US-09-040-725A-2
4	94	58.0	61	2	US-08-202-044-3
5	94	58.0	61	3	US-08-751-344B-3
6	94	58.0	61	3	US-08-751-344B-6
7	94	58.0	61	3	US-08-751-344B-9
8	93	57.4	22	4	US-09-057-363C-50
9	93	57.4	27	3	US-09-051-934-51
10	93	57.4	27	3	US-09-051-934-52
11	93	57.4	61	3	US-08-751-344B-7
12	92	56.8	16	2	US-08-928-358-7
13	92	56.8	16	2	US-08-810-540-3
14	92	56.8	16	2	US-08-810-540-6
15	92	56.8	16	2	US-09-072-429-7
16	92	56.8	16	3	US-08-964-302A-6
17	92	56.8	16	3	US-09-116-294-4
18	92	56.8	16	3	US-09-964-614A-4
19	92	56.8	16	3	US-08-849-486-1
20	92	56.8	16	3	US-08-849-486-4
21	92	56.8	16	3	US-09-208-966-54
22	92	56.8	16	3	US-09-308-935-8
23	92	56.8	16	3	US-09-441-416A-6
24	92	56.8	16	4	US-09-296-089-33
25	92	56.8	16	4	US-09-419-826-35
26	92	56.8	16	4	US-09-302-305C-10
27	92	56.8	16	4	US-09-346-847-1

28	92	56.8	16	4	US-09-346-847-25	Sequence 25, Appl
29	92	56.8	16	4	US-09-057-363C-47	Sequence 47, Appl
30	92	56.8	16	4	US-09-043-560B-3	Sequence 3, Appl
31	92	56.8	17	4	US-09-346-847-17	Sequence 17, Appl
32	92	56.8	17	4	US-09-346-847-20	Sequence 20, Appl
33	92	56.8	17	4	US-09-346-847-22	Sequence 22, Appl
34	92	56.8	17	4	US-09-346-847-27	Sequence 27, Appl
35	92	56.8	18	3	US-08-838-545-20	Sequence 20, Appl
36	92	56.8	18	3	US-09-349-532-20	Sequence 20, Appl
37	92	56.8	19	4	US-09-346-847-23	Sequence 23, Appl
38	92	56.8	19	4	US-09-658-517C-7	Sequence 7, Appl
39	92	56.8	20	4	US-09-466-772-3	Sequence 3, Appl
40	92	56.8	20	4	US-09-346-847-16	Sequence 16, Appl
41	92	56.8	20	4	US-09-346-847-18	Sequence 18, Appl
42	92	56.8	20	4	US-09-346-847-30	Sequence 30, Appl
43	92	56.8	20	4	US-09-658-517C-8	Sequence 8, Appl
44	92	56.8	22	4	US-09-346-847-28	Sequence 28, Appl
45	89	54.9	42	3	US-08-751-344B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-347-504-79
; Sequence 79, Application US/09347504
; Patent No. 639075
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-504-79

Query Match 59.9%; Score 97; DB 4; Length 34;
Best Local Similarity 64.3%; Pred. No. 1.9e-06;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKIWFQNRMRKWKKTALDMSWLQTE 28
:|||||:|||||:|:|
DB 1 ERQIKIWFQNRMRKWKKG--WKHMRLE 26
:

RESULT 2
US-09-419-826-34
; Sequence 34, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTIESTROGEN COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR TREATING BREAST CANCER
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998

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; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: /note= "X = Phosphotyrosine"
US-09-419-826-34

Query Match 58.6%; Score 95; DB 4; Length 24;
Best Local Similarity 85.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRRMKWKKTALD 21
DB 1 RQIKWIFQNRRMKWKKPLXD 20

RESULT 3
US-09-040-725A-2
; Sequence 2, Application US/09040725A
; Patent No. 6399584
; GENERAL INFORMATION:
; APPLICANT: Institut Curie
; APPLICANT: CNRS
; APPLICANT: Arpin, Monique
; APPLICANT: Crepaldi, Tiziana
; APPLICANT: Gautreau, Alexis
; APPLICANT: Louvard, Daniel
; TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated
; TITLE OF INVENTION: on tyrosine 353
; FILE REFERENCE: 391082000100
; CURRENT APPLICATION NUMBER: US/09/040,725A
; CURRENT FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (22)
; OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2

Query Match 58.0%; Score 94; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRRMKWKKTAL 20
DB 1 RQIKWIFQNRRMKWKKRL 19

RESULT 4
US-08-202-044-3
; Sequence 3, Application US/08202044
; Patent No. 5858973
; GENERAL INFORMATION:
; APPLICANT: Habener M.D., Joel F.
; APPLICANT: Miller Ph.D., Christopher P.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
```

```
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,044
; FILING DATE: 23-FEB-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: MGH-124XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-202-044-3

Query Match 58.0%; Score 94; DB 2; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRRMKWKK 17
DB 43 ERQIKWIFQNRRMKWKK 59

RESULT 5
US-08-751-344B-3
; Sequence 3, Application US/08751344B
; Patent No. 6210960
; GENERAL INFORMATION:
; APPLICANT: Habener M.D., Joel F.
; APPLICANT: Miller Ph.D., Christopher P.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,344B
; FILING DATE: 19-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,044
; FILING DATE: 23-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-3

Query Match 58.0%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRMRMKWK 17
Db 43 ERQIKWFOQRMRMKWK 59

RESULT 6
US-08-751-344B-6
; Sequence 6, Application US/08751344B
; Patent No. 6210960
; GENERAL INFORMATION:
; APPLICANT: Habener M.D., Joel P.
; APPLICANT: Miller Ph.D., Christopher P.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,344B
; FILING DATE: 19-Feb-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,044
; FILING DATE: 23-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-751-344B-6

Query Match 58.0%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRMRMKWK 17

Db 43 ERQIKWFOQRMRMKWK 59

RESULT 7
US-08-751-344B-9
; Sequence 9, Application US/08751344B
; Patent No. 6210960
; GENERAL INFORMATION:
; APPLICANT: Habener M.D., Joel P.
; APPLICANT: Miller Ph.D., Christopher P.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,344B
; FILING DATE: 19-Feb-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,044
; FILING DATE: 23-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-751-344B-9

Query Match 58.0%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRMRMKWK 17
Db 43 ERQIKWFOQRMRMKWK 59

RESULT 8
US-09-057-363C-50
; Sequence 50, Application US/09057363C
; Patent No. 6551994
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
; INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle

STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRAINEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-057-363C-50

Query Match 57.4%; Score 93; DB 4; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKFQNRMRKWK 17
Db 6 NRQIKWFQNRMRKWK 22

RESULT 9
US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
TYPE: PRT
LENGTH: 27
ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match 57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.8%; Pred. No. 4.9e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ROIKWFQNRMRKWK 21
Db 1 ROIKWFQNRMRKWK 20

RESULT 10
US-09-051-934-52

Sequence 52, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
TYPE: PRT
LENGTH: 27
ORGANISM: phosphotyrosine binding domain
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (24)
OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match 57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 4.9e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ROIKWFQNRMRKWK 21
Db 1 ROIKWFQNRMRKWK 20

RESULT 11
US-08-751-344B-7
Sequence 7, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-7

Query Match 57.4%; Score 93; DB 3; Length 61;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKWFQNRMRMKWK 17
Db 43 ERQVKIWFQNRMRMKWK 59

RESULT 12
US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEAVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAPFAR, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQIKWIFQNRMRMKWK 17
Db 1 RQIKWIFQNRMRMKWK 16

RESULT 13
US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: TROY, CAROL M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 56.8%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQIKWIFQNRMRMKWK 17
Db 1 RQIKWIFQNRMRMKWK 16

RESULT 14
US-08-810-540-6
Sequence 6, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: TROY, CAROL M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

US-09-072-429-7

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	6	23	Mutated IKKbeta NE
2	41	100.0	6	23	NBD mutant peptide
3	41	100.0	6	23	Anti-inflammatory
4	41	100.0	6	23	Anti-inflammatory
5	41	100.0	6	23	Human NEMO binding
6	41	100.0	7	23	Anti-inflammatory
7	41	100.0	8	23	Anti-inflammatory
8	41	100.0	8	23	Anti-inflammatory
9	41	100.0	9	23	Anti-inflammatory

10	41	100.0	9	23	AA048613	Anti-inflammatory
11	41	100.0	9	23	AA048616	Anti-inflammatory
12	41	100.0	9	23	AA048617	Anti-inflammatory
13	41	100.0	10	23	AA048612	Anti-inflammatory
14	41	100.0	10	23	AA048615	Anti-inflammatory
15	41	100.0	11	23	AA048609	Anti-inflammatory
16	41	100.0	11	23	AA048610	Anti-inflammatory
17	38	92.7	12	21	AA07057	Human IKKbeta muta
18	38	92.7	243	22	AA056674	Human peptide-mimic
19	37	90.2	20	23	AA090327	Propionibacterium
20	37	90.2	70	22	AA049130	Insulin/insulin-li
21	37	90.2	70	22	AA067482	Human liver peptid
22	37	90.2	70	22	AA067482	Human bone marrow
23	37	90.2	70	22	AA067482	Peptide #1807 enco
24	37	90.2	210	20	AA037095	Human peptide enco
25	37	90.2	354	24	AA037451	Schizosaccharomyce
26	37	90.2	379	22	AA096114	Benzodiazepines bi
27	37	90.2	408	22	AA096440	Putative P. abyssi
28	37	90.2	692	22	AA070451	Putative P. abyssi
29	37	90.2	1291	22	AA071544	Micromonospora eve
30	36	87.8	6	23	AA080725	IKKbeta NEMO bindi
31	36	87.8	6	23	AA08530	IKKbeta NEMO bindi
32	36	87.8	6	23	AA08655	NBD mutant peptide
33	36	87.8	6	24	AA080418	Human NEMO binding
34	36	87.8	7	23	AA08534	Anti-inflammatory
35	36	87.8	8	23	AA08527	Anti-inflammatory
36	36	87.8	8	23	AA08535	Anti-inflammatory
37	36	87.8	9	20	AA096182	IKK-alpha polypept
38	36	87.8	9	23	AA08526	Anti-inflammatory
39	36	87.8	9	23	AA08529	Anti-inflammatory
40	36	87.8	9	23	AA08532	Anti-inflammatory
41	36	87.8	9	23	AA08533	Anti-inflammatory
42	36	87.8	10	23	AA077313	IKKbeta NEMO bindi
43	36	87.8	10	23	AA08528	Anti-inflammatory
44	36	87.8	10	23	AA08531	Anti-inflammatory
45	36	87.8	11	23	AA077311	Human NBD peptide

ALIGNMENTS

RESULT 1

ABB08739

ID ABB08739 standard; peptide; 6 AA.

XX

AC ABB08739;

XX

DT 14-JUN-2002 (first entry)

XX

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 17.

XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX Homo sapiens.
OS Synthetic.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

XX Misc-difference 4

XX /note= "Wildtype Ser substituted by Glu"

XX

XX WO200183547-A2.

XX

XX 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US40654.
 XX
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 PI
 XX
 DR WPI; 2002-179350/23.
 XX
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 1 LDWEWL 6
 RESULT 2
 AAM48522
 ID AAM48522 standard; Peptide; 6 AA.
 XX
 AC AAM48522;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 17.
 DE

XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 XX factor kappaB activation, and for treating asthma, lung inflammation,
 XX psoriasis
 PT
 PT Example 6; Page 48; 88pp; English.
 XX
 PS The invention relates to an antiinflammatory compound (especially
 XX AAM48628-AAM48645), comprising a membrane translocation domain
 CC AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 1 LDWEWL 6
 RESULT 3
 AAM48542
 ID AAM48542 standard; Peptide; 6 AA.

XX AAM48542;
 XX 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 45.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX Claim 6; Page 61; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 CC antibacterial, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 6 AA;
 XX Query Match 100.0%; Score 41; DB 23; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 LDWEWL 6
 XX |||||

Db 1 LDWEWL 6
 RESULT 4
 AAM48614
 ID AAM48614 standard; Peptide; 6 AA.
 XX
 XX AAM48614;
 XX 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 117.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 CC antibacterial, immunosuppressive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 6 AA;

Query Match 100.0%; Score 41; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 Db 1 LDWEWL 6

RESULT 5
 ABU08432
 ID ABU08432 standard; peptide; 6 AA.
 XX
 AC ABU08432;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #15.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antiinflammatory; antiarthritic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX
 PD 24-OCT-2002.
 XX
 XX 02-MAY-2001; 2001US-0847940.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (MAYN/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2003-209142/20.
 DR
 XX
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 XX Claim 22; Page 17; 47pp; English.

PS The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 41; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 Db 1 LDWEWL 6

RESULT 6
 AAM48618
 ID AAM48618 standard; Peptide; 7 AA.
 XX
 AC AAM48618;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 121.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 DR
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.

PS The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
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 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 |||||
 Db 1 LDWEWL 6
 |||||
 RESULT 7
 AAM48611
 ID AAM48611 standard; Peptide; 8 AA.
 XX
 AC AAM48611;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 DE Anti-inflammatory peptide SEQ ID NO 114.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
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 PA (PRAE-) PRAECIS PHARM INC.
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 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
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 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 41; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 |||||
 Db 3 LDWEWL 8
 |||||
 RESULT 8
 AAM48619
 ID AAM48619 standard; Peptide; 8 AA.
 XX
 AC AAM48619;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 DE Anti-inflammatory peptide SEQ ID NO 122.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
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 XX 22-AUG-2000; 2000US-0643260.
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 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 41; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 Db 1 LDWEWL 6

RESULT 9
 AAM48610
 ID AAM48610 standard; Peptide; 9 AA.
 XX
 AC AAM48610;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 113.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
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 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 41; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 Db 1 LDWEWL 6

RESULT 10
 AAM48613
 ID AAM48613 standard; Peptide; 9 AA.
 XX
 AC AAM48613;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 116.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
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 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
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 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 XX
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 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 41; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 1 LDWEWL 6
 RESULT 11
 AAM48616
 ID AAM48616 standard; Peptide; 9 AA.
 XX
 AC AAM48616;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 119.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 PR 22-AUG-2000; 2000US-0643260.
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 PA (UYA) UNIV YALE.
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX
 DR WPI; 2002-121889/16.
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 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 41; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 3 LDWEWL 8
 RESULT 12
 AAM48617
 ID AAM48617 standard; Peptide; 9 AA.
 XX
 AC AAM48617;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 120.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 PR 02-MAY-2000; 2000US-201261P.

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PR 22-AUG-2000; 2000US-0643260.
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XX Sequence 9 AA;
XX Query Match 100.0%; Score 41; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
DB 2 LDWEWL 7
RESULT 13
AAM48612
ID AAM48612 standard; Peptide; 10 AA.
XX AC AAM48612;
XX 20-MAR-2002 (first entry)
XX DE Anti-inflammatory peptide SEQ ID NO 115.
XX AAM48615
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX WO200183554-A2.

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XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14346.
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XX Sequence 10 AA;
XX Query Match 100.0%; Score 41; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 4.4;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
DB 2 LDWEWL 7
RESULT 14
AAM48615
ID AAM48615 standard; Peptide; 10 AA.
XX AC AAM48615;
XX 20-MAR-2002 (first entry)
XX DE Anti-inflammatory peptide SEQ ID NO 118.
XX AAM48615
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
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KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.
XX WO200183554-A2.

```

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX
 XX
 PN W0200183554-A2.
 PD 08-NOV-2001.
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 PF 02-MAY-2001; 2001WO-US14346.
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 PR 02-MAY-2000; 2000US-201261P.
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 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 41; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWEWL 6
 Db 3 LDWEWL 8
 RESULT 15
 AAM48609
 ID AAM48609 standard; Peptide; 11 AA.
 XX
 XX AAM48609;
 XX
 XX
 DT 20-MAR-2002 (first entry)
 XX
 XX Anti-inflammatory peptide SEQ ID NO 112.
 XX
 XX Antiinflammatory; antiasthmatic; cytotatic; antipsoriatic; nontropic;

KW anti-rheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX
 XX W0200183554-A2.
 PN
 XX
 PD 08-NOV-2001.
 XX
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 XX
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 41; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWEWL 6
 Db 3 LDWEWL 8
 Search completed: February 18, 2004, 14:26:26
 Job time : 22.7763 secs

No art

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	173	16 Q8E5U2	Q8E5U2 streptococ
2	40	100.0	173	16 Q8E065	Q8E065 streptococ
3	40	100.0	645	2 Q9X6C6	Q9X6C6 thermus bro
4	38	95.0	396	17 Q96XZ8	Q96XZ8 sulfolobus
5	37	92.5	740	6 Q95KV1	Q95KV1 bos taurus
6	37	92.5	745	11 Q8CBT3	Q8CBT3 mus musculu
7	37	92.5	756	6 Q95KV0	Q95KV0 bos taurus
8	36	90.0	27	12 Q9QRU7	Q9QRU7 hepatitis c
9	36	90.0	27	12 Q9QRU6	Q9QRU6 hepatitis c
10	36	90.0	207	5 Q962U3	Q962U3 trypanosoma
11	36	90.0	215	17 Q9V2Z7	Q9V2Z7 pyrococcus
12	36	90.0	251	16 Q07806	Q07806 mycobacteri
13	36	90.0	304	16 Q91719	Q91719 pseudomonas
14	36	90.0	316	16 Q8UBG8	Q8UBG8 agrobacteri
15	36	90.0	444	2 Q9XBD4	Q9XBD4 amycolatops
16	36	90.0	516	10 Q42701	Q42701 catharanthu

17	36	90.0	524	10 Q42700	Q42700 catharanthu
18	36	90.0	544	10 Q9PEE1	Q9PEE1 oryza sativ
19	36	90.0	1083	13 Q90WQ8	Q90WQ8 oncorhynch
20	36	90.0	1083	13 Q8AXU2	Q8AXU2 oncorhynch
21	36	90.0	1100	13 Q90WQ9	Q90WQ9 oncorhynch
22	36	90.0	1127	13 Q9W615	Q9W615 oryza lat
23	36	90.0	1212	16 Q9HX70	Q9HX70 pseudomonas
24	36	90.0	1575	2 P94904	P94904 lysobacter.
25	35	87.5	162	16 Q53756	Q53756 mycobacteri
26	35	87.5	204	16 Q9KER2	Q9KER2 bacillus ha
27	35	87.5	282	16 Q8D354	Q8D354 wigglewort
28	35	87.5	288	2 Q8VTT4	Q8VTT4 pseudomonas
29	35	87.5	299	16 Q9HZ18	Q9HZ18 pseudomonas
30	35	87.5	308	2 Q8KZS2	Q8KZS2 acetobacter
31	35	87.5	311	16 Q92MU7	Q92MU7 rhizobium m
32	35	87.5	313	2 Q8VUQ6	Q8VUQ6 pseudomonas
33	35	87.5	318	16 Q8ZCS8	Q8ZCS8 yersinia pe
34	35	87.5	329	16 Q8XVB4	Q8XVB4 ralestonia s
35	35	87.5	331	16 Q91427	Q91427 pseudomonas
36	35	87.5	337	16 Q8UB44	Q8UB44 agrobacteri
37	35	87.5	341	16 Q8G3A8	Q8G3A8 brucella su
38	35	87.5	344	16 Q8YEH7	Q8YEH7 brucella me
39	35	87.5	353	16 Q9A7F0	Q9A7F0 caulobacter
40	35	87.5	386	16 Q9ZU27	Q9ZU27 rhizobium m
41	35	87.5	393	16 Q987Z1	Q987Z1 rhizobium l
42	35	87.5	394	10 Q9M0Y4	Q9M0Y4 arabidopsis
43	35	87.5	418	10 Q944N8	Q944N8 arabidopsis
44	35	87.5	418	10 Q9M0Y3	Q9M0Y3 arabidopsis
45	35	87.5	439	2 Q93Q61	Q93Q61 klebsiella

ALIGNMENTS

RESULT 1

Q8E5U2 PRELIMINARY; PRT; 173 AA.
AC Q8E5U2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS0887.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevallier F., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766847; CAD46531.1; -.
DR SAGALIST; gbs0887; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 173 AA; 20135 MW; F5F34044F0224CD1 CRC64;

Query Match 100.0%; Score 40; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LDRAWL 6
125 LDRAWL 130

RESULT 2

Q8E065

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ID Q8E065 PRELIMINARY; PRT; 173 AA.
AC Q8E065;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Acetyltransferase, GNAT family.
GN SAG0870.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masingani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobino E.F., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AS014231; AM99756.1; -;
DR TIGR; SAG0870; -;
KW Transferase; Complete proteome.
SQ SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;

Query Match 100.0%; Score 40; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 125 LDRAWL 130
|||||

RESULT 3
Q9X6C6 PRELIMINARY; PRT; 645 AA.
AC Q9X6C6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-galactosidase.
GN BGAT.
OS Thermus brockianus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=56956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ITI360;
RX MEDLINE=99402735; PubMed=10473401;
RA Fridjansson O., Watzlack H., Gehweiler A., Rohrhirsch T., Mattes R.;
RT "Cloning of the gene encoding a novel thermostable alpha-galactosidase
RT from Thermus brockianus ITI360.";
RL Appl. Environ. Microbiol. 65:3955-3963(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ITI360;
RX MEDLINE=20203878; PubMed=10741834;
RA Fridjansson O., Watzlack H., Mattes R.;
RT "The structure of the alpha-galactosidase gene loci in Thermus
RT brockianus ITI360 and Thermus thermophilus TH125.";
RL Extremophiles 4:23-33(2000).
DR EMBL; AF135398; AAD33667.1; -;
DR InterPro; IPR001554; Glyco_hydro_14.
DR InterPro; IPR003476; Glyco_hydro_42.

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```

DR Pfam; PF01373; Glyco_hydro_14; 1.
DR Pfam; PF02449; Glyco_hydro_42; 1.
SQ SEQUENCE 645 AA; 73420 MW; C79A9E1C0020EC40 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 48 LDRAWL 53
|||||

RESULT 4
Q96XZ8 PRELIMINARY; PRT; 396 AA.
AC Q96XZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative anaerobic glycerol-3-phosphate dehydrogenase subunit C.
GN ST2369.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000989; BAB67479.1; -;
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR004017; DUF224.
DR Pfam; PF02754; DUF224; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 396 AA; 45359 MW; 15301A2AF22DDC9F CRC64;

Query Match 95.0%; Score 38; DB 17; Length 396;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 94 MDRAWL 99
|||||

RESULT 5
Q95KV1 PRELIMINARY; PRT; 740 AA.
AC Q95KV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V.T.;
RX Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;

```

RT "Identification and characterisation of the bovine Ikb kinases (IKKs)
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; A414555; CAC93686.1; -.
DR InterPro; IPR000719; Prot Kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot Kinase; 1.
DR SMART; SM00220; S_TKc_1
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BELL1F44D176 CRC64;

Query Match 92.5%; Score 37; DB 6; Length 740;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 733 LDWSWL 738

RESULT 6
Q8CBT3 PRELIMINARY; PRT; 745 AA.
AC Q8CBT3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved helix-loop-helix ubiquitous kinase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK035326; BAC29034.1; -.
SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;

Query Match 92.5%; Score 37; DB 11; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 738 LDWSWL 743

RESULT 7
Q95KV0 PRELIMINARY; PRT; 756 AA.
AC Q95KV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-beta.
GN BIKKBETA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT Identification and characterisation of the bovine Ikb kinases (IKKs)
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; A414555; CAC93687.1; -.
DR InterPro; IPR000719; Prot Kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot Kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176ES CRC64;

Query Match 92.5%; Score 37; DB 6; Length 756;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 737 LDWSWL 742

RESULT 8
Q9QRU7 PRELIMINARY; PRT; 27 AA.
AC Q9QRU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE E2 glycoprotein hypervariable region (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-AS;
RA Yeh C.-T.;
RT "Replication of hepatitis C virus in the ascitic mononuclear cells and
RT development of distinct quasi-species in the ascitic fluid.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF109742; AAD51573.1; -.
FT NON_TER 1 1
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25C84FAB CRC64;

Query Match 90.0%; Score 36; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
Db 12 DWAWL 16

RESULT 9
Q9QRU6 PRELIMINARY; PRT; 27 AA.
AC Q9QRU6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE E2 glycoprotein hypervariable region (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=B-MO;
RA Yeh C.-T.;
RT "Replication of hepatitis C virus in the ascitic mononuclear cells and
RL development of distinct quasi-species in the ascitic fluid.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF109743; AAD51574.1; -
FT NON_TER 1 1
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;

Query Match 90.0%; Score 36; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
DB 12 DWAWL 16

RESULT 10
ID Q962U3 PRELIMINARY; PRT; 207 AA.
AC Q962U3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cathepsin B-like protease (Fragment).
OS Trypanosoma rangeli.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5698;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC 58;
RA Nobrega O.T.; Teixeira A.R.L.; Campbell D.A.; Santana J.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF400046; AAK85411.1; -
DR MEROPS; C01.098; -
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPA1N.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00139; THIOI_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; 1.
KW Hydrolase; Protease; Thiol protease.
FT NON_TER 1 1
FT NON_TER 207 207
SQ SEQUENCE 207 AA; 22968 MW; 7AF0D959D5F81C5B CRC64;

Query Match 90.0%; Score 36; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
DB 71 DWAWL 75

RESULT 11
Q9V227
ID Q9V227 PRELIMINARY; PRT; 215 AA.
AC Q9V227;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Purine phosphoribosyltransferase.
GN GPTA OR PAB2405.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;

RN SEQUENCE FROM N.A.
RP STRAIN=GE5 / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RL structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248283; CAB49171.1; -
DR HSSP; Q26997; 1QK3
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Priboyltran; 1.
KW Glycosyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 215 AA; 24832 MW; A58D71EBED5FD723 CRC64;

Query Match 90.0%; Score 36; DB 17; Length 215;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
DB 141 IDWAWL 146

RESULT 12
O07806
ID O07806 PRELIMINARY; PRT; 251 AA.
AC O07806;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Phosphotransferase (Aminoglycoside 3'-phosphotransferase).
GN RV3817 OR MTCV409.13C OR MT3925.1.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T.; Brosch R.; Parkhill J.; Garnier T.; Churcher C.; Harris D.;
RA Gordon S.V.; Eiglmeier K.; Gas S.; Barry C.E. III; Tekaiia F.;
RA Badcock K.; Basham D.; Brown D.; Chillingworth T.; Connor R.;
RA Davies R.; Devlin K.; Feltwell T.; Gentles S.; Hamlin N.; Holroyd S.;
RA Hornsby T.; Jagels K.; Krogh A.; McLean J.; Moule S.; Murphy L.;
RA Oliver S.; Osborne J.; Quail M.A.; Rajandream M.A.; Rogers J.;
RA Rutter S.; Seeger K.; Skelton S.; Squares S.; Squares R.;
RA Sulston J.E.; Taylor K.; Whitehead S.; Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D.; Alland D.; Eisen J.A.; Carpenter L.; White O.;
RA Peterson J.; DeBoy R.; Dodson R.; Gwinn M.L.; Haft D.; Hickey E.;
RA Kolonay J.F.; Nelson W.C.; Umayam L.A.; Ermolaeva M.D.; Salzberg S.L.;
RA Delcher A.; Utterback T.; Weidman J.; Khouri H.; Gill J.; Mikula A.;
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97188; CAB10016.1; -
DR EMBL; AE007186; AAK48292.1; -
DR TIGR; MT3925; -
DR Tuberculist; RV3817; -
DR InterPro; IPR002575; APH.
DR Pfam; PF01636; APH; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 251 AA; 27241 MW; 52B07FDA006A21B3 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
| | | | |
DB 86 DWAWL 90

RESULT 13

Q91719 ID Q91719 PRELIMINARY; PRT; 304 AA.
AC Q91719; MEDLINE=21608551; PubMed=11743194;
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable cytochrome c oxidase assembly factor.
GN PA0113.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong K.E.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004449; AACG3503.1; -;
DR InterPro: IPR006369; CyOE_CtaB.
DR Pfam: PF01040; UbiA; 1.
DR TIGRFAMs: TIGR01473; CyOE_ctaB; 1.
DR PROSITE: PS00943; UbiA; 1.
KW Complete proteome.
SQ SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 90.0%; Score 36; DB 16; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAW 5
| | | | |
DB 259 LDNAW 263

RESULT 14

Q8UBG8 ID Q8UBG8 PRELIMINARY; PRT; 316 AA.
AC Q8UBG8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ABC transporter, membrane spanning protein.
GN ATU3048 OR AGR_L_3514.
OS Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley P., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT CS8.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens CS8.";
RL Science 294:2323-2328 (2001).
DR EMBL: AE009235; AAL43864.1; -;
DR EMBL: AE008379; AAK90334.1; -;
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 316 AA; 35079 MW; 7137741D79029267 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAW 5
| | | | |
DB 67 LDNAW 71

RESULT 15

Q9XBD4 ID Q9XBD4 PRELIMINARY; PRT; 444 AA.
AC Q9XBD4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative integral membrane sugar transporter.
GN CZA382.17C.
OS Amycolatopsis orientalis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.
OX NCBI_TaxID=31958;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Lennard N., Harris B.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA van Wageningen A., Kirkpatrick P., Williams D., Harris B., Kershaw J.,
RA Lennard N., Jones M., Jones S., Solenberg P.;
RT "Sequencing and analysis of genes involved in the biosynthesis of a
RT vancomycin group antibiotic.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AL078635; CAB45038.1; -;
DR InterPro: IPR007114; MFS.
DR InterPro: IPR005828; Sub_transporter.
DR Pfam: PF00083; sugar tr; 1.
DR PROSITE: PS50850; MFS; 1.
KW Sugar transport; Transmembrane.

SQ SEQUENCE 444 AA; 48039 MW; 51ACE2D9EB121EDA CRC64;
Query Match 90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWAW 5
Db 194 LDWAW 198

Search completed: February 18, 2004, 14:35:58
Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDNAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10	US-09-847-940B-16
2	40	100.0	6	11	US-09-847-946A-16
3	40	100.0	6	11	US-09-847-946A-44
4	40	100.0	6	11	US-09-847-946A-106
5	40	100.0	7	11	US-09-847-946A-110
6	40	100.0	8	11	US-09-847-946A-103
7	40	100.0	8	11	US-09-847-946A-111
8	40	100.0	9	11	US-09-847-946A-102
9	40	100.0	9	11	US-09-847-946A-105
10	40	100.0	9	11	US-09-847-946A-108
11	40	100.0	9	11	US-09-847-946A-109
12	40	100.0	10	11	US-09-847-946A-107
13	40	100.0	10	11	US-09-847-946A-104
14	40	100.0	11	11	US-09-847-946A-101
15	37	92.5	6	10	US-09-847-940B-2

16	37	92.5	6	11	US-09-847-946A-2	Sequence 2, Appl
17	37	92.5	6	11	US-09-847-946A-33	Sequence 33, Appl
18	37	92.5	7	11	US-09-847-946A-37	Sequence 37, Appl
19	37	92.5	8	11	US-09-847-946A-30	Sequence 30, Appl
20	37	92.5	8	11	US-09-847-946A-38	Sequence 38, Appl
21	37	92.5	9	11	US-09-847-946A-29	Sequence 29, Appl
22	37	92.5	9	11	US-09-847-946A-32	Sequence 32, Appl
23	37	92.5	9	11	US-09-847-946A-35	Sequence 35, Appl
24	37	92.5	9	11	US-09-847-946A-36	Sequence 36, Appl
25	37	92.5	10	11	US-09-847-946A-31	Sequence 31, Appl
26	37	92.5	10	11	US-09-847-946A-34	Sequence 34, Appl
27	37	92.5	11	11	US-09-847-946A-28	Sequence 28, Appl
28	37	92.5	11	11	US-09-847-946A-132	Sequence 132, App
29	37	92.5	11	11	US-09-847-946A-140	Sequence 140, App
30	37	92.5	13	11	US-09-847-946A-143	Sequence 143, App
31	37	92.5	13	11	US-09-847-946A-144	Sequence 144, App
32	37	92.5	13	11	US-09-847-946A-145	Sequence 145, App
33	37	92.5	13	11	US-09-847-946A-148	Sequence 148, App
34	37	92.5	17	11	US-09-847-946A-141	Sequence 141, App
35	37	92.5	17	11	US-09-847-946A-142	Sequence 142, App
36	37	92.5	17	11	US-09-847-946A-146	Sequence 146, App
37	37	92.5	17	11	US-09-847-946A-147	Sequence 147, App
38	37	92.5	18	11	US-09-847-946A-131	Sequence 131, App
39	37	92.5	18	11	US-09-847-946A-135	Sequence 135, App
40	37	92.5	18	11	US-09-847-946A-136	Sequence 136, App
41	37	92.5	22	11	US-09-847-946A-133	Sequence 133, App
42	37	92.5	22	11	US-09-847-946A-134	Sequence 134, App
43	37	92.5	22	11	US-09-847-946A-137	Sequence 137, App
44	37	92.5	22	11	US-09-847-946A-138	Sequence 138, App
45	37	92.5	22	11	US-09-847-946A-139	Sequence 139, App

ALIGNMENTS

RESULT 1
US-09-847-940B-16
; Sequence 16, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-16

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNAWL 6
| | | | |
Db 1 LDNAWL 6

RESULT 2
US-09-847-946A-16
; Sequence 16, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-16

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 1 LDRAWL 6

RESULT 3

US-09-847-946A-44
; Sequence 44, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 6

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-44

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 1 LDRAWL 6

RESULT 4

US-09-847-946A-106
; Sequence 106, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 6

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-106

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 1 LDRAWL 6

RESULT 5

US-09-847-946A-110
; Sequence 110, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
; LENGTH: 7

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-110

Query Match 100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 1 LDRAWL 6

RESULT 6

US-09-847-946A-103

; Sequence 103, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 103
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-103

Query Match 100.0%; Score 40; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
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 Db 3 LDRAWL 8

RESULT 7

US-09-847-946A-111
 ; Sequence 111, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 111
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-111

Query Match 100.0%; Score 40; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
 |||||
 Db 1 LDRAWL 6

RESULT 8

US-09-847-946A-102
 ; Sequence 102, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 102
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-102

Query Match 100.0%; Score 40; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
 |||||
 Db 1 LDRAWL 6

RESULT 9

US-09-847-946A-105
 ; Sequence 105, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 105
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-105

Query Match 100.0%; Score 40; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 1 LDRAWL 6

RESULT 10

US-09-847-946A-108
; Sequence 108, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-108

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 3 LDRAWL 8

RESULT 11

US-09-847-946A-109
; Sequence 109, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-109

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 2 LDRAWL 7

RESULT 12

US-09-847-946A-104
; Sequence 104, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-104

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||||
Db 2 LDRAWL 7

RESULT 13

US-09-847-946A-107
; Sequence 107, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-107

US-09-847-946A-107

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
| | | | |
Db 3 LDRAWL 8

RESULT 14

US-09-847-946A-101
; Sequence 101, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-101

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
| | | | |
Db 3 LDRAWL 8

RESULT 15

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 92.5%; Score 37; DB 10; Length 6;

Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
| | | | |
Db 1 LDWSWL 6

Search completed: February 18, 2004, 15:42:01
Job time : 17.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	23	Mutated IKKbeta NE
2	40	100.0	6	23	NBD mutant peptide
3	40	100.0	6	23	AA48521
4	40	100.0	6	23	AA48541
5	40	100.0	6	23	AA48603
6	40	100.0	6	24	ABU08431
7	40	100.0	7	23	AA48607
8	40	100.0	8	23	AA48600
9	40	100.0	9	23	AA48608
10	40	100.0	9	23	AA48599

10	40	100.0	9	23	AA48602	Anti-inflammatory
11	40	100.0	9	23	AA48605	Anti-inflammatory
12	40	100.0	9	23	AA48606	Anti-inflammatory
13	40	100.0	10	23	AA48601	Anti-inflammatory
14	40	100.0	10	23	AA48604	Anti-inflammatory
15	40	100.0	11	23	AA48598	Anti-inflammatory
16	40	100.0	173	23	ABP30297	Streptococcus poly
17	40	100.0	186	23	ABP27565	Streptococcus poly
18	40	100.0	756	23	ABP77306	Human IKKbeta muta
19	38	95.0	342	22	AA40149	Human polypeptide
20	38	95.0	358	22	AA41935	Human polypeptide
21	37	92.5	6	23	AB08725	IKKbeta NEMO bindi
22	37	92.5	6	23	AA48530	Anti-inflammatory
23	37	92.5	6	23	AA48655	NBD mutant peptide
24	37	92.5	6	24	ABU08418	Human NEMO binding
25	37	92.5	7	23	AA48534	Anti-inflammatory
26	37	92.5	8	23	AA48527	Anti-inflammatory
27	37	92.5	8	23	AA48535	Anti-inflammatory
28	37	92.5	9	20	AAW96182	IKK-alpha polypept
29	37	92.5	9	23	AA48526	Anti-inflammatory
30	37	92.5	9	23	AA48529	Anti-inflammatory
31	37	92.5	9	23	AA48532	Anti-inflammatory
32	37	92.5	9	23	AA48533	Anti-inflammatory
33	37	92.5	10	23	ABP77313	IKKbeta NEMO bindi
34	37	92.5	10	23	AA48528	Anti-inflammatory
35	37	92.5	10	23	AA48531	Anti-inflammatory
36	37	92.5	11	23	ABP77311	Human NBD peptide
37	37	92.5	11	23	AA48506	Human IKKbeta pept
38	37	92.5	11	23	AA48525	Anti-inflammatory
39	37	92.5	11	23	AA48653	NBD peptide. Synt
40	37	92.5	13	23	AA48640	Anti-inflammatory
41	37	92.5	13	23	AA48641	Anti-inflammatory
42	37	92.5	13	23	AA48642	Anti-inflammatory
43	37	92.5	13	23	AA48645	Anti-inflammatory
44	37	92.5	17	23	AA48638	Anti-inflammatory
45	37	92.5	17	23	AA48639	Anti-inflammatory

ALIGNMENTS

RESULT 1

AB08738

ID ABB08738 standard; peptide; 6 AA.

XX ABB08738;

XX

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 16.

XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiaesthetic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX

PH NBD mutant peptide

FT Anti-inflammatory

FT Anti-inflammatory

XX Human NEMO binding

PN Anti-inflammatory

XX Anti-inflammatory

PD Anti-inflammatory

XX Anti-inflammatory

Key Location/Qualifiers
Misc-difference 4 /note= "Wildtype Ser substituted by Ala"

WO200183547-A2.

08-NOV-2001.

PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYUA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking NF-kB mediated
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 1 LDWAWL 6
 |||||
 |||||
 RESULT 2
 ID AAM48521
 XX AAM48521 standard; Peptide; 6 AA.
 AC AAM48521;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 16.

XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYUA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16;
 XX
 CC Novel antiinflammatory compound comprising membrane translocation
 CC domain fused to NEMO binding sequence, useful for blocking nuclear
 CC factor kappaB activation, and for treating asthma, lung inflammation,
 CC psoriasis
 CC
 CC Example 6; Page 48; 88pp; English.
 CC
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-NM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 1 LDWAWL 6
 |||||
 |||||
 RESULT 3
 ID AAM48541
 AAM48541 standard; Peptide; 6 AA.

XX AAM48541;
 XX 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 44.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 61; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially:
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 40; DB 23; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 LDWAWL 6
 XX |||||

DB 1 LDWAWL 6
 RESULT 4
 AAM48603
 ID AAM48603 standard; Peptide; 6 AA.
 XX
 XX AAM48603;
 XX
 XX 20-MAR-2002 (first entry)
 XX
 XX Anti-inflammatory peptide SEQ ID NO 106.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially:
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
 DB 1 LDRAWL 6

RESULT 5
 ABU08431
 ID ABU08431 standard; peptide; 6 AA.
 XX
 AC ABU08431;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #14.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antiinflammatory; antiarthritic; mutant; muten.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
 DB 1 LDRAWL 6

RESULT 6
 AAM48607
 ID AAM48607 standard; Peptide; 7 AA.
 XX
 AC AAM48607;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 110.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW cytotoxic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 OS
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYTA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 89pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflamatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
 |||||
 Db 1 LDWAWL 6

RESULT 7
 AAM48600
 ID AAM48600 standard; Peptide; 8 AA.
 XX
 AC AAM48600;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 DE Anti-inflammatory peptide SEQ ID NO 103.
 XX
 XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
 |||||
 Db 3 LDWAWL 8

RESULT 8
 AAM48608
 ID AAM48608 standard; Peptide; 8 AA.
 XX
 AC AAM48608;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 111.
 DE
 XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 PS Novel antiinflammatory compound comprising membrane translocation
 CC domain fused to NEMO binding sequence, useful for blocking nuclear
 CC factor kappaB activation, and for treating asthma, lung inflammation,
 CC psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, antiarthritic, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
 Db 1 LDWAWL 6

RESULT 9
 AAM48599
 ID AAM48599 standard; Peptide; 9 AA.
 AC AAM48599;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 DE Anti-inflammatory peptide SEQ ID NO 102.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 89pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
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 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
 Db 1 LDWAWL 6

RESULT 10
 AAM48602
 ID AAM48602 standard; Peptide; 9 AA.
 AC AAM48602;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 DE Anti-inflammatory peptide SEQ ID NO 105.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
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 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 1 LDWAWL 6
 RESULT 11
 AAM48605
 ID AAM48605 standard; Peptide; 9 AA.
 XX
 AC AAM48605;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 108.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRACIS PHARM INC.
 PA (UYIA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 3 LDWAWL 8
 RESULT 12
 AAM48606
 ID AAM48606 standard; Peptide; 9 AA.
 XX
 AC AAM48606;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 109.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.

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PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYA ) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX Claim 6; Page 62; 88pp; English.
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX Sequence 9 AA;
XX Query Match 100.0%; Score 40; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDRAWL 6
DB 2 LDRAWL 7
RESULT 13
AAM48601
ID AAM48601 standard; Peptide; 10 AA.
XX AC AAM48601;
XX 20-MAR-2002 (first entry)
DT DE Anti-inflammatory peptide SEQ ID NO 104.
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.

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XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14346.
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
XX (UYA ) UNIV YALE.
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX Claim 6; Page 62; 88pp; English.
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CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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CC activation and subsequent decreased phosphorylation of IkappaB. The
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 40; DB 23; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 2.7;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDRAWL 6
DB 2 LDRAWL 7
RESULT 14
AAM48604
ID AAM48604 standard; Peptide; 10 AA.
XX AC AAM48604;
XX 20-MAR-2002 (first entry)
DT DE Anti-inflammatory peptide SEQ ID NO 107.
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.

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KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 DR Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
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 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWAWL 6
 Db 3 LDWAWL 8
 RESULT 15
 AAM48598
 ID AAM48598 standard; Peptide; 11 AA.
 AC AAM48598;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 101.
 DE
 XX Antiinflammatory; antiasthmatic; cytotatic; antipsoriatic; nontropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 DR Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 40; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWAWL 6
 Db 3 LDWAWL 8
 Search completed: February 18, 2004, 14:26:26
 Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	939	16 Q8YQR3	Q8Yqr3 anabaena sp
2	36	100.0	1466	3 Q42930	Q42930 echizosacch
3	34	94.4	317	16 Q8FMV4	Q8fmv4 corynebacte
4	34	94.4	389	17 O58160	O58160 pyrococcus
5	33	91.7	542	3 O60113	O60113 echizosacch
6	32	88.9	75	10 Q94HW4	Q94hw4 arabidopsis
7	32	88.9	136	16 P72919	P72919 synchocyst
8	32	88.9	142	6 Q8HYV0	Q8hyv0 aus scrofa
9	32	88.9	153	16 P73698	P73698 synchocyst
10	32	88.9	172	16 Q9RYF2	Q9ryf2 deinococcus
11	32	88.9	221	10 Q9SJO3	Q9sjg3 arabidopsis
12	32	88.9	229	17 Q8ZYL1	Q8zyl1 pyrobaculum
13	32	88.9	262	10 Q9FNJ0	Q9fnj0 arabidopsis
14	32	88.9	278	10 Q9LUT6	Q9lut6 arabidopsis
15	32	88.9	308	3 Q12010	Q12010 saccharomyc
16	32	88.9	319	5 Q9NEV3	Q9nev3 caenorhabdi

17	32	88.9	337	4 Q9GRE6	Q9gre6 homo sapien
18	32	88.9	362	5 O44634	O44634 caenorhabdi
19	32	88.9	393	16 Q9ZKA8	Q9zka8 helicobacte
20	32	88.9	409	4 Q8N6M5	Q8n6m5 homo sapien
21	32	88.9	412	10 Q8RYL7	Q8ryl7 oryza sativ
22	32	88.9	429	12 Q65111	Q65111 adelaida r1
23	32	88.9	438	16 Q8RHMS	Q8rhms fusobacteri
24	32	88.9	450	16 Q99RI0	Q99ri0 staphylococ
25	32	88.9	450	16 Q8NUY5	Q8nuys staphylococ
26	32	88.9	451	16 Q9L151	Q9l151 streptomyc
27	32	88.9	455	16 Q8CN46	Q8cn46 staphylococ
28	32	88.9	480	16 Q67595	Q67595 aquifex aeo
29	32	88.9	497	10 Q9LZB4	Q9lze4 arabidopsis
30	32	88.9	497	10 Q94EY8	Q94ey8 arabidopsis
31	32	88.9	505	16 Q8PAX6	Q8pax6 xanthomonas
32	32	88.9	542	17 Q30147	Q30147 archaeoglob
33	32	88.9	555	16 Q8PMM9	Q8pmm9 xanthomonas
34	32	88.9	561	16 Q9HTJ2	Q9htj2 pseudomonas
35	32	88.9	567	16 Q8ZGWO	Q8zgw0 yersinia pe
36	32	88.9	573	16 Q8YXB1	Q8yxb1 anabaena sp
37	32	88.9	599	10 Q9PHV3	Q9phv3 arabidopsis
38	32	88.9	620	11 Q8BQG4	Q8bqg4 mus musculu
39	32	88.9	647	2 Q8VUW5	Q8vuws staphylococ
40	32	88.9	673	4 Q9BTT9	Q9btt9 homo sapien
41	32	88.9	708	5 Q9WQD8	Q9wqd8 drosophila
42	32	88.9	738	11 Q8VEB0	Q8veb0 mus musculu
43	32	88.9	793	5 Q9VVY0	Q9vvy0 drosophila
44	32	88.9	828	3 Q74240	Q74240 thielavia h
45	32	88.9	839	10 Q9M0G3	Q9m0g3 arabidopsis

ALIGNMENTS

RESULT 1

Q8YQR3 PRELIMINARY; PRT; 939 AA.
ID Q8YQR3
AC Q8YQR3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Alr3756.
GN ALR3756.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kanieko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003594; BAB75455.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 939 AA; 104233 MW; 8FE0A7CA6C1759A5 CRC64;

Query Match 100.0%; Score 36; DB 16; Length 939;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDWSYL 6

Db 648 LDWSYL 653

RESULT 2

O42930 PRELIMINARY; PRT; 1466 AA.
ID O42930

O42930;
 AC 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-1998 (TrEMBLrel. 23, Last annotation update)
 DE Putative membrane glycoprotein, possible vacuolar protein sorting
 DE /targeting.
 DE SPBC16C6.06.
 GN Schizosaccharomyces pombe (Fission Yeast).
 OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Furnelle B., Goffeau A., Wood V., Lyne M., Barrell B.G.,
 RA Rajadream M.A.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021767; CAA16914.1; -.
 DR GeneDB SPombe; SPBC16C6.06; -.
 DR InterPro; IPR002860; GH_BNR.
 DR InterPro; IPR006581; VPS10.
 DR Pfam; PF02012; BNR; 12.
 DR SMART; SM00602; VPS10; 2.
 SQ SEQUENCE 1466 AA; 165061 MW; CBB315E0F7688D79 CRC64;
 Query Match 100.0%; Score 36; DB 3; Length 1466;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 1046 LDWSYL 1051
 RESULT 3
 Q8FMV4 PRELIMINARY; PRT; 317 AA.
 AC Q8FMV4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 DE CE2395.
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
 RA Usuda Y., Sugimoto S.;
 RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005222; BAC12905.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 317 AA; 33135 MW; 3805DE05030A91C CRC64;
 Query Match 94.4%; Score 34; DB 16; Length 317;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 114 MDWSYL 119
 RESULT 4
 O58160 PRELIMINARY; PRT; 389 AA.
 AC O58160;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein PH0423.
 GN PH0423.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka K., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76 (1998).
 DR EMBL; AP000002; BAA29509.1; -.
 DR InterPro; IPR002934; NTP_transf.
 DR Pfam; PF01909; NTP_transf_2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 389 AA; 46335 MW; 81P32C817B1A53D4 CRC64;
 Query Match 94.4%; Score 34; DB 17; Length 389;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 139 LDWSYL 144
 RESULT 5
 O60113 PRELIMINARY; PRT; 542 AA.
 ID O60113
 AC O60113;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Amino acid permease.
 DE SPBC15C4.04C.
 GN Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Lyne M., Rajadream M.A., Barrell B.G., Xiang Z., Aves S.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL023290; CAA18895.1; -.
 DR GeneDB SPombe; SPBC15C4.04C; -.
 DR InterPro; IPR002293; AA/rei_permease1.
 DR InterPro; IPR004840; AAC_permease.
 DR InterPro; IPR004756; AA_permease.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF00324; aa_permeases; 1.
 DR TIGRFAMs; TIGR00907; 2A0304; 1.
 DR PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.
 SQ SEQUENCE 542 AA; 59726 MW; 17D9B15C04299468 CRC64;
 Query Match 91.7%; Score 33; DB 3; Length 542;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 139 LDWSYL 144

Db 436 LDMSYV 441

RESULT 6

Q94HW4 PRELIMINARY; PRT; 75 AA.
 AC Q94HW4; 75 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 8.8 kDa protein.
 GN T4M14.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
 RA Tallon L.J., Rooney T., Utterback T.R., VanAken S.E., Feldblyum T.V.,
 RA White O., Fraser C.M.;
 RL "Arabidopsis thaliana chromosome 1 BAC T4M14 genomic sequence."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC027036; AAK62781.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 75 AA; 8834 MW; B34EB28B5C41EBB5 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 75;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5
 |||||
 Db 12 LDMSY 16

RESULT 7

P72919 PRELIMINARY; PRT; 136 AA.
 AC P72919;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein slr1082.
 GN SLR1082.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RL "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90901; BAA16936.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match 88.9%; Score 32; DB 16; Length 136;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 6
 |||||
 Db 42 LDMSY 47

RESULT 8

Q8HYV0 PRELIMINARY; PRT; 142 AA.
 AC Q8HYV0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glycogen synthase (Fragment).
 GN GYS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA te Pas M.F., Leenhouders J.I., Knol E.F., Booiij M., Priem J.,
 RA van der Lende T.;
 RL "Marker polymorphism in the porcine muscle glycogen synthase (glycogen
 synthase 1)";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ507152; CAD47844.1; -
 FT NON TER 1 1
 FT NON TER 142 142
 SQ SEQUENCE 142 AA; 15951 MW; C02BAD285PBF8A7E CRC64;

Query Match 88.9%; Score 32; DB 6; Length 142;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSY 6
 |||||
 Db 83 LDMSY 88

RESULT 9

P73698 PRELIMINARY; PRT; 153 AA.
 AC P73698;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein slr1813.
 GN SLR1813.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RL "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90908; BAA17745.1; -
 DR InterPro; IPR002636; DUF29.
 DR Pfam; PF01724; DUF29; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 153 AA; 18387 MW; 6E54EB36EDCB9AF1 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 153;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSY 6
 |||||
 Db 36 LDMSY 41

```

RC STRAIN=cv. Columbia;
RA Lin x.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SQ EMBL; AC006919; AAD24637.1; -.
DR SEQUENCE 221 AA; 25043 MW; D3037BC4CC103990 CRC64;

Query Match      88.9%; Score 32; DB 10; Length 221;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
Db 208 LDWSY 212

RESULT 12
Q8ZYL1 PRELIMINARY; PRT; 229 AA.
ID Q8ZYL1
AC Q8ZYL1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Molybdenum cofactor biosynthesis protein D/E.
GN PAO0727.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thaumarchaeota; Pyrodictaceae; Pyrodicticum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AB009782; AAL62982.1; -.
DR InterPro; IPR003448; Mb_biosynth_MoaE.
DR InterPro; IPR003749; THIS.
DR Pfam; PF02391; MoaE; 1.
DR Pfam; PF02597; This; 1.
KW Complete proteome.
SQ SEQUENCE 229 AA; 25544 MW; 111B06C8F85982EA CRC64;

Query Match      88.9%; Score 32; DB 17; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
Db 60 LDWSY 64

RESULT 13
Q9FNJ0 PRELIMINARY; PRT; 262 AA.
ID Q9FNJ0
AC Q9FNJ0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Genomic DNA, chromosome 5, pl clone:MDJ22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98069011; PubMed=9405937;
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA Tabata S.;

RC STRAIN=cv. Columbia;
RA Lin x.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SQ EMBL; AC006919; AAD24637.1; -.
DR SEQUENCE 221 AA; 25043 MW; D3037BC4CC103990 CRC64;

Query Match      88.9%; Score 32; DB 16; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
Db 96 LDWSY 100

RESULT 11
Q9SJQ3 PRELIMINARY; PRT; 221 AA.
ID Q9SJQ3
AC Q9SJQ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE At2g36550 protein.
GN AT2G36550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Bisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
```

RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned P1 clones."
 RL DNA Res. 4:291-300(1997).
 DR ENBL; AB006899; BAB11677.1; -.
 DR InterPro; IPR006566; FBD.
 DR SMART; SM00579; FBD; 1.
 SQ SEQUENCE 262 AA; 37076 MW; CE15DD9E2CD3C6B9 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 262;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
 |||||
 Db 46 DWSYL 50

RESULT 14

Q9LUT6 PRELIMINARY; PRT; 278 AA.
 AC Q9LUT6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE GB|AAD32889.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones."
 RL DNA Res. 7:131-135(2000).
 DR ENBL; AB022216; BAB02739.1; -.
 SQ SEQUENCE 278 AA; 31217 MW; A16AE1E0910484B2 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 278;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
 |||||
 Db 217 LDWSY 221

RESULT 15

Q12010 PRELIMINARY; PRT; 308 AA.
 AC Q12010;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Chromosome XV reading frame ORF YOL092W.
 GN YOL092W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;
 RX MEDLINE=96021609; PubMed=8533473;
 RA Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
 RT "A 29.425 Kb segment on the left arm of yeast chromosome XV contains
 RT more than twice as many unknown as known open reading frames.";

RL Yeast 11:975-986(1995).
 DR ENBL; Z74834; CAA99104.1; -.
 DR EMBL; X81121; CAA58187.1; -.
 DR SGD; S0005452; YOL092W.
 DR InterPro; IPR006603; CTNS.
 DR SMART; SM00679; CTNS; 2.

SQ SEQUENCE 308 AA; 34872 MW; 38EB1645FA034812 CRC64;

Query Match 88.9%; Score 32; DB 3; Length 308;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 |||||
 Db 267 LDWSYL 272

Search completed: February 18, 2004, 14:35:57
 Job time : 19.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: - 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.76:
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	939	2 AE2275	hypothetical prote
2	36	100.0	1466	2 T39557	vacuolar protein s
3	34	94.4	98	2 H64885	ydas protein - Esc
4	34	94.4	389	2 H71152	hypothetical prote
5	33	91.7	330	1 H69798	conserved hypotet
6	33	91.7	542	2 T39474	amino acid permea
7	32	88.9	136	2 S74785	hypothetical prote
8	32	88.9	153	2 S77187	hypothetical prote
9	32	88.9	172	2 A75592	hypothetical prote
10	32	88.9	221	2 H84781	hypothetical prote
11	32	88.9	265	2 T40878	probable FAD synth
12	32	88.9	308	2 S57377	probable membrane
13	32	88.9	362	2 T32669	hypothetical prote
14	32	88.9	392	2 T45032	hypothetical prote
15	32	88.9	393	2 B71857	probable lipopolys
16	32	88.9	445	2 S27492	hypothetical prote
17	32	88.9	450	2 D90047	hypothetical prote
18	32	88.9	476	2 T43863	cardiolipin syntha
19	32	88.9	480	2 B70446	hypothetical prote
20	32	88.9	497	2 T48367	hypothetical prote
21	32	88.9	542	2 A69261	probable acid-CoA
22	32	88.9	561	2 B82975	choline dehydrogen
23	32	88.9	567	2 AC0143	choline dehydrogen
24	32	88.9	573	2 AE1969	sulfate permease f
25	32	88.9	707	2 T40070	origin recognition
26	32	88.9	735	2 A33369	glycogen(starch) s
27	32	88.9	737	2 A32156	glycogen(starch) s
28	32	88.9	839	2 F85334	myosin heavy chain
29	32	88.9	1446	2 T04528	myosin heavy chain

30	32	88.9	1556	2 F96587	hypothetical prote
31	32	88.9	1583	2 T00727	myosin heavy chain
32	32	88.9	1611	2 A84743	probable myosin he
33	32	88.9	1643	2 T07961	myosin heavy chain
34	32	88.9	1736	2 F86178	hypothetical prote
35	32	88.9	2245	2 T18278	myosin heavy chain
36	32	88.9	2658	2 A86216	protein T23G18.2 (
37	31	86.1	223	2 T24188	hypothetical prote
38	31	86.1	231	2 G81026	inositol monophosp
39	31	86.1	237	2 B82644	5-amino-6-(5-phosp
40	31	86.1	264	2 D81971	hypothetical prote
41	31	86.1	506	2 T50211	WD-repeat protein
42	31	86.1	703	2 S45686	glycogen(starch) s
43	31	86.1	703	2 A35362	glycogen(starch) s
44	31	86.1	745	1 I49101	conserved helix-lo
45	31	86.1	757	2 A39283	gamma-glutamyl car

ALIGNMENTS

RESULT 1
AE2275

Hypothetical protein alr3756 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE2275
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-939 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA075455.1; PID:gl17132890; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3756

Query Match 100.0%; Score 36; DB 2; Length 939;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
|||
DB 648 LDWSYL 653

RESULT 2

T39557
vacuolar protein sorting - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39557
R;Furnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21863
A:Accession: T39557
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1466 <PUR>
A:Cross-references: EMBL:AL021767; PIDN:CAA16914.1; GSPDB:GN00067; SPDB:SPBC16C6.06
A:Experimental source: strain 972h; cosmid c16C6
C:Genetics:
A:Gene: SPDB:SPBC16C6.06
A:Map position: 2
A:Introns: 58/93
Query Match 100.0%; Score 36; DB 2; Length 1466;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

superfamily: serinocysteine isoenzymes hydrolytic protein 000000

N;Alternate names: hyponeuric protein 0522; protein 18K14W homolog

C:Species: Saccharomyces cerevisiae
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 19-Apr-2002
 C:Accession: S57377; S66786; S50413
 R:Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
 Yeast 11, 975-986, 1995
 A:Title: A 28.425 kb segment on the left arm of yeast chromosome XV contains more than 1
 A:Reference number: S57374; MUID:96021609; PMID:8533473
 A:Accession: S57377
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-308 <ZUM>
 A:Cross-references: EMBL:X83121; NID:G600461; PIDN:CAA58187.1; PID:G600466
 R:Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66775
 A:Accession: S66786
 A:Molecule type: DNA
 A:Residues: 1-308 <ZUM>
 A:Cross-references: EMBL:Z74834; NID:G1419937; PID:G1419938; MIPS:YOL092W
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0005452
 A:Map position: 15L
 C:Superfamily: Saccharomyces probable membrane protein YBR147W
 C:Keywords: transmembrane protein
 F:14-30/Domain: transmembrane #status predicted <TM1>
 F:45-61/Domain: transmembrane #status predicted <TM2>
 F:73-89/Domain: transmembrane #status predicted <TM3>
 F:168-184/Domain: transmembrane #status predicted <TM4>
 F:249-265/Domain: transmembrane #status predicted <TM5>
 F:278-294/Domain: transmembrane #status predicted <TM6>

Query Match 88.9%; Score 32; DB 2; Length 308;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 |||||
 Db 267 LDWKYL 272

RESULT 13
 Hypothetical protein F16B4.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32669
 R:Davidson, S.; Wohldmann, P.; Bauer, C.; O'Neal, D.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid F16B4.
 A:Reference number: Z21208
 A:Accession: T32669
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-362 <DAV>
 A:Cross-references: EMBL:AF039048; PIDN:AAB94233.1; GSPDB:GN00023; CBSP:F16B4.2
 A:Experimental source: strain Bristol N2; clone F16B4
 C:Genetics:
 A:Gene: CBSP:F16B4.2
 A:Map position: 5
 A:Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 88.9%; Score 32; DB 2; Length 362;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 |||||
 Db 26 LDWSFL 31

hypothetical protein Y3986B.f [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T45032
 R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; John B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.
 Nature 368, 32-38, 1994
 A:Authors: Showkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, E.; E tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
 A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
 A:Reference number: S43531; MUID:94150718; PMID:7906398
 A:Accession: T45032
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-392 <WIL>
 A:Cross-references: EMBL:AL132896; NID:G6434440; PIDN:CAB60911.1; PID:G6434446
 A:Experimental source: clone Y3986B
 C:Genetics:
 A:Map position: 3
 A:Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
 A:Note: Y3986B.f

Query Match 88.9%; Score 32; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
 |||||
 Db 289 DWSYL 293

RESULT 15
 B71857
 probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 C:Accession: B71857
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: B71857
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-393 <ARN>
 A:Cross-references: GB:AE001531; GB:AE001439; NID:G4155617; PIDN:AAD06611.1; PID:G415562
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp1031

Query Match 88.9%; Score 32; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
 |||||
 Db 284 DWSYL 288

Search completed: February 18, 2004, 14:38:51
 Job time : 7.5921 secs

RESULT 14
 T45032

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	829	4 US-09-252-991A-27150	Sequence 27150, A
2	32	88.9	462	4 US-09-134-001C-4300	Sequence 4300, Ap
3	32	88.9	597	4 US-09-252-991A-17139	Sequence 17139, A
4	32	88.9	651	4 US-09-107-532A-4902	Sequence 4902, Ap
5	32	88.9	706	1 US-08-484-105-16	Sequence 16, Appl
6	32	88.9	706	1 US-08-484-106-16	Sequence 16, Appl
7	32	88.9	911	1 US-08-596-985-2	Sequence 2, Appl
8	31	86.1	745	2 US-08-887-518-3	Sequence 3, Appl
9	31	86.1	745	2 US-09-023-321-3	Sequence 3, Appl
10	31	86.1	745	2 US-08-890-853-4	Sequence 4, Appl
11	31	86.1	745	2 US-09-032-475-3	Sequence 3, Appl
12	31	86.1	745	2 US-09-039-125A-4	Sequence 4, Appl
13	31	86.1	745	2 US-09-099-124A-4	Sequence 4, Appl
14	31	86.1	745	3 US-09-032-476-4	Sequence 4, Appl
15	31	86.1	745	3 US-08-890-854-4	Sequence 4, Appl
16	31	86.1	745	3 US-09-023-324-4	Sequence 4, Appl
17	31	86.1	745	3 US-09-168-629-2	Sequence 2, Appl
18	31	86.1	745	3 US-08-910-820-10	Sequence 10, Appl
19	31	86.1	745	3 US-08-810-131A-2	Sequence 2, Appl
20	31	86.1	745	4 US-09-109-986-4	Sequence 4, Appl
21	31	86.1	745	4 US-09-844-908-10	Sequence 10, Appl
22	31	86.1	745	4 US-08-868-758-3	Sequence 3, Appl
23	31	86.1	756	2 US-08-887-518-4	Sequence 4, Appl
24	31	86.1	756	2 US-09-023-321-4	Sequence 4, Appl
25	31	86.1	756	2 US-08-890-853-2	Sequence 2, Appl
26	31	86.1	756	2 US-09-032-475-4	Sequence 4, Appl
27	31	86.1	756	2 US-09-099-125A-2	Sequence 2, Appl

28	31	86.1	756	2 US-09-099-124A-2	Sequence 2, Appl
29	31	86.1	756	3 US-09-032-476-2	Sequence 2, Appl
30	31	86.1	756	3 US-08-890-854-2	Sequence 2, Appl
31	31	86.1	756	3 US-09-023-324-2	Sequence 2, Appl
32	31	86.1	756	3 US-09-168-629-15	Sequence 15, Appl
33	31	86.1	756	3 US-08-910-820-9	Sequence 9, Appl
34	31	86.1	756	4 US-09-109-986-2	Sequence 9, Appl
35	31	86.1	756	4 US-09-844-908-9	Sequence 9, Appl
36	31	86.1	756	4 US-08-868-758-4	Sequence 4, Appl
37	31	86.1	758	1 US-07-756-250-16	Sequence 16, Appl
38	31	86.1	996	4 US-09-417-197-123	Sequence 123, App
39	31	86.1	997	4 US-09-417-197-121	Sequence 121, App
40	30	83.3	122	4 US-08-936-165A-397	Sequence 397, App
41	30	83.3	363	1 US-07-681-704A-2	Sequence 2, Appl
42	30	83.3	417	3 US-08-640-906-4	Sequence 4, Appl
43	30	83.3	417	3 US-08-640-906-18	Sequence 18, Appl
44	30	83.3	417	4 US-09-395-936-4	Sequence 4, Appl
45	30	83.3	417	4 US-09-395-936-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-252-991A-27150
; Sequence 27150, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27150
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27150

Query Match 100.0%; Score 36; DB 4; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 486 LDWSYL 491

RESULT 2
US-09-134-001C-4300
; Sequence 4300, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4300
; LENGTH: 462
; TYPE: PRT

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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4300

Query Match      88.9%; Score 32; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSY 5
Db      159 LDWSY 163

RESULT 3
US-09-252-991A-17139
; Sequence 17139, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17139
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17139

Query Match      88.9%; Score 32; DB 4; Length 597;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSYL 6
Db      153 DWSYL 157

RESULT 4
US-09-107-532A-4902
; Sequence 4902, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
```

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; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4902:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 651 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...651
; SEQUENCE DESCRIPTION: SEQ ID NO: 4902:
US-09-107-532A-4902

Query Match      88.9%; Score 32; DB 4; Length 651;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSY 5
Db      360 LDWSY 364

RESULT 5
US-08-484-105-16
; Sequence 16, Application US/08484105
; Patent No. 5589341
; GENERAL INFORMATION:
; APPLICANT: STILLMAN, Bruce
; APPLICANT: BELL, Stephen P
; APPLICANT: KOBAYASHI, Ryuji
; APPLICANT: RINE, Jasper
; APPLICANT: FOSS, Margit
; APPLICANT: MCNALLY, Francis J
; APPLICANT: LAURENSEN, Patricia
; APPLICANT: HERSKOWITZ, Ira
; APPLICANT: LI, Joachim J
; APPLICANT: GAVIN, Kimberly
; TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,105
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELE: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 706 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-105-16

Query Match 88.9%; Score 32; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
|
|
|
|
|
Db 193 LDWSY 197

RESULT 6
US-08-484-106-16

; Sequence 16, Application US/08484106
; Patent No. 5614618

; GENERAL INFORMATION:

; APPLICANT: STILLMAN, Bruce
; APPLICANT: BELL, Stephen P
; APPLICANT: KOBAYASHI, Ryuji
; APPLICANT: RINE, Jasper
; APPLICANT: FOSS, Margit
; APPLICANT: McNALLY, Francis J
; APPLICANT: LAURENSEN, Patricia
; APPLICANT: HERSKOWITZ, Ira
; APPLICANT: LI, Joachim J
; APPLICANT: GAVIN, Kimberly
; TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR, HOBBACH, TRST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,106

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman Ph.D., Richard Aron

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO

; TELEPHONE: (415) 494-8700

; TELEFAX: (415) 494-8771

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 706 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-484-106-16

Query Match 88.9%; Score 32; DB 1; Length 706;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
|
|
|
|
|
Db 193 LDWSY 197

RESULT 7

US-08-596-985-2

; Sequence 2, Application US/08596985

; Patent No. 5736374

; GENERAL INFORMATION:

; APPLICANT: Berkha, Randy M.

; APPLICANT: Hucul, John A.

; APPLICANT: Ward, Michael

; TITLE OF INVENTION: Increased Production of

; TITLE OF INVENTION: Beta-galactosidase in Aspergillus oryzae

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genencor International, Inc

; STREET: 180 Kimball Way

; CITY: South San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/596,985

; FILING DATE: 05-FEB-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/267,631

; FILING DATE: 29-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Horn, Margaret A

; REGISTRATION NUMBER: 33,401

; REFERENCE/DOCKET NUMBER: GC250

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 742-7536

; TELEFAX: (415) 742-7217

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 911 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-596-985-2

Query Match 88.9%; Score 32; DB 1; Length 911;

Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSYL 6

|
|
|
|
|

Db 675 LDWKYL 680

RESULT 8

US-08-887-518-3

; Sequence 3, Application US/08887518

; Patent No. 5843721

; GENERAL INFORMATION:

; APPLICANT: Rothe, Mike

; APPLICANT: Wu, Lin

; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/887,518
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 9
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/023,321
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 10
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goettel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
Db 738 LDWSWL 743

RESULT 11
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;; STREET: 268 BUSH STREET, SUITE 3200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/032.475
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/887,518
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-032-475-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
DB 738 LDWSWL 743

RESULT 12
US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-099-125A-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
DB 738 LDWSWL 743

RESULT 13
US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6

Db 738 LDWSWL 743
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RESULT 14

US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-032-476-4

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Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
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Db 738 LDWSWL 743

RESULT 15

US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	10	US-09-847-940B-15
2	36	100.0	6	11	US-09-847-946A-15
3	34	94.4	98	12	US-10-287-274-432
4	32	88.9	6	10	US-09-847-940B-14
5	32	88.9	6	11	US-09-847-946A-14
6	32	88.9	27	11	US-09-974-879-385
7	32	88.9	27	11	US-09-305-736-385
8	32	88.9	27	12	US-09-818-683-385
9	32	88.9	376	12	US-10-369-493-12565
10	32	88.9	412	12	US-10-374-780A-1378
11	32	88.9	445	15	US-10-156-761-8567
12	32	88.9	525	12	US-10-369-493-267
13	32	88.9	542	12	US-10-369-493-913
14	32	88.9	560	12	US-10-369-493-13768
15	32	88.9	561	9	US-09-815-242-12101

16	32	88.9	562	12	US-10-032-585-7639	Sequence 7639, Ap
17	32	88.9	583	12	US-10-369-493-15366	Sequence 15366, A
18	32	88.9	724	12	US-10-369-493-2523	Sequence 2523, Ap
19	32	88.9	1024	15	US-10-213-990-30	Sequence 30, Appl
20	32	88.9	1689	15	US-10-080-943-2	Sequence 2, Appl
21	31	86.1	6	10	US-09-847-940B-2	Sequence 2, Appl
22	31	86.1	6	11	US-09-847-946A-2	Sequence 33, Appl
23	31	86.1	7	11	US-09-847-946A-33	Sequence 37, Appl
24	31	86.1	8	11	US-09-847-946A-30	Sequence 30, Appl
25	31	86.1	8	11	US-09-847-946A-38	Sequence 38, Appl
26	31	86.1	9	11	US-09-847-946A-29	Sequence 29, Appl
27	31	86.1	9	11	US-09-847-946A-32	Sequence 32, Appl
28	31	86.1	9	11	US-09-847-946A-35	Sequence 35, Appl
29	31	86.1	9	11	US-09-847-946A-36	Sequence 36, Appl
30	31	86.1	10	11	US-09-847-946A-31	Sequence 31, Appl
31	31	86.1	10	11	US-09-847-946A-34	Sequence 34, Appl
32	31	86.1	11	11	US-09-847-946A-28	Sequence 28, Appl
33	31	86.1	11	11	US-09-847-946A-132	Sequence 132, App
34	31	86.1	11	11	US-09-847-946A-140	Sequence 140, App
35	31	86.1	11	11	US-09-847-946A-141	Sequence 141, App
36	31	86.1	13	11	US-09-847-946A-143	Sequence 143, App
37	31	86.1	13	11	US-09-847-946A-144	Sequence 144, App
38	31	86.1	13	11	US-09-847-946A-145	Sequence 145, App
39	31	86.1	13	11	US-09-847-946A-148	Sequence 148, App
40	31	86.1	17	11	US-09-847-946A-141	Sequence 141, App
41	31	86.1	17	11	US-09-847-946A-142	Sequence 142, App
42	31	86.1	17	11	US-09-847-946A-146	Sequence 146, App
43	31	86.1	17	11	US-09-847-946A-147	Sequence 147, App
44	31	86.1	18	11	US-09-847-946A-131	Sequence 131, App
45	31	86.1	18	11	US-09-847-946A-135	Sequence 135, App

ALIGNMENTS

RESULT 1
US-09-847-940B-15
; Sequence 15, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-15

Query Match 100.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSYL 6
Db 1 LDWSYL 6

RESULT 2
US-09-847-946A-15
; Sequence 15, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15

Query Match 100.0%; Score 36; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDWSYL 6
Db 1 LDWSYL 6

RESULT 3
US-10-287-274-432
; Sequence 432, Application US/10287274
; Publication No. US20030181408A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Alllyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
; FILE REFERENCE: ELITRA.008DVI
; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 432
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-287-274-432

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Matches 5; Conservative 1; Mismatches 0;

QY 1 LDWSYL 6
Db 67 IDWSYL 72

RESULT 4
US-09-847-940B-14
; Sequence 14, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP

; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-14

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Best Local Similarity 83.3%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 LDWSYL 6
Db 1 LDWSYL 6

RESULT 5
US-09-847-946A-14
; Sequence 14, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
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; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-14

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Best Local Similarity 83.3%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 LDWSYL 6
Db 1 LDWSYL 6

RESULT 6
US-09-974-879-385
; Sequence 385, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: PZ02092
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683

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; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
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; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
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; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
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; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
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; PRIOR FILING DATE: 1997-11-07
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; PRIOR FILING DATE: 1997-11-17
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; PRIOR FILING DATE: 1997-11-17
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; PRIOR FILING DATE: 1997-11-17
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; ORGANISM: Homo sapiens
US-09-974-879-385

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Best Local Similarity 100.0%; Pred. No. 93;
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Db      8 LDWSY 12

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; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
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; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
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; EARLIER APPLICATION NUMBER: 60/064,987

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; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
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US-09-305-736-385

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Query Match      88.9%; Score 32; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
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Qy      1 LDWSY 5
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Db      8 LDWSY 12

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RESULT 8
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; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; CURRENT FILING DATE: 2001-03-28
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-683-385

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Query Match      88.9%; Score 32; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 LDWSY 5
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Db      8 LDWSY 12

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RESULT 9
US-10-369-493-12565
; Sequence 12565, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

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;/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
;/ FILE REFERENCE: 38-10(52052)B
;/ CURRENT APPLICATION NUMBER: US/10/369,493
;/ CURRENT FILING DATE: 2003-02-28
;/ PRIOR APPLICATION NUMBER: US 60/360,039
;/ PRIOR FILING DATE: 2002-02-21
;/ NUMBER OF SEQ ID NOS: 47374
;/ SEQ ID NO 12565
;/ LENGTH: 376
;/ TYPE: PRT
;/ ORGANISM: Aspergillus nidulans
;/ FEATURE:
;/ NAME/KEY: unsure
;/ LOCATION: (1)..(376)
;/ OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12565

Query Match 88.9%; Score 32; DB 12; Length 376;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSY 5
Db 372 LDWSY 376

RESULT 10
US-10-374-780A-1378
;/ Sequence 1378, Application US/10374780A
;/ Publication No. US20040019927A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Sherman, Bradley K
;/ APPLICANT: Riechmann, Jose Luis
;/ APPLICANT: Jiang, Cai-Zhong
;/ APPLICANT: Heard, Jacqueline E
;/ APPLICANT: Haake, Volker
;/ APPLICANT: Creelman, Robert A
;/ APPLICANT: Ratcliffe, Oliver
;/ APPLICANT: Adam, Luc J
;/ APPLICANT: Reuber, T. Lynne
;/ APPLICANT: Keddle, James
;/ APPLICANT: Broun, Pierre E
;/ APPLICANT: Pilgrim, Marsha L
;/ APPLICANT: Dubell III, Arnold T
;/ APPLICANT: Pineda, Omaira
;/ APPLICANT: Yu, Guo-Liang
;/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
;/ FILE REFERENCE: MBI-0047 CIP
;/ CURRENT APPLICATION NUMBER: US/10/374,780A
;/ CURRENT FILING DATE: 2003-02-25
;/ PRIOR APPLICATION NUMBER: 09/837,944
;/ PRIOR FILING DATE: 2001-04-18
;/ PRIOR APPLICATION NUMBER: 60/310,847
;/ PRIOR FILING DATE: 2001-08-09
;/ PRIOR APPLICATION NUMBER: 09/934,455
;/ PRIOR FILING DATE: 2001-08-22
;/ PRIOR APPLICATION NUMBER: 60/336,049
;/ PRIOR FILING DATE: 2001-11-19
;/ PRIOR APPLICATION NUMBER: 60/338,692
;/ PRIOR FILING DATE: 2001-12-11
;/ PRIOR APPLICATION NUMBER: 10/171,468
;/ PRIOR FILING DATE: 2002-06-14
;/ PRIOR APPLICATION NUMBER: 10/225,066
;/ PRIOR FILING DATE: 2002-08-09
;/ PRIOR APPLICATION NUMBER: 10/225,067
;/ PRIOR FILING DATE: 2002-08-09
;/ PRIOR APPLICATION NUMBER: 10/225,068
;/ PRIOR FILING DATE: 2002-08-09
;/ NUMBER OF SEQ ID NOS: 2906
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 1378
;/ LENGTH: 412
;/ TYPE: PRT

;/ ORGANISM: Oryza sativa
;/ FEATURE:
;/ OTHER INFORMATION: Orthologous to G1062
US-10-374-780A-1378

Query Match 88.9%; Score 32; DB 12; Length 412;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
Db 57 DWSYL 61

RESULT 11
US-10-156-761-8567
;/ Sequence 8567, Application US/10156761
;/ Publication No. US20030119018A1
;/ GENERAL INFORMATION:
;/ APPLICANT: OMURA, SATOSHI
;/ APPLICANT: IKEDA, HARUO
;/ APPLICANT: ISHIKAWA, JUN
;/ APPLICANT: HORIKAWA, HIROSHI
;/ APPLICANT: SHIBA, TADAYOSHI
;/ APPLICANT: SAKAKI, YOSHIYUKI
;/ APPLICANT: HATTORI, MASAHIRA
;/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;/ FILE REFERENCE: 249-262
;/ CURRENT APPLICATION NUMBER: US/10/156,761
;/ CURRENT FILING DATE: 2002-05-29
;/ PRIOR APPLICATION NUMBER: JP 2001-204089
;/ PRIOR FILING DATE: 2001-05-30
;/ PRIOR APPLICATION NUMBER: JP 2001-272697
;/ PRIOR FILING DATE: 2001-08-02
;/ NUMBER OF SEQ ID NOS: 15109
;/ SEQ ID NO 8567
;/ LENGTH: 445
;/ TYPE: PRT
;/ ORGANISM: Streptomyces avermitilis
US-10-156-761-8567

Query Match 88.9%; Score 32; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
Db 394 DWSYL 398

RESULT 12
US-10-369-493-267
;/ Sequence 267, Application US/10369493
;/ Publication No. US20030233675A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Cao, Yongwei
;/ APPLICANT: Hinkle, Gregory J.
;/ APPLICANT: Slater, Steven C.
;/ APPLICANT: Goldman, Barry S.
;/ APPLICANT: Chen, Xianfeng
;/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;/ FILE REFERENCE: 38-10(52052)B
;/ CURRENT APPLICATION NUMBER: US/10/369,493
;/ CURRENT FILING DATE: 2003-02-28
;/ PRIOR APPLICATION NUMBER: US 60/360,039
;/ PRIOR FILING DATE: 2002-02-21
;/ NUMBER OF SEQ ID NOS: 47374
;/ SEQ ID NO 267
;/ LENGTH: 525
;/ TYPE: PRT
;/ ORGANISM: Xenorhabdus nematophilus
US-10-369-493-267

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Query Match      88.9%; Score 32; DB 12; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSYL 6
      |||||
Db      87 DWSYL 91

RESULT 13
US-10-369-493-913
; Sequence 913, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 913
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Archaeoglobus fulgidus
US-10-369-493-913

Query Match      88.9%; Score 32; DB 12; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSYL 6
      |||||
Db      292 DWSYL 296

RESULT 14
US-10-369-493-13768
; Sequence 13768, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13768
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13768

Query Match      88.9%; Score 32; DB 12; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSYL 6
      |||||
```

```
Db      117 DWSYL 121

RESULT 15
US-09-815-242-12101
; Sequence 12101, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12101
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12101

Query Match      88.9%; Score 32; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSYL 6
      |||||
Db      117 DWSYL 121

Search completed: February 18, 2004, 15:42:00
Job time : 16.7529 secs
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OM protein - protein search, using sw model

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Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LWSYL 6

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	23	Mutated IKKbeta NE
2	36	100.0	6	23	NBD mutant peptide
3	36	100.0	6	24	Human NEMO binding
4	36	100.0	756	23	Human IKKbeta muta
5	34	94.4	98	22	E. coli growth and
6	33	91.7	193	22	Micromonospora eve
7	32	88.9	6	23	Mutated IKKbeta NE
8	32	88.9	6	23	NBD mutant peptide
9	32	88.9	6	24	Human NEMO binding

10	32	88.9	320	22	ABG13516	Novel human diagno
11	32	88.9	320	22	ABG27654	Novel human diagno
12	32	88.9	393	19	AAV11025	H. pylori ORF 02ge
13	32	88.9	393	23	AAU76667	Helicobacter pylor
14	32	88.9	455	22	AA82777	S. epidermidis ope
15	32	88.9	462	23	ABP39455	Staphylococcus epi
16	32	88.9	465	22	ABG18718	Novel human diagno
17	32	88.9	561	22	AAU36508	Pseudomonas aerugi
18	32	88.9	562	23	ABP73802	Candida albicans e
19	32	88.9	706	18	AAW22231	S. pombe origin of
20	32	88.9	707	18	AAW14137	Schizosaccharomyce
21	32	88.9	708	22	ABBS8681	Drosophila melanog
22	32	88.9	737	23	ABP65156	Hypoxia-regulated
23	32	88.9	756	23	ABB77300	Human IKKbeta muta
24	32	88.9	793	22	ABB68973	Drosophila melanog
25	32	88.9	911	17	AA929508	A. oryzae beta-gal
26	32	88.9	937	22	ABG66195	Drosophila melanog
27	32	88.9	952	22	ABG23297	Novel human diagno
28	32	88.9	1005	18	AAW11238	Beta-galactosidase
29	32	88.9	1317	22	ABG18723	Novel human diagno
30	32	88.9	1483	21	AAG48640	Arabidopsis thalia
31	32	88.9	1493	21	AAG48639	Arabidopsis thalia
32	32	88.9	1495	21	AAG30440	Arabidopsis thalia
33	32	88.9	1505	21	AAG30439	Arabidopsis thalia
34	32	88.9	1544	21	AAG48638	Arabidopsis thalia
35	32	88.9	1556	21	AAG30438	Arabidopsis thalia
36	32	88.9	1675	22	AAU00418	Mouse cell regulat
37	32	88.9	1689	22	AAU00415	Mouse cell regulat
38	32	88.9	1894	22	ABG18725	Novel human diagno
39	32	88.9	5464	22	ABG11810	Novel human diagno
40	31	86.1	6	23	ABB08725	IKKbeta NEMO bindi
41	31	86.1	6	23	AAW48530	Anti-inflammatory
42	31	86.1	6	23	AAW48530	NBD mutant peptide
43	31	86.1	6	24	ABU08418	Human NEMO binding
44	31	86.1	7	23	AAW48534	Anti-inflammatory
45	31	86.1	8	23	AAW48527	Anti-inflammatory

ALIGNMENTS

RESULT 1

ABB08737
ID ABB08737 standard; peptide; 6 AA.
XX
AC ABB08737;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.
XX

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX autoimmune disease; transplant rejection; osteoporosis; cancer;
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
XX osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;
XX antiarteriosclerotic; virucide; antiaesthetic; antiallergic;
XX dermatological; antibacterial; antipsoriatic; antirheumatic;
XX antiarthritic; osteopathic; antiulcer; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers
XX Misc-difference 5 /note= "Wildtype Trp substituted by Tyr"

XX WO200183547-A2.

XX 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 Db 1 LDWSYL 6
 |||||
 |||||
 RESULT 2
 ID AAM48520
 XX AAM48520 standard; Peptide; 6 AA.
 AC AAM48520;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 15.

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 PA (PRAE-) PRAECIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX Novel antinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 PT
 XX Example 6; Page 48; 88pp; English.
 PS
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-NM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 Db 1 LDWSYL 6
 |||||
 |||||
 RESULT 3
 ID ABU08430
 ABU08430 standard; peptide; 6 AA.

XX AC ABU08430;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #13.
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IKKalpha kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN US2002156000-A1.
 XX PD 24-OCT-2002.
 XX PF 02-MAY-2001; 2001US-0847940.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (MAYW/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX PI May MJ, Ghosh S;
 XX PI WPI; 2003-209142/20.
 XX DR N-PSDB; ABX94271, ABX94272.
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX PS Claim 22; Page 17; 47pp; English.
 XX CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDMSYL 6
 |||||
 Db 1 LDMSYL 6
 RESULT 4
 ABB77301
 ID ABB77301 standard; protein; 756 AA.

XX AC ABB77301;
 XX DT 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant W741Y.
 XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nontropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200183547-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US40654.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (UYVA) UNIV YALE.
 XX PI May MJ, Ghosh S;
 XX PI WPI; 2002-179350/23.
 XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX PS Example 11; Page -; 82pp; English.
 XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for

CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. 014920 (AB077294).
 XX
 SQ Sequence 756 AA;

Query Match 100.0%; Score 36; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 |||||
 Db 737 LDMSYL 742

RESULT 5
 AAG98962
 ID AAG98962 standard; Protein; 98 AA.

XX AAG98962;

AC AAG98962;

DT 26-SEP-2001 (first entry)

XX E. coli growth and proliferation related protein sequence SEQ ID NO:432.

DE Escherichia coli; growth; proliferation; microbial; antimicrobial;

KW bacterial infection; microorganism.

XX Escherichia coli.

XX WO200134810-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30950.

XX 09-NOV-1999; 99US-0164415.

XX (ELIT-) ELITRA PHARM INC.

XX Forsyth RA, Ohlsen K, Zyskind J;

XX WPI: 2001-335933/35.

XX N-PSDB; AAH84633.

PT Novel nucleic acids that inhibit Escherichia coli proliferation, useful
 PT for screening for homologous genes and for designing expression vectors
 PT -

PS Claim 19; Page 490-491; 522pp; English.

XX AAH84373 to AAH84499 represent Escherichia coli growth and proliferation
 CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli
 CC growth and proliferation related proteins given in AAG99078 and AAG98830
 CC to AAG98999. (I) can be used as potential targets for the generation of
 CC new antimicrobial agents, and for identification of compounds which
 CC interact with the gene products of (I). In addition the expression of
 CC (I) and the purification of the proteins, the purified proteins or other
 CC used to generate reagents and screen small molecule libraries or other
 CC candidate compound libraries for compounds that can be further developed
 CC to yield novel antimicrobial compounds. In addition, nucleic acid probes
 CC complementary to (I) that are specific for particular species of
 CC microorganisms can be used to identify particular microorganism species
 CC in clinical specimens, therefore, providing a rapid and dependable
 CC method by which to identify the causative agents of a bacterial
 CC infection. Also, antibodies generated against proteins translated from

CC mRNA transcribed from proliferation-required sequences can also be used
 CC to screen for specific microorganisms that produce such proteins in a
 CC species-specific manner. AAH84371 and AAH84670 represent sequencing
 CC primers used in the isolation of E. coli growth and proliferation
 CC related sequence, which are used in an example from the present
 CC invention.
 XX

SQ Sequence 98 AA;

Query Match 94.4%; Score 34; DB 22; Length 98;
 Best Local Similarity 83.3%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6
 :|||||
 Db 67 LDMSYL 72

RESULT 6

AAU04899
 ID AAU04899 standard; Protein; 193 AA.

XX AAU04899;

XX 26-SEP-2001 (first entry)

XX Micromonospora everninomicin biosynthetic enzyme evrMR2.

DE Everninomicin; antibiotic; bottle-neck gene; orthomycin;

KW fermentation; resistance mechanism gene; evrMR2.

XX Micromonospora carbonacea var. africana.

XX WO200151639-A2.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US01187.

XX 12-JAN-2000; 2000US-0175751.

XX (SCHE) SCHERING CORP.

XX Hosted TJ, Horan AC, Wang TX;

XX WPI: 2001-442147/47.

XX N-PSDB; AAS08693.

PT New nucleic acid molecules encoding everninomicin pathway gene
 PT products, useful for improving yields of everninomicin, to produce new
 PT everninomicin and as probes to identify homologous sequences -

XX Claim 19; Fig 11; 109pp; English.

XX The sequence is a protein, evrMR2, encoded by a resistance mechanism
 CC gene. The protein comprises one of 98 enzymes of the
 CC everninomicin antibiotic biosynthetic pathway. A vector comprising a
 CC M. carbonacea everninomicin biosynthetic pathway resistance gene
 CC product is useful for selecting for a transfected or transformed host
 CC cell. An integrative version of the vector is useful for introducing a
 CC everninomicin pathway gene (a bottle-neck gene) into an actinomycete of
 CC the genus Micromonospora. The DNA encoding the biosynthetic proteins is
 CC useful for synthesising novel everninomicin-related compounds, arising
 CC from modifications of the DNA sequence designed to change glycosyl and
 CC modified orsellinic acid groups contained in everninomicin, for
 CC expressing functional or mutant everninomicin biosynthetic enzyme for
 CC evaluation, diagnosis and preferably biosynthesis of everninomicin or
 CC other secondary metabolic products, improving the yield of everninomicins
 CC and to produce novel everninomicins and also as a hybridisation probe to
 CC identify homologous sequences. The encoded polypeptides are useful for
 CC combinatorial biosynthesis to generate libraries of orthomycins, e.g.
 CC everninomicin analogues/homologues and drug discovery. The
 CC DNA encoding the integrase allows for increasing a given gene dosage. The

CC integrative vector can be used to permanently integrate copies of a
 CC heterologous gene of choice into chromosomes of different hosts and to
 CC integrate genes which increase the yield of known products or to generate
 CC novel products such as hybrid antibiotics or other novel secondary
 CC metabolites. The vector can also be used to integrate antibiotic
 CC resistance genes in order to carry out bioconversions with compounds to
 CC which the strain is normally sensitive and is thus useful in fermentation
 CC processes involving e.g. Streptomyces antibioticus.

XX Sequence 193 AA;

Query Match 91.7%; Score 33; DB 22; Length 193;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 DB 139 LDWAYL 144
 |||:|

RESULT 7

ABB08736
 ID ABB08736 standard; peptide; 6 AA.

AC ABB08736;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antitumor; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 5 /note= "Wildtype Trp substituted by Phe"

FT WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

PA (UYA) UNIV YALE.

XX May WJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -

PS Claim 23; Page 45; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain

CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spindylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.

XX Sequence 6 AA;

Query Match 88.9%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
 DB 1 LDWSFL 6
 |||:|

RESULT 8

AAW48519

ID AAW48519 standard; Peptide; 6 AA.

XX AAW48519;

XX 20-MAR-2002 (first entry)

DE NBD mutant peptide SEQ ID NO 14.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRACIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Example 6; Page 48; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48620-AA48645), comprising a membrane translocation domain
 CC (AAM48620-AA48627 or AAM48646-AA48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC brucellosis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 88.9%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. NO. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 1 LDWSFL 6
 RESULT 9
 ABU08429
 ID ABU08429 standard; peptide; 6 AA.
 AC
 XX ABU08429;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 XX Human NEMO binding site (NBD) mutant peptide #12.
 DE
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cystostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX US2002156000-A1.
 XX

PD 24-OCT-2002.
 XX
 XX 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 XX May MJ, Ghosh S;
 PI
 XX WPI; 2003-209142/20.
 DR
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 88.9%; Score 32; DB 24; Length 6;
 Best Local Similarity 83.3%; Pred. NO. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 1 LDWSFL 6
 RESULT 10
 ABG13516
 ID ABG13516 standard; Protein; 320 AA.
 XX
 XX ABG13516;
 XX
 XX 18-FEB-2002 (first entry)
 DT
 XX Novel human diagnostic protein #13507.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US08631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA

XX PI Drmanac RT, Liu C, Tang YT;
 XX XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS77703.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 43875; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 320 AA;
 Query Match 88.9%; Score 32; DB 22; Length 320;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSYL 6
 Db 240 DWSYL 244
 |||||
 RESULT 11
 ABG27654
 ID ABG27654 standard; Protein; 320 AA.
 AC
 AC ABG27654;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #27645.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.
 DR N-PSDB; AAS91841.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 58013; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 320 AA;
 Query Match 88.9%; Score 32; DB 22; Length 320;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSYL 6
 Db 240 DWSYL 244
 |||||
 RESULT 12
 AAY11025
 ID AAY11025 standard; Protein; 393 AA.
 XX
 AC AAY11025;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE H. pylori ORF 02ge41622_14875000_c2_65 outer membrane protein.
 XX
 KW Vaccine; probe; diagnostic; ORF; cell envelope protein;
 KW secreted protein; cytoplasmic protein; cellular protein.
 XX
 OS Helicobacter pylori.
 XX
 PN WO9824475-A1.
 XX
 PD 11-JUN-1998.
 XX
 PF 05-DEC-1997; 97WO-US22104.
 XX
 PR 14-JUL-1997; 97US-0891928.
 PR 05-DEC-1996; 96US-0759625.
 PR 25-MAR-1997; 97US-0823745.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Alm RA, Castriotta LM, Doig PC, Kabok Z, Smith D;
 XX

DR WPI; 1998-333051/29.
 DR N-PSDB; AAH30554.
 XX
 PT New isolated Helicobacter pylori nucleic acids - used to develop
 PT products for the diagnosis, prevention and treatment of infection by
 PT H. pylori and other Helicobacter species
 XX
 PS Claims 37, 41; Page 187-188; 339pp; English.
 XX
 CC Recombinant or substantially pure preparations of H. pylori polypeptides
 CC are disclosed, together with the nucleic acids encoding them. In all,
 CC 97 ORFs are shown. The proteins are variously cell envelope proteins,
 CC cytoplasmic proteins, secreted proteins or other cellular proteins.
 CC Vaccines containing the nucleic acids or proteins are claimed, as are
 CC probes containing at least 8 nucleotides from the nucleic acid
 CC sequences. The vaccines are useful for treating or reducing the risk of
 CC H. pylori infections, and the probes can be used diagnostically for
 CC detecting the presence of Helicobacter in a sample. The products are
 CC also of use in screening for compounds having the ability to interfere
 CC with the H. pylori life cycle or to inhibit H. pylori infection.
 XX
 SQ Sequence 393 AA;
 Query Match 88.9%; Score 32; DB 19; Length 393;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSYL 6
 DB 284 DMSYL 288
 |||||
 RESULT 13
 AAU76667
 ID AAU76667 standard; Protein; 393 AA.
 AC
 XX AAU76667;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Helicobacter pylori LPS biosynthesis enzyme HP1031 from strain J99.
 XX
 DE LPS; lipopolysaccharide; biosynthesis enzyme; HP1031; strain J99;
 KW antibiotic; vaccine; human self epitope.
 XX
 OS Helicobacter pylori.
 XX
 XX WO200207763-A2.
 XX
 XX 31-JAN-2002.
 XX
 PF 12-JUL-2001; 2001WO-1B01536.
 XX
 PR 12-JUL-2000; 2000GB-0017149.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Del Giudice G, Rappuoli R;
 XX
 DR WPI; 2002-217026/27.
 XX
 XX Novel Helicobacter pylori useful for prophylaxis and treatment of
 PT Helicobacter pylori infection, comprises mutation that prevents
 PT synthesis of auto-reactive lipopolysaccharide -
 XX
 PS Disclosure; Fig 1; 23pp; English.
 XX
 CC The present invention relates to a new Helicobacter pylori bacterium
 CC having a mutation that affects lipopolysaccharide (LPS) biosynthesis,
 CC where either LPS is not expressed or LPS which is expressed does not
 CC induce antibodies which cross-react with human self epitopes. The
 CC invention is useful for treating or preventing, and in the manufacture
 CC of a vaccine for treatment or prophylaxis of Helicobacter pylori

CC infection. The vaccine does not induce antibodies which cross-react
 CC with human self epitopes. The present amino acid sequence represents
 CC the Helicobacter pylori LPS biosynthesis enzyme HP1031 that was
 CC isolated from strain J99 and was used in the methods of the invention.
 XX
 SQ Sequence 393 AA;
 Query Match 88.9%; Score 32; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSYL 6
 DB 284 DMSYL 288
 |||||
 RESULT 14
 AAG82777
 ID AAG82777 standard; Protein; 455 AA.
 AC
 XX AAG82777;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:2648.
 XX
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW vaccination; endocarditis.
 XX
 OS Staphylococcus epidermidis.
 XX
 XX WO200134809-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 09-NOV-2000; 2000WO-US30782.
 XX
 PR 09-NOV-1999; 99US-0164258.
 XX
 XX* (GLAXO) GLAXO GROUP LTD.
 PA
 XX
 PI Kimmerly WJ;
 XX
 DR WPI; 2001-316495/33.
 DR N-PSDB; AAH53627.
 XX
 XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis -
 PT
 PS Claim 18; Page 694-695; 2188pp; English.
 XX
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
 CC (I) and (II) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC S. epidermidis polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
 CC polynucleotide sequences from the present invention. AAH55091 to
 CC AAH55098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 XX
 SQ Sequence 455 AA;

Query Match 88.9%; Score 32; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSY 5
 Db 152 LDWSY 156

RESULT 15

ABP39455
 ID ABP39455 standard; Protein; 462 AA.

XX AC ABP39455;
 XX 24-JUL-2002 (first entry)
 XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4300.
 XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy.
 XX Staphylococcus epidermidis.

OS US6380370-B1.
 XX PN 30-APR-2002.
 XX PF 13-AUG-1998; 98US-0134001.
 XX PR 14-AUG-1997; 97US-055779P.
 XX PR 08-NOV-1997; 97US-064964P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX Doucette-Stamm LA, Bush D;
 XX WPI; 2002-381255/41.
 XX N-PSDB; ABN92000.
 XX Novel isolated nucleic acid encoding a Staphylococcus epidermidis
 PT polypeptide, useful for diagnosing and treating bacterial infections -
 XX Disclosure; SEQ ID 4300; 267pp; English.

XX AN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP3124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences
 CC can also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life
 CC cycle or inhibit S. epidermidis infection.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site.

SQ Sequence 462 AA;

Query Match 88.9%; Score 32; DB 23; Length 462;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSY 5
 Db 159 LDWSY 163

Search completed: February 18, 2004, 14:26:25
 Job time : 22.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-14
Perfect score: 35
Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_23.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_nhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	136	16	P72919 synchocyst
2	35	100.0	362	5	O44634 caenorhabdi
3	35	100.0	573	16	Q8YXB1 anabaena sp
4	35	100.0	2621	10	Q9LMZ3 arabidopsis
5	35	100.0	2658	10	Q9SGE4 arabidopsis
6	33	94.3	208	16	Q8E014 streptococc
7	33	94.3	216	16	Q8E559 streptococc
8	33	94.3	556	16	Q8DC15 vibrio vuln
9	33	94.3	608	5	Q9VXS9 drosophila
10	33	94.3	732	5	O61565 crassostrea
11	33	94.3	962	10	Q9SVS7 arabidopsis
12	32	91.4	176	5	O44486 caenorhabdi
13	32	91.4	203	16	Q98GA7 rhizobium l
14	32	91.4	203	16	Q8UDW9 agrobacteri
15	32	91.4	284	2	O86850 streptomyce
16	32	91.4	284	16	Q9RKS7 streptomyce

17	32	91.4	339	16	Q9CE52 lactococcus
18	32	91.4	377	16	Q924X8 streptomyce
19	32	91.4	556	16	Q55814 synchocyst
20	32	91.4	744	4	Q8N261 homo sapien
21	32	91.4	870	4	Q8N639 homo sapien
22	32	91.4	927	16	Q928S2 listeria in
23	32	91.4	927	16	Q8Y4S2 listeria mo
24	32	91.4	939	16	Q8YQR3 anabaena sp
25	32	91.4	1466	3	O42930 schizosacch
26	31	88.6	124	11	Q9D247 mus musculu
27	31	88.6	131	12	Q9QPQ1 tomato leaf
28	31	88.6	134	12	Q8QY77 tomato leaf
29	31	88.6	134	12	Q88558 tomato leaf
30	31	88.6	134	12	Q8QL10 tobacco cur
31	31	88.6	134	12	O56991 papaya leaf
32	31	88.6	134	12	O72708 cotton leaf
33	31	88.6	134	12	Q91MF1 pepper leaf
34	31	88.6	134	12	Q99DR2 chilli leaf
35	31	88.6	134	12	Q8V019 cotton leaf
36	31	88.6	134	12	Q993Y9 cotton leaf
37	31	88.6	134	12	Q98742 tomato leaf
38	31	88.6	134	12	Q8JZ16 tomato leaf
39	31	88.6	134	12	Q8JLL0 cotton leaf
40	31	88.6	134	12	O72711 cotton leaf
41	31	88.6	134	12	Q91BQ2 ageratum ye
42	31	88.6	134	12	Q8V012 hollyhock l
43	31	88.6	134	12	O9IGX4 tobacco gem
44	31	88.6	134	12	Q9IN49 cotton leaf
45	31	88.6	134	12	Q9QDE5 tomato leaf

ALIGNMENTS

RESULT 1

P72919 ID P72919 PRELIMINARY; PRT; 136 AA.
AC P72919;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein slr1082.
GN SLR1082.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyama M., Saezamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synchocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90901; BAA16936.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match 100.0%; Score 35; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 42 LDWSFL 47

RESULT 2

O44634

ID O44634 PRELIMINARY; PRT; 362 AA.
AC O44634;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 42.3 kDa protein.
GN F16B4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Davidson S., Wohlmann P., Bauer C., O'Neal D.;
RT "The sequence of C. elegans cosmid F16B4.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039048; AAB94233.1; -
DR WormPep; F16B4.2; CEI7012.
DR InterPro; IPR001810; F-box.1.
DR Pfam; PF00646; F-box.1.
KW Hypothetical protein.
SQ SEQUENCE 362 AA; 42255 MW; 33D99EF0FD114006 CRC64;
Query Match 100.0%; Score 35; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSFL 6
Db 26 LDWSFL 31
RESULT 3
Q8YXB1 PRELIMINARY; PRT; 573 AA.
AC Q8YXB1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sulfate permease family protein.
GN ALL1304.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
DR EMBL; AF003585; BAB73261.1; -
DR InterPro; IPR002645; STAS.
DR InterPro; IPR001902; Sulph_transp.

DR Pfam; PF01740; STAS; 1.
DR Pfam; PF00916; Sulfate_transp; 1.
DR PROSITE; PS50801; STAS; 1.
KW Complete proteome.
SQ SEQUENCE 573 AA; 60239 MW; F2D1C2F66A8E36CC CRC64;
Query Match 100.0%; Score 35; DB 16; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSFL 6
Db 357 LDWSFL 362
RESULT 4
Q9LMZ3 PRELIMINARY; PRT; 2621 AA.
AC Q9LMZ3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE T6D22.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome
RT I.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC026875; AAF79832.1; -
DR InterPro; IPR006153; Na_Hporter.
DR Pfam; PF00999; Na_H_Exchange; 1.
SQ SEQUENCE 2621 AA; 297067 MW; E3534E176F2370A4 CRC64;
Query Match 100.0%; Score 35; DB 10; Length 2621;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSFL 6
Db 2184 LDWSFL 2189
RESULT 5

Q9SGE4 Q9SGE4 PRELIMINARY; PRT; 2658 AA.
 AC Q9SGE4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE T23G18.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vayenberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T23G18 from chromosome
 I.",
 RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC011438; AAF18257.1; -.
 DR InterPro; IPR006153; Na.H.porter.
 DR Pfam; PF00999; Na.H.Exchange; 1.
 SQ SEQUENCE 2658 AA; 301830 MW; 77ECF93667B4293F CRC64;
 Query Match 100.0%; Score 35; DB 10; Length 2658;
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 DB 2221 LDWSFL 2226
 RESULT 6
 Q8E014 PRELIMINARY; PRT; 208 AA.
 AC Q8E014;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Riboflavin synthase, alpha subunit.
 GN RIBE OR SAG0747.
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=216466;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=12200547;
 RA Tettelin H., Masiogni V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J.J., Brinkac L.M., Daugherty S.C.,
 RA Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.B., Gill J., Scariselli M., Moxa M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014225; AAM99634.1; -.
 DR TIGR; SAG0747; -.
 KW Complete proteome.
 SQ SEQUENCE 208 AA; 22666 MW; 4C25AB59FC1EE601 CRC64;
 Query Match 94.3%; Score 33; DB 16; Length 208;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 DB 198 MDWSFL 203
 RESULT 7
 Q8E659 PRELIMINARY; PRT; 216 AA.
 AC Q8E659;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN GBS0768.
 OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=216495;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NEM316 / Serotype III;
 RX MEDLINE=2242508; PubMed=12354221;
 RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
 RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513(2002).
 DR EMBL; AL766847; CAD46412.1; -.
 DR Sagaliss; gbs0768; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 216 AA; 23587 MW; E55556DSF751CEEFC CRC64;
 Query Match 94.3%; Score 33; DB 16; Length 216;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 DB 206 MDWSFL 211
 RESULT 8
 Q8DC15 PRELIMINARY; PRT; 556 AA.
 AC Q8DC15;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Sulfate permease and.
 GN VW11638.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OC NCBI_TaxID=672;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016802; AB010056.1; -.
 KW Complete proteome.
 SQ SEQUENCE 556 AA; 59064 MW; 1EC2AC082F0602DA CRC64;
 Query Match 94.3%; Score 33; DB 16; Length 556;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QV 1 LDWSFL 6
Db 356 LDWSFI 361
|||||:

RESULT 9
Q9VXS9 PRELIMINARY; PRT; 608 AA.
AC Q9VXS9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CG9220 protein.
GN CG9220.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabriellista A.E., Ferraz C., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Anantides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Patel S., Pfeiffer B.,

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RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.D., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003499; AAF48479.2; -
DR FlyBase; FBgn0030662; CG9220.
SQ SEQUENCE 608 AA; 70423 MW; 9278ADD434745CA CRC64;

Query Match 94.3%; Score 33; DB 5; Length 608;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 151 LDWSFI 156
|||||:

RESULT 10
O61565 PRELIMINARY; PRT; 732 AA.
ID O61565;
AC O61565;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE I-kappa-B kinase.
GN IKK.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99332074; PubMed=10405163;
RA Escoubas J.M., Briant L., Montagnani C., Hez S., Devaux C., Roch P.;
RT "Oyster IKK-like protein shares structural and functional properties
RT with its mammalian homologues.";
RL FEBS Lett. 453:293-298(1999).
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF051320; AAC05683.1; -
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot Kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 732 AA; 84215 MW; 871EE8D1CA3E39AF CRC64;

Query Match 94.3%; Score 33; DB 5; Length 732;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDMSFL 6
DB      719 MDMSFL 724

RESULT 11
Q9SVS7 ID Q9SVS7 PRELIMINARY; PRT; 962 AA.
AC Q9SVS7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 108.9 kDa protein.
GN F17L22.160 OR A74G21700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.-J., Voet M., Robben J.,
RA Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Van Der Schueren J., Vandenbussche F., Chuang Y.J., Braeken M.,
RA Robben J., Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035527; CAB36814.1; -.
DR EMBL; AL161555; CAB81277.1; -.
DR InterPro; IPR000269; CUNH_oxidase.
DR PROSITE; PS01164; COPPER_AMINE_OXID_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 962 AA; 108894 MW; 5F48A946474B8927 CRC64;

Query Match 94.3%; Score 33; DB 10; Length 962;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSFL 6
DB      889 LDMSFI 894

RESULT 12
O44486 ID O44486 PRELIMINARY; PRT; 176 AA.
AC O44486
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 20.6 kDa protein.
GN F42A6.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99089613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for

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RT Investigating biology, The C. elegans Sequencing Consortium.;
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Scheet P., Andrews S.;
RT "The sequence of C. elegans cosmid F42A6.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038613; AAB92050.1; -.
DR WormPep; F42A6.5; CE17057.
DR InterPro; IPR001357; BRCT.
DR Pfam; PF00533; BRCT; 1.
DR SMART; SM00292; BRCT; 1.
DR PROSITE; PS01172; BRCT; 1.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 20612 MW; 1F8E5E23AF3E25BD CRC64;

Query Match 91.4%; Score 32; DB 5; Length 176;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSFL 6
DB      37 LDWNFL 42

RESULT 13
Q98GA7 ID Q98GA7 PRELIMINARY; PRT; 203 AA.
AC Q98GA7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein ml13416.
GN ML13416.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res 7:331-338(2000).
DR EMBL; AF003001; BAB50309.1; -.
DR InterPro; IPR000534; Semialdh_dh.
DR Pfam; PF01118; Semialdehyde_dh; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 203 AA; 21716 MW; FC61A9883F2E3BEF CRC64;

Query Match 91.4%; Score 32; DB 16; Length 203;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSFL 6
DB      140 LDWTFLL 145

RESULT 14

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Q8UDW9
ID Q8UDW9 PRELIMINARY; PRT; 203 AA.
AC Q8UDW9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein Atu1999.
GN Atu1999 OR AGR C 3633.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA William C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
DR EMBL; AB009151; AAL42992.1; -.
DR EMBL; AB008117; AAK87755.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 203 AA; 21846 MW; D5BF6AC4E3C6B7CB CRC64;

Query Match 91.4%; Score 32; DB 16; Length 203;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 140 LDWTF 145
|||:|

RESULT 15
O86850 PRELIMINARY; PRT; 284 AA.
AC O86850;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 31.0 kDa protein.
GN ORFA.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M145;
RA Takano E., Chakraborty R., Nihira T., Yamada Y., Bibb M.;
RT "Characterisation of scbR, and scbA genes involved in gamma-
RT butyrolactone binding and synthesis in Streptomyces coelicolor."

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RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ007731; CAA07626.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 30969 MW; 38DE00712A09BE7D CRC64;

Query Match 91.4%; Score 32; DB 2; Length 284;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 125 LDWTF 130
|||:|

Search completed: February 18, 2004, 14:35:55
JOB time : 18.3684 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-14
Perfect score: 35
Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	35	100.0	136	2 S74785	hypothetical prote
2	35	100.0	362	2 T32669	hypothetical prote
3	35	100.0	573	2 AE1969	sulfate permease f
4	35	100.0	2658	2 A86216	protein T23G18.2 (
5	33	94.3	962	2 T05845	hypothetical prote
6	32	91.4	176	2 T32618	hypothetical prote
7	32	91.4	203	2 AB2822	conserved hypotet
8	32	91.4	203	2 B97600	hypothetical prote
9	32	91.4	339	2 C86874	ABC transporter pe
10	32	91.4	377	2 T36246	probable glycolate
11	32	91.4	404	2 A64151	hypothetical prote
12	32	91.4	556	2 S76624	integral membrane
13	32	91.4	927	2 AG1739	transmembrane prot
14	32	91.4	927	2 AH1369	transmembrane prot
15	32	91.4	939	2 AE2275	hypothetical prote
16	32	91.4	1466	2 T39557	vacuolar protein s
17	31	88.6	21	2 A60420	lens intrinsic mem
18	31	88.6	134	2 S59886	C2 protein - tomat
19	31	88.6	135	1 QOCV04	AL2 protein - toma
20	31	88.6	135	2 S07533	hypothetical prote
21	31	88.6	204	2 AB0188	phosphoribosyl-ATP
22	31	88.6	225	2 T17795	hypothetical prote
23	31	88.6	242	2 B96571	hypothetical prote
24	31	88.6	264	2 S51829	alpha-amylase inhi
25	31	88.6	266	2 B84848	hypothetical prote
26	31	88.6	350	2 G29800	dibenzothioephene d
27	31	88.6	350	2 G98302	thermophilic desul
28	31	88.6	355	2 A12867	endo-1,4-beta-xyla
29	31	88.6	356	1 A42053	gap junction prote

30	31	88.6	357	2 A49024	connexin40 - dog
31	31	88.6	358	2 S23111	connexin 40 - mous
32	31	88.6	358	2 I38429	connexin40 - human
33	31	88.6	365	2 E97644	endo-1,4-beta-xyla
34	31	88.6	369	2 B37819	connexin-42 - chic
35	31	88.6	383	2 T38772	protein phosphatas
36	31	88.6	400	2 T11921	NADH2 dehydrogenas
37	31	88.6	400	2 I50219	connexin 45.6 - ch
38	31	88.6	402	2 I46053	connexin44 - bovin
39	31	88.6	416	2 S25764	connexin 46 - rat
40	31	88.6	432	2 I39176	intrinsic membrane
41	31	88.6	440	2 I49624	gap junction prote
42	31	88.6	510	2 A45338	connexin-56 - chic
43	31	88.6	569	2 T43531	probable potassium
44	31	88.6	570	2 H87368	copper-binding pro
45	31	88.6	575	2 D84668	hypothetical prote

ALIGNMENTS

RESULT 1

S74785

hypothetical protein slr1082 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C:Accession: S74785

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74785

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAAL6936.1; PID:g16520 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: *Synechocystis* hypothetical protein slr0489

Query Match 100.0%; Score 35; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
Db 42 LDWSFL 47

RESULT 2

T32669

hypothetical protein F16B4.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T32669

R;Davidson, S.; Wohlmann, P.; Bauer, C.; O'Neal, D.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of *C. elegans* cosmid F16B4.

A:Reference number: Z21208

A:Accession: T32669

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-362 <DAV>

A:Cross-references: EMBL:AF039048; PIDN:AA894233.1; GSPDB:GN00023; CESP:F16B4.2

A:Experimental source: strain Bristol N2; clone F16B4

C:Genetics:

A:Gene: CESP:F16B4.2

A:Map position: 5

A:Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 100.0%; Score 35; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
DB 26 LDWSFL 31

RESULT 3
AE1969
sulfate permease family protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1969
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073261.1; PID:G17130651; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1304
C:Superfamily: integral membrane protein HP0228

Query Match 100.0%; Score 35; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
DB 357 LDWSFL 362

RESULT 4
A86216
protein T23G18.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana [mouse-ear cress]
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A86216
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huiziar, L. Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86216
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2658 <STO>
A:Cross-references: GB:AE005172; NID:G6579214; PIDN:AAF18257.1; GSPDB:GN00141
C:Genetics:
A:Gene: T23G18.2
A:Map position: 1

Query Match 100.0%; Score 35; DB 2; Length 2658;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
DB 2221 LDWSFL 2226

RESULT 5
T05845
hypothetical protein F17L22.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 24-Nov-1999
C:Accession: T05845
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15454
A:Accession: T05845
A:Molecule type: DNA
A:Residues: 1-962 <BEV>
A:Cross-references: EMBL:AL035527
A:Experimental source: cultivar Columbia; BAC clone F17L22
C:Genetics:
A:Map position: 4
A:Note: F17L22.160
C:Superfamily: Arabidopsis thaliana hypothetical protein F17L22.160

Query Match 94.3%; Score 33; DB 2; Length 962;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
DB 889 LDWSFL 894

RESULT 6
T32618
hypothetical protein F42A6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32618
R:Du, Z.; Scheet, P.; Andrews, S.
A:Submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F42A6.
A:Reference number: Z21201
A:Accession: T32618
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176 <DUZ>
A:Cross-references: EMBL:AF038613; PIDN:AA092050.1; GSPDB:GN000022; CESP:F42A6.5
A:Experimental source: strain Bristol N2; clone F42A6
C:Genetics:
A:Gene: CESP:F42A6.5
A:Map position: 4
A:Introns: 51/3; 109/3

Query Match 91.4%; Score 32; DB 2; Length 176;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
DB 37 LDWSFL 42

RESULT 7
AB2822
conserved hypothetical protein Atul199 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AB2822
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, P.; Roneo, P.; Zhang, S.
A:Reference number: 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AB2822
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAU42992.1; PID:g17740453; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul1999
A;Map position: circular chromosome

Query Match 91.4%; Score 32; DB 2; Length 203;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
Db 140 LDWTF 145

RESULT 8
B97600
hypothetical protein AGR_C_3633 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97600
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97600
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87755.1; PID:g15157123; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_3633
A;Map position: circular chromosome

Query Match 91.4%; Score 32; DB 2; Length 203;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
Db 140 LDWTF 145

RESULT 9
C86874
ABC transporter permease protein ec5B [imported] - Lactococcus lactis subsp. lactis (str
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86874
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86825; MUID:21235186; PMID:111337471
A;Accession: C86874
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <STO>
A;Cross-references: GB:AE005176; PID:g12725040; PIDN:AAK06093.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ec5B

Query Match 91.4%; Score 32; DB 2; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||

Db 158 LDWAF 163

RESULT 10
T36246
probable glycolate oxidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: T36246
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21602
A;Accession: T36246
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-377 <SAU>
A;Cross-references: EMBL:AL035640; PIDN:CAB38520.1; GSPDB:GN00070; SCOEDB:SC563.05
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC563.05
C;Superfamily: (S)-2-hydroxy-acid oxidase: (S)-2-hydroxy-acid oxidase homology
F;2-296/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>

Query Match 91.4%; Score 32; DB 2; Length 377;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
Db 207 LDWSFV 212

RESULT 11
A64151
hypothetical protein HI0396 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: A64151
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
G.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64151
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-404 <TIGR>
A;Cross-references: GB:U32723; GB:L42023; NID:g1573363; PIDN:AAK22055.1; PID:g1573367;
A;Note: best homolog was a hypothetical protein from Escherichia coli

Query Match 91.4%; Score 32; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||||
Db 366 LDWAF 371

RESULT 12
S76624
integral membrane protein HP0228 homolog 2 - Synechocystis sp. (strain PCC 6803)
N;Alternate names: low affinity sulfate transporter; protein sir0096
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S76624
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasu
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

8.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76624
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-556 <KAN>
A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10568.1; PID:g100173
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: integral membrane protein HP0228

Query Match 91.4%; Score 32; DB 2; Length 556;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 364 VDWSFL 369

RESULT 13
AG1739
transmembrane protein [imported] - *Listeria innocua* (strain Clp11262)
C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1739
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria* species
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1739
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-927 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97687.1; PID:g16414982; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin2460

Query Match 91.4%; Score 32; DB 2; Length 927;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 83 LDWNFL 88

RESULT 14
AH1369
transmembrane protein [imported] - *Listeria monocytogenes* (strain EGD-e)
C:Species: *Listeria monocytogenes*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH1369
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1369
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-927 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00438.1; PID:g16411848; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmc2360

Query Match 91.4%; Score 32; DB 2; Length 927;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 83 LDWNFL 88

RESULT 15
AE2275
hypothetical protein alr3756 [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A>Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE2275
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2275
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-939 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA075455.1; PID:g17132890; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3756

Query Match 91.4%; Score 32; DB 2; Length 939;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 648 LDWSYL 653

Search completed: February 18, 2004, 14:38:50
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	23	Mutated IKKbeta NE
2	35	100.0	6	23	NBD mutant peptide
3	35	100.0	6	23	Human NEMO binding
4	35	100.0	24	ABU08429	Human IKKbeta muta
5	33	94.3	59	22	Propionibacterium
6	33	94.3	208	23	Streptococcus poly
7	33	94.3	216	23	Streptococcus poly
8	33	94.3	788	22	Drosophila melanog
9	32	91.4	6	23	Mutated IKKbeta NE

10	32	91.4	6	23	AAW48520	NBD mutant peptide
11	32	91.4	6	24	ABU08430	Human NEMO binding
12	32	91.4	37	21	AAW59894	Arabidopsis thalia
13	32	91.4	37	21	AAW60632	Arabidopsis thalia
14	32	91.4	56	22	ABB03835	Human musculoskele
15	32	91.4	56	24	ABU13129	Novel human muscul
16	32	91.4	339	23	ABW55349	Lactococcus lactis
17	32	91.4	756	23	ABB77301	Human IKKbeta muta
18	32	91.4	927	23	ABB49720	Listeria monocytog
19	31	88.6	71	22	AAU63276	Propionibacterium
20	31	88.6	83	21	AAW00107	Human secreted pro
21	31	88.6	97	22	AAU55876	Propionibacterium
22	31	88.6	124	21	AAW58122	Lung cancer associ
23	31	88.6	137	22	AAW67051	Human dihydroorota
24	31	88.6	149	21	AAW233584	Arabidopsis thalia
25	31	88.6	150	21	AAW35712	CLCIV AC3 protein
26	31	88.6	157	22	AAW91029	C glutamic protei
27	31	88.6	178	21	AAW23583	Arabidopsis thalia
28	31	88.6	234	21	AAW49093	Arabidopsis thalia
29	31	88.6	234	21	AAW49116	Arabidopsis thalia
30	31	88.6	242	23	ABB91342	Herbicidally activ
31	31	88.6	259	21	AAW26244	Zea mays zmet2b me
32	31	88.6	264	21	AAW16701	Bacteriophage Dp-1
33	31	88.6	266	21	AAW11935	Arabidopsis thalia
34	31	88.6	277	15	AAW48747	G-protein coupled
35	31	88.6	277	17	AAW02719	G-protein coupled
36	31	88.6	280	21	AAW11934	Arabidopsis thalia
37	31	88.6	315	21	AAW49092	Arabidopsis thalia
38	31	88.6	315	21	AAW49115	Arabidopsis thalia
39	31	88.6	317	22	AAW69701	Bifidobacterium lo
40	31	88.6	317	23	AAW69607	Human NOV8 protein
41	31	88.6	343	21	AAW49114	Arabidopsis thalia
42	31	88.6	358	19	AAW233968	Connexin protein C
43	31	88.6	373	23	ABP65723	Bifidobacterium lo
44	31	88.6	382	17	AAW00496	Candida albicans s
45	31	88.6	417	19	AAW49009	Mouse alpha 3 conn

ALIGNMENTS

RESULT 1

ABB08736

ID ABB08736 standard; peptide; 6 AA.

XX ABB08736;

XX 14-JUN-2002 (first entry)

XX Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 5

XX /note= "Wildtype Trp substituted by Phe"

PN WO200183547-A2.

XX 08-NOV-2001.

PD 08-NOV-2001.

XX 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US40654.
 XX
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 XX
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking NF-kB mediated
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 |||||
 Db 1 LDWSFL 6
 RESULT 2
 ID AAM48519
 XX AAM48519 standard; Peptide; 6 AA.
 AC AAM48519;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 14.
 DE

XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW cytotoxic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 XX
 DR Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX Example 6; Page 48; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-NM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, The
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSFL 6
 |||||
 Db 1 LDWSFL 6
 RESULT 3
 ID ABU08429
 ID ABU08429 standard; peptide; 6 AA.

XX AC ABU08429;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #12.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IKKalpha kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US2002156000-A1.
 XX
 XX 24-OCT-2002.
 XX
 XX 02-MAY-2001; 2001US-0847940.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (MAYM/) MAY M J.
 XX (GHOS/) GHOSH S.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2003-209142/20.
 XX
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 XX Claim 22; Page 17; 47pp; English.
 XX
 XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWSFL 6
 Db | | | | |
 1 LDWSFL 6
 RESULT 4
 ID ABU08418 standard; protein; 756 AA.
 XX

AC ABB77300;
 XX
 XX 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant W741P.
 XX
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nontropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antipruritic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 741 /note= "Wildtype Trp substituted by Phe"
 FT
 XX WO200183547-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX Example 11; Page -: 82pp; English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polynyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. 014920 (AB077294).
 CC
 XX SQ Sequence 756 AA;

Query Match 100.0%; Score 35; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
 :|||||
 Db 737 LDWSFL 742

RESULT 5
 AAU58740
 ID AAU58740 standard; Protein; 59 AA.

XX AC AAU58740;

DT 13-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #19636.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX DR WPI; 2001-616774/71.

XX DR N-PSDB; AAS59594.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -

XX PS Example 1; SEQ ID No 19935; 1069pp; English.

XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 59 AA;

Query Match 94.3%; Score 33; DB 22; Length 59;
 Best Local Similarity 83.3%; Pred. No. 61;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
 :|||||
 Db 18 LDWSFL 23

RESULT 6
 ABP30274
 ID ABP30274 standard; Protein; 208 AA.

XX AC ABP30274;

DT 02-JUL-2002 (first entry)

XX DE Streptococcus polypeptide SEQ ID NO 9724.

XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW Group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS Streptococcus agalactiae.

XX PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PF 29-OCT-2001; 2001WO-GB04789.

XX PR 27-OCT-2000; 2000GB-0026333.

XX PR 24-NOV-2000; 2000GB-0028727.

XX PR 07-MAR-2001; 2001GB-0005640.

XX PA (CHIR-) CHIRON SPA.

XX PA (GENO-) INST GENOMIC RES.

XX PI Telford J, Masignani V, Margarit Ros VI, Grandi G, Fraser C;

XX PI Tettein H;

XX DR WPI; 2002-352536/38.

XX DR N-PSDB; ABN70905.

XX PS Claim 1; Page 4099; 4525pp; English.

XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX Sequence 208 AA;
 SQ Query Match 94.3%; Score 33; DB 23; Length 208;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
 Db 198 MDMSFL 203

RESULT 7
 ABP25952
 ID ABP25952 standard; Protein; 216 AA.
 XX AC
 AC ABP25952;
 XX DT
 DT 02-JUL-2002 (first entry)
 XX XX
 XX Streptococcus polypeptide SEQ ID NO 1080.
 DE Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX OS
 OS Streptococcus agalactiae.
 XX PN
 PN WO200234771-A2.
 XX PD
 PD 02-MAY-2002.
 XX PF
 PF 29-OCT-2001; 2001WO-GB04789.
 XX PR
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX XX
 XX (CHIR-) CHIRON SPA
 PA (GENO-) INST GENOMIC RES.
 XX PI
 PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Frazer C;
 PI Tettelin H;
 XX XX
 XX WPI: 2002-352536/38.
 DR N-PSDB; ABN66583.
 XX XX
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX XX
 PS Claim 1; Page 3263; 4525pp; English.
 XX XX
 XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

XX Sequence 216 AA;
 SQ Query Match 94.3%; Score 33; DB 23; Length 216;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
 Db 206 MDMSFL 211

RESULT 8
 ABB64315
 ID ABB64315 standard; Protein; 788 AA.
 XX AC
 AC ABB64315;
 XX DT
 DT 26-MAR-2002 (first entry)
 XX XX
 XX Drosophila melanogaster polypeptide SEQ ID NO 19737.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS
 OS Drosophila melanogaster.
 XX PN
 PN WO200171042-A2.
 XX PD
 PD 27-SEP-2001.
 XX PF
 PF 23-MAR-2001; 2001WO-US09231.
 XX PR
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX XX
 XX (PEKE) PE CORP NY.
 XX PI
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX XX
 XX WPI: 2001-656860/75.
 DR N-PSDB; ABL08418.
 XX XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX XX
 PS Disclosure; SEQ ID NO 19737; 21pp + Sequence Listing; English.
 XX XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX XX
 SQ Sequence 788 AA;
 XX Query Match 94.3%; Score 33; DB 22; Length 788;
 Best Local Similarity 83.3%; Pred. No. 9.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6
 Db 331 LDMSFI 336

RESULT 9
 ABB08737 ID ABB08737 standard; peptide; 6 AA.
 AC ABB08737;
 DT 14-JUN-2002 (first entry)
 XX
 DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.
 XX
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; anti-allergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5 /note= "Wildtype Trp substituted by Tyr"
 FT
 XX WO200183547-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US40654.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 XX
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 XX inflammatory disorders, osteoporosis and cancer, comprises contacting a
 XX cell with an anti-inflammatory compound comprising at least one NEMO
 XX binding domain -
 XX
 XX Claim 23; Page 45; 82pp; English.
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 XX comprises contacting a cell with an anti-inflammatory compound
 XX (ABB08725-ABB08742) comprising at least one NEMO binding domain
 XX (ABB73113). The compound has acts through selective inhibition of
 XX cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 XX with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 XX interaction results in inhibition of IKKbeta kinase activation and
 XX subsequent decreased phosphorylation of IkappaB. The compound may also
 XX act (directly or indirectly) by blocking the recruitment of leukocytes
 XX into sites of acute and chronic inflammation, by down-regulating the
 XX expression of E-selectin on leukocytes or by blocking osteoclast
 XX differentiation. The compound is useful in treating NF-kB mediated
 XX conditions, where the condition is an inflammatory disorder, an
 XX autoimmune disease, transplant rejection, osteoporosis, cancer,
 XX Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 XX telangiectasia. The inflammatory disorder is asthma, allergies,
 XX urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 XX rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 XX bowel disease, chronic obstructive pulmonary disease, vasculitis and
 XX burititis. The inflammatory disorder may also be dermatitis, eczema,
 XX psoriasis, osteoarthritis, psoriatic arthritis, lupus and

CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 91.4%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. NO. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSPL 6
 DB 1 LDWSYL 6
 RESULT 10
 AAM48520 ID AAM48520 standard; Peptide; 6 AA.
 AC AAM48520;
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 15.
 DE
 KW Antiinflammatory; antiasthmatic; cytostatic; antiapsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 XX factor kappaB activation, and for treating asthma, lung inflammation,
 XX psoriasis -
 XX
 XX Example 6; Page 48; 88pp; English.
 PS
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
 CC cytoskeletal, anti-psoriatic, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutrotropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
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 Db 1 LDWSYL 6

RESULT 11
 ABU08430
 ID ABU08430 standard; peptide; 6 AA.
 XX
 AC ABU08430;

DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #13.
 XX

KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytoskeletal; neutrotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasototropic; antirheumatic; antiarthritic; mutant; mutein.

XX Homo sapiens.
 OS Synthetic.

XX US2002156000-A1.

XX 24-OCT-2002.

XX 02-MAY-2001; 2001US-0847940.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.
 XX (GHOS/) GHOSH S.

XX May MJ, Ghosh S;

XX WPI; 2003-209142/20.

XX N-PSDB; ABX94271, ABX94272.

XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,

PT
 XX

XX psoriasis, vasculitis -
 PS Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 24; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSFL 6
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 Db 1 LDWSYL 6

RESULT 12
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 ID AAG59894 standard; Protein; 37 AA.
 XX
 AC AAG59894;

DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 7522.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridization assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 03-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

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XX 19-APR-1999; 99US-0130077.

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XX 06-MAY-1999; 99US-0132486.

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Query Match 91.4%; Score 32; DB 21; Length 37;
Best Local Similarity 83.3%; Pred. No. 57;
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Qy 1 LDWSFL 6
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Db 3 LDWAF 8

RESULT 13
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ID AAG60632 standard; Protein; 37 AA.
XX
AC AAG60632;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 78557.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match          91.4%; Score 32; DB 21; Length 37;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSEL 6
Db 3 LDWAF 8

RESULT 14
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ID ABB03835 standard; Protein; 56 AA.
XX
AC ABB03835;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polypeptide SEQ ID NO 1782.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system.
XX
OS Homo sapiens.
XX
PN WO200155367-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01338.
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PR 31-JAN-2000; 2000US-0179065.
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PR 14-AUG-2000; 2000US-0224519.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225759.
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PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 08-SEP-2000; 2000US-0231242.
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PR 12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0233065.
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PR 21-SEP-2000; 2000US-0234274.
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PR 27-SEP-2000; 2000US-0235836.
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PR 29-SEP-2000; 2000US-0236367.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 17-NOV-2000; 2000US-0249265.
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PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-451937/48.

DR N-PSDB; AAL35417.

XX Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -

XX Claim 11; SEQ ID NO 1782; 781pp + Sequence Listing; English.

XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 56 AA;

Query Match 91.4%; Score 32; DB 22; Length 56;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 27 LDWNFL 32

RESULT 15
ABU13129
ID ABU13129 standard; Protein; 56 AA.
XX
AC ABU13129;
XX
DT 26-FEB-2003 (first entry)
XX
DE Novel human musculoskeletal system antigen #749.
XX
KW Musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height;
KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
OS Homo sapiens.
XX
PN US2002147140-A1.
XX
PD 10-OCT-2002.
XX
PF 17-JAN-2001; 2001US-0764877.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218230P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
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PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.

PR 29-SEP-2000; 2000US-236368P.
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PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI WPI; 2003-128199/12.
XX N-PSDB; ABX58405.
DR
DR
XX
XX Isolated nucleic acid molecules encoding musculoskeletal system
XX associated polypeptides, useful for detecting disorders, e.g. cancer -
XX Claim 11; SEQ ID NO 1782; 321pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals
CC or humans. The nucleic acid; stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC used to enhance bone and periodontal regeneration and aid in tissue
CC transports or bone grafts; prevents skin aging due to sunburn by
CC stimulating keratinocyte growth; prevents hair loss, since FGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells, besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g. cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorhythms,
CC mammalian rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This is the amino acid sequence of a
CC novel human musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.secdta.uspto.gov/sequence.html?DocID=20020147140.
XX
XX Sequence 56 AA;
SQ

Query Match 91.4%; Score 32; DB 24; Length 56;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSFL 6
|||:
Db 27 LDWNFL 32

Search completed: February 18, 2004, 14:26:25
Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LMSAL 6

Scoring table: BLOSUM62

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Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	33	100.0	235	Q9RL11	Q9RL11 streptomyc
2	31	93.9	192	Q9PCP5	Q9PCP5 xylella fas
3	31	93.9	266	Q9EUB5	Q9EUB5 corynebacte
4	31	93.9	345	Q9VXR2	Q9VXR2 drosophila
5	31	93.9	399	Q9NE98	Q9NE98 leishmania
6	31	93.9	455	Q8PM34	Q8PM34 xanthomonas
7	31	93.9	652	Q9V553	Q9V553 drosophila
8	31	93.9	666	Q8L311	Q8L311 vitreosocill
9	31	93.9	666	Q8SX14	Q8SX14 drosophila
10	31	93.9	1006	Q07324	Q07324 saccharomyc
11	31	93.9	1040	Q94147	Q94147 saccharomyc
12	31	93.9	1394	Q08409	Q08409 saccharomyc
13	31	93.9	2297	Q54155	Q54155 streptomyc
14	31	93.9	10917	Q93NM6	Q93NM6 streptomyc
15	30	90.9	90	Q50164	Q50164 mycobacteri
16	30	90.9	124	Q9VP65	Q9VP65 drosophila

Q9N5H2 caenorhabdi
Q9HPE2 halobacteri
Q9RY28 deinococcus
Q9RHB7 bradyrhizob
Q9CUA9 mus musculu
Q9CXU7 mus musculu
Q97GH1 clostridium
Q16933 ancylostoma
Q9K123 vibrio chol
Q9KPM8 vibrio chol
Q8ZGR2 versinia pe
Q98FD4 rhizobium l
Q916R0 pseudomonas
Q91111 streptomyc
Q8DKE4 synecococc
Q19242 caenorhabdi
Q9PF46 xylella fas
Q8LR21 oryza sativ
Q8BXR2 mus musculu
Q9CTV2 mus musculu
Q9A1S8 streptomyc
Q8B400 porcine lym
Q8B417 porcine lym
Q8B3X0 porcine lym
Q8JYD0 porcine lym
Q9UF13 homo sapien
Q9RXV9 deinococcus
Q8GR31 streptomyc
Q42948 schizosacch

154 5 Q9N5H2
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578 12 Q8B417
578 12 Q8B3X0
580 12 Q8JYD0
600 4 Q9UF13
638 16 Q9RXV9
660 2 Q8GR31
1026 3 Q42948

ALIGNMENTS

RESULT 1

Q9RL11 PRELIMINARY; PRT; 295 AA.

ID Q9RL11
AC Q9RL11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO0307.
GN SCO0307 OR SC5G9.16.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapalce D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdono-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabbintowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT Coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939105; CAB55664.1; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR Pfam; PF01381; HTH_3; 1.
DR SMART; SM00530; HTH_XRE; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 295 AA; 32188 MW; 91AF744D77736075 CRC64;
Query Match 100.0%; Score 33; DB 16; Length 295;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSAL 6
Db 234 LDWSAL 239
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Q9PCP5 ID Q9PCP5 PRELIMINARY; PRT; 192 AA.
AC Q9PCP5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tryptophan repressor binding protein.
GN XF1733.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Arya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Perseu J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003996; AAF84542.1; -.

DR InterPro; IPR001226; Flavodoxin.
DR Pfam; PF00258; Flavodoxin; 1.
DR PROSITE; PS00201; FLAVODOXIN; 1.
KW Complete proteome.
SQ SEQUENCE 192 AA; 20309 MW; 38474F2CAC40A7D4 CRC64;
Query Match 93.9%; Score 31; DB 16; Length 192;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSAL 6
Db 43 MDWSAL 48
RESULT 3
Q9EU85 ID Q9EU85 PRELIMINARY; PRT; 266 AA.
AC Q9EU85;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 29.4 kDa protein.
GN ORF55.
OS Corynebacterium equi (Rhodococcus equi).
OG Plasmid pREAT701 (p33701), and Plasmid virulence.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=43767;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC33701; PLASMID=pREAT701 (p33701);
RA Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC33701, and 103; PLASMID=pREAT701 (p33701), and virulence;
RX PubMed=11083803;
RA Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A.,
RA Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,
RA Dan H., Prescott J.F.;
RT "DNA sequence and comparison of virulence plasmids from Rhodococcus
RT equi ATCC 33701 and 103.";
RL Infect Immun. 68:6840-6847(2000).
DR EMBL; AP001204; BAB16664.1; -.
DR EMBL; AF116907; AAG21758.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 266 AA; 29450 MW; 26B9B0B9717FF8B6 CRC64;
Query Match 93.9%; Score 31; DB 2; Length 266;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSAL 6
Db 30 LDWSAL 35
RESULT 4
Q9VXR2 ID Q9VXR2 PRELIMINARY; PRT; 345 AA.
AC Q9VXR2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG8191 protein (RE17665p).
GN CG8191.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananadis P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butcher H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foelele K., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003500; AAF48496.1; -.
DR EMBL; AY071134; AAL48756.1; -.
DR FlyBase; FBgn0030675; CG8191.
SQ SEQUENCE 345 AA; 39831 MW; 0513409F8F007B9C CRC64;

Query Match 93.9%; Score 31; DB 5; Length 345;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 136 LDWSAI 141
|||||
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011792; AAM36468.1; -.
DR InterPro; IPR000733; Flay_monooxygenase.
DR InterPro; IPR003042; Rng_monooxygenase.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RINGMONOXNASE.
KW Monooxygenase; Complete proteome.
SQ SEQUENCE 455 AA; 50857 MW; D4D9F44E9761A618 CRC64;

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GN L4803.06.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Masuy D., Furnelle B., Goffeau A., Ivens A.C., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL161416; CAB77684.1; -.
KW Hypothetical protein.
SQ SEQUENCE 399 AA; 43458 MW; BB86021C2BBB3E18 CRC64;

Query Match 93.9%; Score 31; DB 5; Length 399;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 388 LDWSAI 393
|||||
RESULT 6
Q8PM34 PRELIMINARY; PRT; 455 AA.
ID Q8PM34
AC Q8PM34;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kynurenine 3-monooxygenase.
DE XAC1600.
GN Xanthomonas axonopodis (pv. citri).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Chapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.P., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011792; AAM36468.1; -.
DR InterPro; IPR000733; Flay_monooxygenase.
DR InterPro; IPR003042; Rng_monooxygenase.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RINGMONOXNASE.
KW Monooxygenase; Complete proteome.
SQ SEQUENCE 455 AA; 50857 MW; D4D9F44E9761A618 CRC64;

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Query Match 93.9%; Score 31; DB 16; Length 455;
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 DB 435 LDWSAL 440

RESULT 7
 QYV553 PRELIMINARY; PRT; 652 AA.
 AC Q9V553;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE CG8027 protein.
 GN CG8027.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupek M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtka R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003834; AAF58967.1; --
 DR FlyBase; FBgn033392; CG8027.
 DR InterPro; IPR000800; Nocth.
 DR Pfam; PF00066; nocth; 1.
 SQ SEQUENCE 652 AA; 75752 MW; 2728764810039458 CRC64;

Query Match 93.9%; Score 31; DB 5; Length 652;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 DB 447 LDWSAM 452

RESULT 8
 QBL311 PRELIMINARY; PRT; 666 AA.
 ID QBL311;
 AC QBL311;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Cytochrome b subunit B.
 GN CYOB.
 OS Vitreoscilla sp. (strain C1).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Vitreoscilla.
 OX NCBI_TaxID=96942;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C1;
 RA Webster D.A., Hwang K.-W., Kim S.-K., Kim K.-J., Chung Y.-T.,
 RA Stark B.C.;
 RT "Sequence and Characterization of the Cytochrome b Operon of
 RT Vitreoscilla.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF439739; AAM20915.1; --
 DR InterPro; IPR000883; COX1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Electron transport; Heme; Oxidoreductase; Respiratory chain;
 KW Transmembrane; Transport.
 SQ SEQUENCE 666 AA; 74470 MW; B5F3EAE67282E7C CRC64;

Query Match 93.9%; Score 31; DB 2; Length 666;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 DB 5 LDWSAI 10

RESULT 9
 QBSX14 PRELIMINARY; PRT; 666 AA.
 ID QBSX14;
 AC QBSX14;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE RE35033p.
 GN CG8027.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragae V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY089618; AAL90356.1; --

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DR FlyBase; FBgn033392; CG8027.
DR InterPro; IPR000800; Notch.
DR Pfam; PF00066; notch; 1.
SQ SEQUENCE 666 AA; 77745 MW; F6FDB6D1C1C39248 CRC64;

Query Match      93.9%; Score 31; DB 5; Length 666;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      461 LDMSAM 466

RESULT 10
Q07324 ID Q07324 PRELIMINARY; PRT; 1006 AA.
AC Q07324;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ATP dependent permease (yeast homolog).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA De haan M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL EMBL; 274920; CAA99202.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
KW ATP-binding.
FT NON_TER 1
SQ SEQUENCE 1040 AA; 117840 MW; B32B0F1D33906B5C CRC64;

Query Match      93.9%; Score 31; DB 3; Length 1040;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      663 LDMSAL 668

RESULT 12
Q08409 ID Q08409 PRELIMINARY; PRT; 1394 AA.
AC Q08409;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chromosome XV reading frame ORF YOR011W.
GN AUS1 OR YOR011W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-842 FROM N.A.
RA Pettersson B.; Sterky F.; Uhlen M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN [3]
RP SEQUENCE OF 355-1394 FROM N.A.
RA De haan M.; Grivell L.A.; Maarse A.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL EMBL; 274919; CAA99199.1; -.
DR SGD; S0005537; AUS1.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC transporter; 2.
DR SMART; SM00382; AAA; 1.

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DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 DR PROSITE; PS01159; WW_DOMAIN_1; 1.
 KW ATP-binding.
 SQ SEQUENCE 1394 AA; 157749 MW; 357A35A0FC9C93B CRC64;

Query Match 93.9%; Score 31; DB 3; Length 1394;
 Best Local Similarity 83.3%; Pred. No. 2.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 :|||||
 Db 1017 IDWSAL 1022

RESULT 13

ID O54155 PRELIMINARY; PRT; 2297 AA.
 AC O54155;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Polyketide synthase.
 GN SC05892 OR SC3F7.12.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 RL EMBL; AL939125; CAA16183.1; --
 DR HSSP; P25715; IMLA.
 DR InterPro; IPR001227; Ac transferase.
 DR InterPro; IPR003408; Ala synthase.
 DR InterPro; IPR004839; Aminotransf1/2.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR001917; NHtransf.2.
 DR InterPro; IPR006163; Pp_bind.
 DR Pfam; PF00698; Acyl_transf; 1.
 DR Pfam; PF02490; ALA_synthase; 1.

DR Pfam; PF00155; aminotran_1.2; 1.
 DR Pfam; PF00501; AMP-binding_1.
 DR Pfam; PF00109; ketoacyl-synt; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF00550; pp-binding; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
 DR PROSITE; PS00075; AC DOMAIN_2.
 DR PROSITE; PS00506; B_KETOACYL_SYNTHASE; 1.
 DR Phosphopantetheine; Transferase; Complete proteome.
 KW SEQUENCE 2297 AA; 241989 MW; C67B58461535EB46 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 2297;
 Best Local Similarity 83.3%; Pred. No. 4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 :|||||
 Db 1641 IDWSAL 1646

RESULT 14

ID Q93NW6 PRELIMINARY; PRT; 10917 AA.
 AC Q93NW6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE AmphC.
 GN AMPHC.
 OS Streptomyces nodosus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=40318;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., O'Liynyk M.;
 RT "The amphoterin biosynthetic gene cluster from Streptomyces
 nodosus.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -|- COFACTOR: ZINC (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR EMBL; AF357202; AAK73514.1; --
 DR InterPro; IPR001227; Ac transferase.
 DR InterPro; IPR002328; Adh_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR InterPro; IPR004410; FabD.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR006162; Peantne attach.
 DR InterPro; IPR006163; Pp_bind.
 DR Pfam; PF00698; Acyl_transf; 6.
 DR Pfam; PF00107; adh_zinc; 1.
 DR Pfam; PF00109; ketoacyl-synt; 6.
 DR Pfam; PF02801; ketoacyl-synt_C; 6.
 DR Pfam; PF00550; pp-binding; 6.
 DR TIGRFAMs; TIGR00128; fabd; 6.
 DR PROSITE; PS00075; ACP_DOMAIN; 6.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 DR PROSITE; PS00059; B_KETOACYL_SYNTHASE; 6.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 5.
 KW Metal-binding; Oxidoreductase; Phosphopantetheine; Transferase; Zinc.
 SQ SEQUENCE 10917 AA; 1132905 MW; 15AC5956BB5810A1 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 10917;
 Best Local Similarity 83.3%; Pred. No. 1.9e+04;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 :|||||
 Db 8165 IDWSAL 8170

RESULT 15

Q50164
ID Q50164 PRELIMINARY; PRT; 90 AA.
AC Q50164;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE U2966.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15187; AAA63116.1; -.
SQ SEQUENCE 90 AA; 9642 MW; F0187130F441A846 CRC64;

Query Match 30.9%; Score 30; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 65 LDWSAV 70

Search completed: February 18, 2004, 14:35:54
Job time : 19.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-13
Perfect score: 33
Sequence: 1 LDWSAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	330	YD31_ARCFU	O28938 archaeoglob
2	31	93.9	226	1 CXB2_SHEEP	P46691 ovis aries
3	31	93.9	333	1 YZ37_SYNY3	Q55480 synochocyst
4	31	93.9	666	1 CO14_BRAJA	P98057 bradyrhizob
5	31	93.9	984	1 PKL2_HUMAN	Q16513 homo sapien
6	30	90.9	208	1 TRPF_DEIRA	Q3728 deinococcus
7	30	90.9	261	1 YFJR_BACSU	Q34969 bacillus su
8	30	90.9	377	1 Y4WD_RHISN	P55682 rhizobium s
9	30	90.9	516	1 PROD_HUMAN	O43272 homo sapien
10	29	87.9	223	1 SAMP_HUMAN	P02743 homo sapien
11	29	87.9	224	1 SAMP_PIG	O19063 sus scrofa
12	29	87.9	234	1 SAMP_MESAU	P07629 mesocricetu
13	29	87.9	286	1 CXA6_RAT	P28233 rattus norv
14	29	87.9	286	1 SGBU_ECOLI	P37679 escherichia
15	29	87.9	296	1 CYCG_RHOSH	Q53143 rhodobacter
16	29	87.9	313	1 Y763_TRSPA	O83744 treponema p
17	29	87.9	378	1 CXAL_XENLA	P16863 xenopus lae
18	29	87.9	380	1 CXAL_BRARE	O57474 brachydanio
19	29	87.9	380	1 CXAL_CHICK	P14154 gallus gall
20	29	87.9	381	1 CXAL_HUMAN	P17302 homo sapien
21	29	87.9	381	1 CXAL_MOUSE	P23242 mus musculu
22	29	87.9	381	1 CXAL_RAT	P08050 rattus norv
23	29	87.9	382	1 CXAL_BOVIN	P18246 bos taurus
24	29	87.9	394	1 PGK_BACST	P18912 bacillus st
25	29	87.9	446	1 SHT_BOMMO	Q17239 bombyx mori
26	29	87.9	451	1 GUDH_PSEPU	P42206 pseudomonas
27	29	87.9	455	1 UHPT_CHLPN	Q92759 chlamydia p
28	29	87.9	456	1 UHPT_CHLMU	Q92759 chlamydia p
29	29	87.9	456	1 UHPT_CHLTR	O84548 chlamydia t
30	29	87.9	482	1 TRPE_SPIAU	P21690 spirochaeta
31	29	87.9	517	1 LADI_HUMAN	O00515 homo sapien
32	29	87.9	528	1 LADI_MOUSE	P57016 mus musculu
33	29	87.9	548	1 NOLQ_BRAJA	Q45269 bradyrhizob

34	29	87.9	600	1 GLMS_HALN1	Q9ht00 h glucosami
35	29	87.9	630	1 GLMS_SYNY3	P72720 s glucosami
36	29	87.9	644	1 VP4_BTvl1	P33428 bluetongue
37	29	87.9	644	1 VP4_BTvl3	P33429 bluetongue
38	29	87.9	644	1 VP4_BTv2A	P33427 bluetongue
39	29	87.9	654	1 VP4_BTv10	P07132 bluetongue
40	29	87.9	754	1 RIRI_BPT4	P32282 bacterioph
41	29	87.9	842	1 PKL2_RAT	O08874 rattus norv
42	29	87.9	926	1 MAY3_SCHCO	P37934 schizophyll
43	29	87.9	941	1 GCSP_MYCTU	Q50601 mycobacteri
44	29	87.9	946	1 PKL1_RAT	Q63433 rattus norv
45	29	87.9	958	1 YA7B_SCHPO	Q09764 schizosacch

ALIGNMENTS

RESULT 1
YD31_ARCFU STANDARD; PRT; 330 AA.
ID YD31_ARCFU STANDARD; PRT; 330 AA.
AC O28938;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein AF1331.
GN AF1331.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-15 / DSM 4104 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).

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EMBL; AB001012; AAB89926.1; -;
PIR; B69416; B69416.
TIGR; AF1331; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 330 AA; 38741 MW; 1B32F8BF5E9C7621 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 177 LDWSAL 182

RESULT 2

```

CXB2_SHEEP
ID _CXB2_SHEEP STANDARD; PRT; 226 AA.
AC P46631;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction beta-2 protein (Connexin 26) (Cx26).
GN GJB2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Cornea;
RC
RA Dong Y., Green C., Donaldson P.J., Kistler J.;
RA Submitted (NOV-1994) to the EMBL/GenBank/DBEJ databases.
CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -!- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP I)
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U17592; AAA67446.1; -.
CC InterPro; IPR000500; Connexin.
CC Pfam; PF00029; connexin; 1.
CC PRINTS; PR00206; CONNEXIN.
CC SMART; SM00037; CNX; 1.
CC PROSITE; PS00407; CONNEXINS_1; 1.
CC PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 40 POTENTIAL.
FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 98 POTENTIAL.
FT DOMAIN 99 131 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 132 154 POTENTIAL.
FT DOMAIN 155 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 215 POTENTIAL.
FT DOMAIN 216 226 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 226 AA; 26215 MW; DCE2F0C1B4FCE7D CRC64;

Query Match 93.9%; Score 31; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 1 MDWSAL 6
:|||||
146 MDWSAL 151

RESULT 3
YZ37_SYNY3
ID YZ37_SYNY3 STANDARD; PRT; 333 AA.
AC Q55480;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical sugar kinase slr0537.
GN SLR0537.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.

```

```

OX NCBI_TaxID=1148;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64 to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
CC -----
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CC -----
CC EMBL; D64006; BAA10827.1; -.
CC PIR; S75980; S75980.
CC HSP; Q9TWM2; IDG.
CC InterPro; IPR002173; PFKB.
CC PRINTS; PR00294; pfkb; 1.
CC PROSITE; PS00950; RIBOKINASE.
CC PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG.
CC PROSITE; PS00584; PFKB_KINASES_2; 1.
KW Hypothetical protein; Transferase; Kinase; Complete proteome.
SQ SEQUENCE 333 AA; 35184 MW; CBCE13D0F7EEF9D CRC64;

Query Match 93.9%; Score 31; DB 1; Length 333;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 146 MDWSAL 151
:|||||

RESULT 4
CO14_BRAJA
ID CO14_BRAJA STANDARD; PRT; 666 AA.
AC P98057;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fourth
DE terminal oxidase).
GN BLR2715.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=94259305; PubMed=8200541;
RA Surpin M.A., Moshiri F., Murphy A.M., Maier R.J.;
RT "Genetic evidence for a fourth terminal oxidase in Bradyrhizobium
RT japonicum.";
RL Gene 143:73-77(1994).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=USDA 110;
RC MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).

```

CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- PATHWAY: Respiratory chain; terminal step.
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L25841; AAA26210.1; --
CC EMBL: AP005944; BAC47980.1; --
CC HSP: P18401; 1PFT.
CC InterPro: IPR000883; COX1.
CC Pfam: PF00115; COX1; 1.
CC PRINTS; P01165; CYCOXIDASE1.
CC PROSITE; PS00077; COX1; 1.
CC Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
CC Complete proteome. 105
CC METAL 105 IRON (LOW-SPIN HEME AXIAL LIGAND)
CC (BY SIMILARITY).
CC METAL 283 COPPER B (BY SIMILARITY).
CC METAL 287 COPPER B (BY SIMILARITY).
CC METAL 332 COPPER B (BY SIMILARITY).
CC METAL 333 COPPER B (BY SIMILARITY).
CC METAL 418 IRON (HIGH-SPIN HEME AXIAL LIGAND)
CC (BY SIMILARITY).
CC METAL 420 IRON (LOW-SPIN HEME AXIAL LIGAND)
CC (BY SIMILARITY).
CC CROSSLINK 283 1'-histidyl-3'-tyrosine (By similarity).
CC CONFLICT 204 G -> D (IN REF. 1). CRC64;
CC SEQUENCE 666 AA; 74469 MW; F04F4870CD039861 CRC64;
Query Match 93.9%; Score 31; DB 1; Length 666;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSAL 6
DB 5 LDWSAI 10
RESULT 5
PKL2_HUMAN STANDARD; PRT; 984 AA.
AC Q16513; Q9H1W4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C-like 2 (EC 2.7.1.-) (protein-kinase C-related kinase
DE 2).
GN PRKCL2 OR PRK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95080426; PubMed=7988719;
RX Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
RT products.";
RL FEBS Lett. 356:5-8(1994).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=B-cell;
RX MEDLINE=95154310; PubMed=7851406;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Cloning and expression patterns of two members of a novel protein-
RT kinase-C-related kinase family.";

RL Eur. J. Biochem. 227:344-351(1995).
[3]
RN SEQUENCE OF 17-984 FROM N.A.
RA Brown A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: EXHIBITS A PREFERENCE FOR HIGHLY BASIC PROTEIN
CC SUBSTRATES (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
CC AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS AND
CC UNSATURATED FATTY ACIDS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PFM: AUTOPHOSPHORYLATED.
CC -1- PFM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
CC EMBL: U33052; AAC50208.1; --
CC EMBL: S75548; AAB33346.1; --
CC EMBL: AL136381; CAC17575.1; --
CC PIR: S67527; S67527.
CC HSP: Q63450; 1A06.
CC Genew; HGNC:9406; PRKCL2.
CC MIM: 602549; --
CC GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
CC GO: GO:0007165; P:signal transduction; TAS.
CC InterPro: IPR000008; C2.
CC InterPro: IPR000961; Kinase C.
CC InterPro: IPR000719; Prot kinase.
CC InterPro: IPR000861; REM repeat.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF02185; HR1; 3.
CC Pfam: PF00069; kinase; 1.
CC Pfam: PF00433; kinase C; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00074; HR1; 3.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TK_X; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Transferase; ATP-binding; Serine/threonine-protein kinase;
CC Phosphorylation.
CC DOMAIN 657 916 PROTEIN KINASE.
CC NP_BIND 663 671 ATP (BY SIMILARITY).
CC BINDING 686 686 ATP (BY SIMILARITY).
CC ACT_SITE 782 782 BY SIMILARITY.
CC CONFLICT 207 207 N -> NGDGINCPSPVEHN (IN REF. 3).
CC SEQUENCE 984 AA; 112034 MW; 687EC417A0F51C1D CRC64;
Query Match 93.9%; Score 31; DB 1; Length 984;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSAL 6
DB 919 IDWSAL 924
RESULT 6
TRPF_DEIRA
ID TRPF_DEIRA STANDARD; PRT; 208 AA.
AC Q9RY28;
DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).
 GN TRPF OR DR0123.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCBI 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarchova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."; 1577(1999).
 RL Science 286:1571-1577(1999).
 CC -I- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-ribose)-anthranilate = 1-
 CC (2-carboxyphenylamino)-1-deoxy-D-ribose 5-phosphate.
 CC -I- PATHWAY: Tryptophan biosynthesis; third step.
 CC -I- SIMILARITY: BELONGS TO THE TRPF FAMILY.
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 CC -----
 CC EMBL; AE001875; AAF09715.1; -;
 DR PIR; D75556; D75556.
 DR HSP; Q56320; 1DL3.
 DR TIGR; DR0123; -;
 DR HAMAP; MF_00135; -; 1.
 DR InterPro; IPR001240; PRAI.
 DR Pfam; PF00697; PRAI; 1.
 KW Isomerase; Tryptophan biosynthesis; Complete proteome.
 SQ SEQUENCE 208 AA; 21156 MW; CF98D22E23AC2833 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 208;
 Best Local Similarity 83.3%; Pred. No. 85;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 144 LDWAAL 149
 RESULT 7
 YFUR_BACSU STANDARD; PRT; 261 AA.
 ID YFJR_BACSU
 AC Q34969;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase yfjr (EC 1.1.1.-).
 GN YFJR.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AC327;
 RX MEDLINE=97124190; PubMed=8969503;
 RA Yamamoto H., Uchiyama S., Sekiguchi J.;
 RT "Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76
 RT degrees region of the Bacillus subtilis chromosome containing genes

RT for trehalose metabolism and acetoin utilization.";
 RL Microbiology 142:3057-3065(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Chou S.K., Codani J.J., Connerton I.F., Cummings N.J., Carter N.M.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz C., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis".
 RL Nature 390:249-256(1997).
 CC -I- SIMILARITY: BELONGS TO THE 3-HYDROXYISOBUTYRATE DEHYDROGENASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; D83967; BAA23388.1; -;
 DR EMBL; D78509; BAA24303.1; -;
 DR EMBL; Z99108; CAB12628.1; -;
 DR PIR; A69807; A69807.
 DR Subtilist; BG12914; yfjr.
 DR InterPro; IPR002204; 3hydroxisobut dh.
 KW PROSITE; PS00895; 3_HYDROXYISOBUT DH; FALSE NEG.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT ACT_SITE 146 146 BY SIMILARITY.
 SQ SEQUENCE 261 AA; 27866 MW; 6C9A8CAC8C71CA66 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 261;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 251 LDWAAL 256
 RESULT 8
 Y4WD_RHISN
 ID Y4WD_RHISN STANDARD; PRT; 377 AA.
 AC P55682;
 DT 01-NOV-1997 (Rel. 35, Created)

```
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical transport protein Y4WD.
GN Y4WD.
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97305956; PubMed=9163424;
RX Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- FUNCTION: COULD BE INVOLVED IN A TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: TO R.MELILOTI MOSC.
CC -----
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CC -----
DR EMBL; AE000103; AAB91911.1; -.
DR InterPro; IPR007114; MFS.
KW Hypothetical protein; Transmembrane; Transport; Plasmid.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 85 105 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 192 212 POTENTIAL.
FT TRANSMEM 278 298 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 327 347 POTENTIAL.
FT TRANSMEM 356 376 POTENTIAL.
SQ SEQUENCE 377 AA; 39051 MW; 49CF6E44AA0D74BD CRC64;

Query Match 90.9%; Score 30; DB 1; Length 377;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 221 LDWSAV 226

RESULT 9
PROD HUMAN
ID -SAMP_HUMAN STANDARD; PRT; 516 AA.
AC O43272;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Proline oxidase, mitochondrial precursor (BC 1.5.3.-) (Proline
DE dehydrogenase).
GN PRODH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98046348; PubMed=9385373;
RA Campbell H.D., Webb G.C., Young I.G.;
RT "A human homologue of the Drosophila melanogaster sluggish-A (proline
RT oxidase) gene maps to 22q11.2, and is a candidate gene for type-I
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RT hyperprolinaemia.";
RL Hum. Genet. 101:69-74(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum, and Kidney;
RX MEDLINE=99206616; PubMed=10192398;
RA Gogos J.A., Santha M., Takacs Z., Beck K.D., Luine V., Lucas L.R.,
RA Nadler J.V., Karayiorgou M.;
RT "The gene encoding proline dehydrogenase modulates sensorimotor gating
RT in mice.";
RL Nat. Genet. 21:434-439(1999).
CC -1- FUNCTION: CONVERTS PROLINE TO DELTA-1-PYRROLINE-5-CARBOXYLATE.
CC -1- PATHWAY: Conversion from proline to glutamate; first step.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKELETAL MUSCLE AND BRAIN,
CC TO A LESSER EXTENT IN HEART AND KIDNEY, AND WEAKLY IN LIVER,
CC PLACENTA AND PANCREAS.
CC -1- DISEASE: Defects in PRODH are the cause of type I hyperprolinaemia
CC [MIM:239500]; a disorder characterized by elevated serum proline
CC levels. May be involved in the psychiatric and behavioral
CC phenotypes associated in the 22q11 velocardiofacial syndrome.
CC -1- SIMILARITY: BELONGS TO THE PROLINE OXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; U82381; AAB88789.1; -.
DR EMBL; AF120278; AAD24775.1; -.
DR Genew; HGNC:9453; PRODH.
DR GK; O43272; -.
DR MIM; 606810; -.
DR MIM; 239500; -.
DR GO; GO:0004657; F:proline dehydrogenase activity; TAS.
DR InterPro; IPR002872; Pro_dh.
DR Pfam; PF01619; Pro_dh; 1.
KW Oxidoreductase; Proline metabolism; Mitochondrion; Transit peptide.
FT TRANSIT 1 7 MITOCHONDRION (POTENTIAL).
FT CHAIN ? 516 PROLINE OXIDASE.
FT CONFLICT 80 80 S -> T (IN REF. 2).
SQ SEQUENCE 516 AA; 59216 MW; 2PASB1E481C450A CRC64;

Query Match 90.9%; Score 30; DB 1; Length 516;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 231 LDWSSL 236

RESULT 10
SAMP_HUMAN
ID -SAMP_HUMAN STANDARD; PRT; 223 AA.
AC P02743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glycoprotein).
GN APCS OR PTX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207828; PubMed=2987268;
RA Mantzouranis E.C., Downton S.B., Whitehead A.S., Edge M.D.,
RA Bruns G.A.P., Colten H.R.;
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RT "Human serum amyloid P component. cDNA isolation, complete sequence
 of pre-serum amyloid P component, and localization of the gene to
 chromosome 1.";
 RL J. Biol. Chem. 260:7752-7756(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87137351; PubMed=3029048;
 RA Ohnishi S., Maeda S., Shimada K., Arai T.;
 RT "Isolation and characterization of the complete complementary and
 genomic DNA sequences of human serum amyloid P component.";
 RL J. Biochem. 100:849-858(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Skeletal muscle;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Udwin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 20-223.
 RX MEDLINE=86033713; PubMed=4055725;
 RA Prelli F., Pras M., Frangione B.;
 RT "The primary structure of human tissue amyloid P component from a
 patient with primary idiopathic amyloidosis.";
 RL J. Biol. Chem. 260:12895-12898(1985).
 RN [5]
 RP SEQUENCE OF 20-49.
 RX MEDLINE=79042150; PubMed=81686;
 RA Thompson A.R., Enfield D.L.;
 RT "Human plasma P component: Isolation and characterization.";
 RL Biochemistry 17:4304-4311(1978).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94159098; PubMed=8114934;
 RA Emsley J., White H.E., O'Hara B., Oliva G., Srinivasan N.,
 RA Tickle I.J., Blundell T.L., Pepys M.B., Wood S.P.;
 RT "Structure of pentameric human serum amyloid P component.";
 RL Nature 367:338-345(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=97360233; PubMed=9217261;
 RA Hohenester E., Hutchinson W.L., Pepys M.B., Wood S.P.;
 RT "Crystal structure of a decameric complex of human serum amyloid P
 component with bound DAMP.";
 RL J. Mol. Biol. 269:570-578(1997).
 CC -!- FUNCTION: CAN INTERACT WITH DNA AND HISTONES AND MAY SCAVENGE
 CC NUCLEAR MATERIAL RELEASED FROM DAMAGED CIRCULATING CELLS. MAY ALSO
 CC FUNCTION AS A CALCIUM-DEPENDENT LECTIN.
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: D00097; BAA00060.1; -;
 CC EMBL: M10944; AAA60302.1; -;
 CC EMBL: X04608; CAA28275.1; -;
 CC EMBL: BC007039; AAH07039.1; -;
 CC EMBL: BC007058; AAH07058.1; -;
 CC PIR: A25503; YLRHUP.
 CC PDB: 1SAC; 31-JUL-94.
 CC PDB: 1LGN; 24-DEC-97.
 CC GlycoSuiteDB; P02743; -;
 CC SWISS-2DPAGE; P02743; HUMAN.
 CC Genew; HGNC:584; APCs.
 CC MIM; 104770; -;
 CC GO: GO:0005615; C:extracellular space; TAS.
 CC GO: GO:0003794; F:acute-phase response protein activity; TAS.
 CC GO: GO:0005208; F:amyloid protein; TAS.
 CC GO: GO:0003754; F:chaperone activity; TAS.
 CC GO: GO:0005211; F:plasma glycoprotein; TAS.
 CC GO: GO:0005209; F:plasma protein; TAS.
 CC GO: GO:0006462; P:protein complex assembly, multichaperone pa. .; TAS.
 CC GO: GO:0006457; P:protein folding; TAS.
 CC InterPro; IPR001759; Pentaxin.
 CC Pfam; PF00354; pentaxin; 1.
 CC PRINTS; PR00895; PENTAXIN.
 CC ProDom; PD002153; Pentaxin; 1.
 CC SMART; SM00159; PTX; 1.
 CC PROSITE; PS00289; PENTAXIN; 1.
 CC Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal; Polymorphism;
 KW 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 223 SERUM AMYLOID P-COMPONENT.
 FT DOMAIN 20 223 PENTAXIN.
 FT DISULFID 55 114
 FT CARBOHYD 51 51 N-LINKED (GLCNAc. .).
 FT VARIANT 152 152 /FTID=VAR_000169.
 FT VARIANT 155 155 L -> G.
 FT VARIANT 158 158 E -> G.
 FT VARIANT 158 158 /FTID=VAR_006054.
 FT CONFLICT 101 101 S -> G.
 FT STRAND 21 21 /FTID=VAR_006055.
 FT TURN 24 25 S -> P (IN REF. 1).
 FT STRAND 26 30
 FT STRAND 38 42
 FT STRAND 49 49
 FT STRAND 51 59
 FT STRAND 66 73
 FT TURN 74 75
 FT STRAND 76 86
 FT TURN 87 88
 FT STRAND 89 94
 FT TURN 95 96
 FT STRAND 97 102
 FT TURN 111 118
 FT TURN 119 121
 FT STRAND 123 128
 FT TURN 129 130
 FT STRAND 131 132
 FT STRAND 136 137
 FT TURN 140 141
 FT STRAND 144 144
 FT STRAND 149 152
 FT HELIX 165 167
 FT STRAND 171 179
 FT HELIX 185 193

FT TURN 194 194
FT STRAND 202 203
FT TURN 204 205
FT STRAND 207 212
FT STRAND 216 219
SQ SEQUENCE 223 AA; 25387 MW; 6C88A515FE88B393 CRC64;
Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
||| ||
Db 202 LDWQAL 207

RESULT 11
SAMP_PIG STANDARD; PRT; 224 AA.
AC O19063;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component precursor (SAP).
GN APCs.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace; TISSUE=Liver;
RA Ozawa A., Matsumoto M., Kajikawa M., Hanazono M., Yaeue H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AB005546; BAA21474.1; -;
CC HSSP; P02743; ISAC.
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; Pentaxin; 1.
CC PRINTS; PR00895; PENTAXIN.
CC ProDom; PD002153; Pentaxin; 1.
CC SMART; SM00159; PTX; 1.
CC PROSITE; PS00289; PENTAXIN; 1.
CC Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CHAIN 20 224 SERUM AMYLOID P-COMPONENT.
FT DOMAIN 20 224 PENTAXIN.
FT DISULFID 55 114 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 224 AA; 25641 MW; 9D1867691EBDC66 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 224;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
||| ||
Db 203 LDWQAL 208

RESULT 12
SAMP_MESAU STANDARD; PRT; 234 AA.
AC P07629;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component precursor (female protein) (FP) (SAP(FP)).
GN PTX2 OR SAP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94012761; PubMed=7691816;
RA Rudnick C.M., Dowton S.B.;
RT "Serum amyloid P (female protein) of the Syrian hamster. Gene
RT structure and expression.";
RL J. Biol. Chem. 268:21760-21769(1993).
RN [2]
RP SEQUENCE OF 24-234 FROM N.A.
RX MEDLINE=85218787; PubMed=2408337;
RA Dowton S.B., Woods D.E., Mantzouranis E.C., Colten H.R.;
RT "Syrian hamster female protein: analysis of female protein primary
RT structure and gene expression.";
RL Science 228:1206-1208(1985).
RN [3]
RP SEQUENCE OF 25-48.
RX MEDLINE=8124137; PubMed=6166709;
RA Coe J.E., Margossian S.S., Slayter H.S., Sogn J.A.;
RT "Hamster female protein. A new Pentraxin structurally and
RT functionally similar to C-reactive protein and amyloid P component.";
RL J. Exp. Med. 153:977-991(1981).
RN [4]
RP 3D-STRUCTURE MODELING
RX MEDLINE=95187705; PubMed=7881902;
RA Srinivasan N., White H.E., Emsley J., Wood S.P., Pepys M.B.,
RA Blundell T.L.;
RT "Comparative analyses of pentraxins: implications for protomer
RT assembly and ligand binding.";
RL Structure 2:1017-1027(1994).
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: PLASMA CONCENTRATION OF FP ARE ALTERED BY SEX
CC STEROIDS AND BY STIMULI THAT ELICIT AN ACUTE PHASE RESPONSE.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.

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CC or send an email to license@isb-sib.ch).

CC EMBL; L22024; AAA03577.1; -;
CC EMBL; M11342; AAA36980.1; -;
CC PIR; A44177; A44177.
CC PIR; A48593; A48593.
CC PDB; 1HAS; 15-OCT-95.
CC InterPro; IPR001759; Pentaxin.
CC Pfam; PF00354; Pentaxin; 1.
CC PRINTS; PR00895; PENTAXIN.
CC ProDom; PD002153; Pentaxin; 1.
CC SMART; SM00159; PTX; 1.
CC PROSITE; PS00289; PENTAXIN; 1.
CC Lectin; Pentaxin; Plasma; Acute phase; Signal; Amyloid; Glycoprotein;
FT 3D-structure. 1 22 POTENTIAL.
FT SIGNAL

FT CHAIN 23 234
 FT DOMAIN 23 234
 FT DISULFID 58 117
 FT CARBOHYD 54 54
 FT CONFLICT 27 27
 FT CONFLICT 43 43
 FT CONFLICT 76 76
 FT STRAND 24 24
 FT TURN 27 28
 FT STRAND 29 33
 FT STRAND 41 44
 FT STRAND 52 52
 FT STRAND 54 62
 FT STRAND 69 76
 FT TURN 77 78
 FT STRAND 79 89
 FT TURN 90 91
 FT STRAND 92 97
 FT TURN 98 99
 FT STRAND 100 105
 FT STRAND 113 121
 FT TURN 122 125
 FT STRAND 126 131
 FT TURN 132 133
 FT STRAND 134 135
 FT STRAND 139 140
 FT TURN 143 144
 FT STRAND 147 147
 FT STRAND 152 155
 FT STRAND 168 170
 FT STRAND 174 182
 FT HELIX 188 196
 FT TURN 197 197
 FT STRAND 205 205
 FT TURN 207 208
 FT STRAND 210 210
 FT STRAND 212 215
 FT STRAND 219 222
 FT HELIX 226 234
 SQ SEQUENCE 234 AA; 26463 MW; 6161F0383062D2DB CRC64;

SERUM AMYLOID P-COMPONENT.
 PENTAXIN.
 BY SIMILARITY.
 N-LINKED (GLCNAC...) (POTENTIAL).
 T -> S (IN REF. 3).
 K -> N (IN REF. 3).
 A -> T (IN REF. 2).

Query Match 87.9%; Score 29; DB 1; Length 234;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWSAL 6
 DB 205 LDWQAL 210

RESULT 13
 CXA6 RAT
 ID CXA6 RAT STANDARD; PRT; 286 AA.
 AC P28233;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gap junction alpha-6 protein (Connexin 33) (Cx33).
 GN GJA6 OR CXN-33.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=92112940; PubMed=1370487;
 RA Haefliger J.-A., Bruzzone R., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Paul D.L.;
 RA "Four novel members of the connexin family of gap junction proteins.
 RT Molecular cloning, expression, and chromosome mapping."
 RL J. Biol. Chem. 267:2057-2064(1992).
 CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which

materials of low mw diffuse from one cell to a neighboring cell.
 -!- SUBUNIT: A connexon is composed of a hexamer of connexins.
 -!- SUBCELLULAR LOCATION: Integral membrane protein.
 -!- TISSUE SPECIFICITY: Expressed in testis.
 -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II) SUBFAMILY.

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EMBL; M76534; AAA40998.1; -.
 DR PIR; C42053; C42053.
 DR InterPro; IPR000500; Connexin.
 DR Pfam; PF00029; connexin; 1.
 DR PRINTS; PR00206; CONNEXIN.
 DR SMART; SM00037; CNX; 1.
 DR PROSITE; PS00407; CONNEXINS_1; 1.
 DR PROSITE; PS00408; CONNEXINS_2; 1.
 KW Gap junction; Transmembrane.
 FT DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 24 41 POTENTIAL.
 FT DOMAIN 42 76 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 77 99 POTENTIAL.
 FT DOMAIN 100 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 174 POTENTIAL.
 FT DOMAIN 175 209 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 210 232 POTENTIAL.
 FT DOMAIN 233 286 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 286 AA; 32860 MW; A585266ACA2ACC2 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSAL 6
 DB 3 DWSAL 7

RESULT 14
 SGBU_ECOLI
 ID SGBU_ECOLI STANDARD; PRT; 286 AA.
 AC P37679;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative hexulose-6-phosphate isomerase (EC 5.-.-.-) (HUMPI).
 GN SGBU OR B3582.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=94316500; PubMed=8041620;
 RX STRAIN=K12 / MG1655;
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner P.R.;
 RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
 RT region from 76.0 to 81.5 minutes."
 RL Nucleic Acids Res. 22:2576-2586(1994).
 RN [2]
 DISCUSSION OF SEQUENCE.
 RA Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
 RA "Novel phosphotransferases system genes revealed by bacterial genome
 RT analysis: operons encoding homologues of sugar-specific permease
 RT domains of the phosphotransferase system and pentose catabolic
 RT enzymes."
 RL Genome Sci. Technol. 1:53-75(1996).

CC -1- FUNCTION: ISOMERIZATION OF D-ARABINO-6-HEXULOSE 3-PHOSPHATE TO
CC D-FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
CC SGBH.
CC -1- SIMILARITY: BELONGS TO THE HUMPI FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; U00039; AAB18559.1; ALT INIT.
DR ENBL; AE000435; AAC76606.1; ALT_INIT.
DR EcoGene; EG12286; sgbu.
DR InterPro; IPR004560; Hx16Piso_put.
DR Pfam; PF03809; Hx16Piso_put; 1.
DR TIGRFAMs; TIGR00542; hx16Piso_put; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 286 AA; 32455 MW; 4C849F575E937BF9 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSA 5
Db |||||
48 LDWSA 52

RESULT 15
CYCG_RHOSH STANDARD; PRT; 296 AA.
AC Q53143;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diheme cytochrome C-type.
GN CYCG.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=95362655; PubMed=7543472;
RA Flory J.E., Donohue T.J.;
RT "Organization and expression of the Rhodobacter sphaeroides cycFG
operon";
RL J. Bacteriol. 177:4311-4320(1995).
CC -1- FUNCTION: DIHEME C-TYPE CYTOCHROME, THAT IS PARTICULARLY EXPRESSED
CC WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C
CC SUBUNIT.
CC -----
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CC -----
CC ENBL; L36880; AAD09146.1; -.
DR InterPro; IPR003088; Cyt C1.
DR InterPro; IPR003219; CytC adh.
DR InterPro; IPR000345; CytC heme bind.
DR Pfam; PF00034; cytochrome_c; 1.

DR ProDom; PD011584; CytC adh; 1.
DR PROSITE; PS00190; CYTOCHROME C; 2.
KW Electron transport; Heme; Membrane.
FT BINDING 52 52 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 55 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT METAL 56 56 IRON (HEME 1 AXIAL LIGAND)
FT (BY SIMILARITY).
FT BINDING 202 202 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 206 206 IRON (HEME 2 AXIAL LIGAND)
FT (BY SIMILARITY).
SQ SEQUENCE 296 AA; 31727 MW; 4C4A9D8F695B5BFD CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSA 5
Db |||||
241 LDWSA 245

Search completed: February 18, 2004, 14:28:11
Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-13
Perfect score: 33
Sequence: 1 LDWSAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	330	2 B69416	hypothetical prote
2	31	93.9	192	2 F82645	tryptophan repress
3	31	93.9	333	2 S75980	hypothetical prote
4	31	93.9	984	2 S67527	protein kinase (EC
5	31	93.9	1394	2 S66876	ATP-dependent tran
6	31	93.9	2297	2 T34918	polyketide synthas
7	30	90.9	163	2 D84320	hypothetical prote
8	30	90.9	208	2 D75556	phosphoribosylanth
9	30	90.9	261	2 A69807	3-hydroxyisobutyra
10	30	90.9	280	2 D97195	probable xylanase/
11	30	90.9	365	2 F82398	transcription regu
12	30	90.9	380	2 D82088	chromate resistanc
13	30	90.9	384	2 AG0149	probable membrane
14	30	90.9	401	2 D83618	beta-ketoadipyl Co
15	30	90.9	442	2 T20638	hypothetical prote
16	30	90.9	476	2 E82758	siroheme synthase
17	30	90.9	572	2 T37128	hypothetical prote
18	30	90.9	638	2 F75547	anthranilate synth
19	30	90.9	1026	2 T39612	hypothetical prote
20	30	90.9	1293	2 T30871	orsellinic acid sy
21	30	90.9	1471	2 F86218	protein F22013.8 [
22	30	90.9	1616	2 T00713	helicase homolog F
23	29	87.9	32	2 A24047	gap junction prote
24	29	87.9	94	2 S77047	transposase srr17
25	29	87.9	119	2 S74925	transposase srr1065
26	29	87.9	119	2 S75488	transposase srr211
27	29	87.9	119	2 S74836	transposase srr085
28	29	87.9	119	2 S75590	transposase srr125
29	29	87.9	150	2 A83754	hypothetical prote

transposase srr152
hypothetical prote
female protein - g
probable permease
conserved hypochet
serum amyloid P-co
conserved hypochet
serum amyloid P-co
hypothetical prote
hypothetical prote
transposase srr1043
transposase srr023
transposase srr035
transposase srr135
transposase srr199
gap junction prote

ALIGNMENTS

RESULT 1

B69416
hypothetical protein AFI331 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69416
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69416
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-330 <KLE>
A;Cross-references: GB:AE0001012; GB:AE000782; NID:g2689335; PIDN:AAB89926.1; PID:g26492

Query Match 100.0%; Score 33; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 177 LDWSAL 182

RESULT 2

F82645
tryptophan repressor binding protein XF1733 [imported] - Xylella fastidiosa (strain 9a5
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82645
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <SIM>
A;Cross-references: GB:AE003996; GB:AE003849; NID:g9106790; PIDN:AAF84542.1; GSPDB:GN00

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XFI733

Query Match 93.9%; Score 31; DB 2; Length 192;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 43 MDWSAL 48
:|||||

RESULT 3
S75980
hypothetical protein slr0537 - *Synechocystis* sp. (strain PCC 6803)
A;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
R;Accession: S75980
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75980
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-333 <KAN>
A;Cross-references: EMBL:D64006; GB:AB001339; NID:gl001291; PIDN:BAAL0827.1; PID:gl00134
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: probable ribokinase

Query Match 93.9%; Score 31; DB 2; Length 333;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 146 MDWSAL 151
:|||||

RESULT 4
S67527
protein kinase (BC 2.7.1.1-) PRK2 - human
C;Species: *Homo sapiens* (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jul-2000
C;Accession: S67527; I67464
R;Palmer, R.H.; Ridden, J.; Parker, P.J.
Eur. J. Biochem. 227, 344-351, 1995
A;Title: Cloning and expression patterns of two members of a novel protein-kinase-C-rela
A;Reference number: I53327; MUID:95154310; PMID:7851406
A;Accession: S67527
A;Molecule type: mRNA
A;Residues: 1-984 <PAL>
A;Cross-references: EMBL:S75548; NID:G914099; PIDN:AAB33346.1; PID:G914100
A;Experimental source: fetal brain
A;Accession: I67464
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-984 <RES>
A;Cross-references: GB:S75548; NID:G914099; PIDN:AAB33346.1; PID:G914100
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase
F;655-916/Domain: protein kinase homology <KIN>

F;663-671/Region: protein kinase ATP-binding motif
F;686/Active site: Lys #status predicted

Query Match 93.9%; Score 31; DB 2; Length 984;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
DB 919 IDWSAL 924
:|||||

RESULT 5

S66876

ATP-dependent transport protein homolog YOR011w - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: ATP-dependent permease homolog; protein O2601; protein UNA841
C;Species: *Saccharomyces cerevisiae*
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
A;Accession: S66876; S54617; S61995; S72144
R;Pettersson, B.; Sterky, F.; Uhlen, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66882
A;Accession: S66876
A;Molecule type: DNA
A;Residues: 1-841 <PET>
A;Cross-references: EMBL:Z74919; MIPS:YOR011w
A;Experimental source: strain S288C
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
A;Accession: S66877
A;Molecule type: DNA
A;Residues: 355-1394 <DEH>
A;Cross-references: EMBL:Z74919; MIPS:YOR011w
A;Experimental source: strain S288C
R;de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Accession: S54617
A;Molecule type: DNA
A;Residues: 355-1394 <DEW>
A;Cross-references: EMBL:X87331
R;Sterky, F.; Uhlen, M.
submitted to the EMBL Data Library, December 1995
A;Reference number: S61981
A;Accession: S61995
A;Molecule type: DNA
A;Residues: 389-841 <STE>
A;Cross-references: EMBL:U43491; NID:gl150992; PIDN:AAC49491.1; PID:gl151007
R;Sterky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.
Yeast 12, 1091-1095, 1996
A;Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from *Sacchar*

A;Cross-references: EMBL:U43491; NID:gl150992; PIDN:AAC49491.1; PID:gl151007
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C;Genetics:
A;Gene: SGD:AUS1
A;Cross-references: SGD:S0005537
A;Map position: 15R
A;Note: YOR011w
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
F;49-249/Domain: ATP-binding cassette homology <ABC1>
F;391-407/Domain: transmembrane #status predicted <TM1>
F;421-437/Domain: transmembrane #status predicted <TM2>
F;476-492/Domain: transmembrane #status predicted <TM3>
F;501-517/Domain: transmembrane #status predicted <TM4>
F;527-543/Domain: transmembrane #status predicted <TM5>
F;640-656/Domain: transmembrane #status predicted <TM6>

F;766-954/Domain: ATP-binding cassette homology <ABC2>
 F;782-789/Region: nucleotide-binding motif A (P-loop)
 F;1107-1123/Domain: transmembrane #status predicted <TM7>
 F;1166-1182/Domain: transmembrane #status predicted <TM8>
 F;1226-1242/Domain: transmembrane #status predicted <TM9>

Query Match 93.9%; Score 31; DB 2; Length 1394;
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
 :|||||
 Db 1017 IDWSAL 1022

RESULT 6

T34918 polyketide synthase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Nov-2000
 C;Accession: T34918

R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998

A;Reference number: Z21558
 A;Accession: T34918

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2297 <OLI>

A;Cross-references: EMBL:AL021409; PIDN:CAA16183.1; GSPDB:GN00070; SCOEDB:SC3F7.12
 A;Experimental source: strain A3(2)

C;Genetics:

C;Superfamily: [acyl-carrier-protein] synthase I homology; acetate-CoA ligase

A;Gene: SCOEDB:SC3F7.12

C;Keywords: carrier protein

F;80-583/Domain: acetate-CoA ligase homology <ACL>

F;701-771/Domain: acyl carrier protein homology <ACP>

F;818-1205/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F;1315-1600/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

Query Match 93.9%; Score 31; DB 2; Length 2297;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
 :|||||
 Db 1641 IDWSAL 1646

RESULT 7

D84320

hypothetical protein Vng1679h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: D84320

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alam, M.; Freitas T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: D84320

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-163 <STO>

A;Cross-references: GB:AE004437; NID:g10581148; PIDN:AAG19928.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG1679H

Query Match 90.9%; Score 30; DB 2; Length 163;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
 :|||||
 Db 142 LDWAAL 147

RESULT 8

D75556

phosphoribosylthranilate isomerase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C;Accession: D75556

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: D75556

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-208 <WHI>

A;Cross-references: GB:AE001875; GB:AE000513; NID:g6457790; PIDN:AAF09715.1; PID:g64577

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0123

A;Map position: 1

C;Superfamily: phosphoribosylthranilate isomerase; trpF homology

Query Match 90.9%; Score 30; DB 2; Length 208;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
 :|||||
 Db 144 LDWAAL 149

RESULT 9

A69807

3-hydroxyisobutyrate dehydrogenase homolog yfjR - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000

C;Accession: A69807

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Barte

C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmeron, P.I.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, K.; Tognoni, K.; Uchiyama

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,

A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: A69807

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-261 <KUN>

A;Cross-references: GB:299108; GB:AL009126; NID:g2633055; PIDN:CAB12628.1; PID:g2633123

A;Experimental source: strain 168

C;Genetics:

A;Gene: yfjR

C;Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase h

F;2-240/Domain: 3-hydroxyisobutyrate dehydrogenase homology #status atypical <HIB>

Query Match 90.9%; Score 30; DB 2; Length 261;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 |||:|
 Db 251 LDWAAL 256

RESULT 10

D82088
 Probable xylanase/chitin deacetylase [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: D97195
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97195
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-280 <HEI>
 A:Cross-references: GB:AE001437; PIDN:AAK80351.1; PID:gi15025409; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC2396

Query Match 90.9%; Score 30; DB 2; Length 280;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 |||:|
 Db 212 LDWAL 217

RESULT 11

F82398
 transcription regulator AraC/XylS family VCA0926 [imported] - Vibrio cholerae (strain N1
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: F82398
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-365 <HEI>
 A:Cross-references: GB:AE004420; GB:AE003853; NID:g9658361; PIDN:AAF96823.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VCA0926
 A:Map position: 2

Query Match 90.9%; Score 30; DB 2; Length 365;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 :|||
 Db 70 VDWSAL 75

RESULT 12

D82088
 Chromate resistance protein-related protein VC2339 [imported] - Vibrio cholerae (strain
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: D82088
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: D82088
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <HEI>
 A:Cross-references: GB:AE004304; GB:AE003852; NID:g9656905; PIDN:AAF95482.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2339
 A:Map position: 1
 C:Superfamily: chromate resistance protein A

Query Match 90.9%; Score 30; DB 2; Length 380;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 |||:|
 Db 344 LDWAAL 349

RESULT 13

AG0149
 probable membrane protein YPO1221 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AG0149
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0149
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-384 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC90058.1; PID:gi5979278; GSPDB:GN00175
 C:Genetics:
 A:Gene: YPO1221

Query Match 90.9%; Score 30; DB 2; Length 384;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 |||:|
 Db 228 LDWSAV 233

RESULT 14

D83618
 beta-ketoadipyl CoA thiolase PcaP PA0228 [imported] - Pseudomonas aeruginosa (strain PA
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: D83618
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: D83618
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-401 <STO>
 A:Cross-references: GB:AE004460; GB:AE004091; NID:g9946055; PIDN:AAG03617.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:

A;Gene: pcaf; PA0228
C;Superfamily: acetyl-CoA acetyltransferase

Query Match 90.9%; Score 30; DB 2; Length 401;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 45 VDWSAL 50

RESULT 15
T20638
hypothetical protein T06H11.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20638; T24630
R;Kershaw, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19303
A;Accession: T20638
A;Status: preliminary; translated from GE/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-442 <WIL>
A;Cross-references: EMBL:Z49887; PIDN:CAA90060.1; GSPDB:GN00028; CESP:T06H11.4
A;Experimental source: clone F09B9
R;Kershaw, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19914
A;Accession: T24630
A;Status: preliminary; translated from GE/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-442 <WT2>
A;Cross-references: EMBL:Z49889; PIDN:CAA90069.1; GSPDB:GN00028; CESP:T06H11.4
A;Experimental source: clone T06H11
C;Genetics:
A;Gene: CESP:T06H11.4
A;Map position: X
A;Introns: 45/1; 95/3; 150/2; 208/3; 250/2; 292/3
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2

Query Match 90.9%; Score 30; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 39 VDWSAL 44

Search completed: February 18, 2004, 14:38:49
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-13
Perfect score: 33
Sequence: 1 LDMSAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	6	10	US-09-847-940B-13
2	33	100.0	6	11	US-09-847-946A-13
3	31	93.9	53	12	US-10-148-786A-25
4	31	93.9	77	12	US-10-148-786A-8
5	31	93.9	333	12	US-10-369-493-2852
6	31	93.9	334	12	US-10-217-574-18
7	31	93.9	334	12	US-10-217-555-18
8	31	93.9	502	9	US-09-895-072-13
9	31	93.9	502	10	US-09-986-552-13
10	31	93.9	502	12	US-10-023-894-16
11	31	93.9	502	12	US-10-024-197-16
12	31	93.9	502	12	US-10-306-686-13
13	31	93.9	502	15	US-10-023-888-16
14	31	93.9	502	15	US-10-023-889-16
15	31	93.9	502	15	US-10-023-890-16

31	93.9	652	12	US-10-120-801-91	Sequence 91, Appl
31	93.9	984	12	US-10-354-358-106	Sequence 106, Appl
31	93.9	984	14	US-10-029-905-10	Sequence 10, Appl
31	93.9	1394	12	US-10-369-493-22353	Sequence 22353, A
30	90.9	138	12	US-10-029-386-34138	Sequence 34138, A
21	90.9	208	12	US-10-369-493-23401	Sequence 23401, A
22	90.9	403	15	US-10-156-761-14428	Sequence 14428, A
23	90.9	476	12	US-10-310-154-397	Sequence 397, Appl
24	90.9	516	14	US-10-119-635-2	Sequence 2, Appl
30	90.9	1293	12	US-10-084-846A-50	Sequence 50, Appl
26	90.9	2747	12	US-10-402-842-2	Sequence 2, Appl
27	90.9	19725	12	US-10-084-846A-4	Sequence 4, Appl
28	90.9	175	12	US-10-320-797-3024	Sequence 3024, Ap
29	87.9	203	12	US-10-262-473-4	Sequence 4, Appl
30	87.9	223	12	US-10-262-473-2	Sequence 2, Appl
31	87.9	228	12	US-10-084-846A-16	Sequence 16, Appl
32	87.9	267	15	US-10-156-761-14290	Sequence 14290, A
33	87.9	292	12	US-10-238-075-301	Sequence 301, Appl
34	87.9	297	11	US-09-557-796-30	Sequence 30, Appl
35	87.9	300	12	US-10-314-657-11	Sequence 11, Appl
36	87.9	324	15	US-10-156-761-7691	Sequence 7691, Ap
37	87.9	345	11	US-09-735-056-34	Sequence 34, Appl
38	87.9	352	12	US-10-289-762-702	Sequence 702, Appl
39	87.9	382	12	US-10-024-298A-113	Sequence 113, Appl
40	87.9	382	12	US-10-024-298A-115	Sequence 115, Appl
41	87.9	382	12	US-10-042-211A-113	Sequence 113, Appl
42	87.9	382	12	US-10-042-211A-115	Sequence 115, Appl
43	87.9	382	12	US-10-438-537-6	Sequence 6, Appl
44	87.9	382	12	US-10-372-683-28	Sequence 28, Appl
45	87.9	426	12	US-10-369-493-3236	Sequence 3236, Ap

ALIGNMENTS

RESULT 1
US-09-847-940B-13
; Sequence 13, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-13

Query Match 100.0%; Score 33; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6
Db 1 LDMSAL 6

RESULT 2
US-09-847-946A-13
; Sequence 13, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-13

Query Match 100.0%; Score 33; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 1 LDWSAL 6

RESULT 3
US-10-148-786A-25
; Sequence 25, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario
; APPLICANT: Blondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-25

Query Match 93.9%; Score 31; DB 12; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 12 IDWSAL 17

RESULT 4
US-10-148-786A-8
; Sequence 8, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario
; APPLICANT: Blondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-8

Query Match 93.9%; Score 31; DB 12; Length 77;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 12 IDWSAL 17

RESULT 5
US-10-369-493-2852
; Sequence 2852, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2852
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-10-369-493-2852

Query Match 93.9%; Score 31; DB 12; Length 333;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
Db 146 MDWSAL 151

RESULT 6
US-10-217-574-18
; Sequence 18, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18

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; LENGTH: 334
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-574-18

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Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDWSAL 6
Db      269 IDWSAL 274

RESULT 7
US-10-217-555-18
; Sequence 18, Application US/10217555
; Publication No. US2004009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-555-18

Query Match          93.9%; Score 31; DB 12; Length 334;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDWSAL 6
Db      269 IDWSAL 274

RESULT 8
US-09-895-072-13
; Sequence 13, Application US/09895072
; Patent No. US20020025550A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 210119USCONT
; CURRENT APPLICATION NUMBER: US/09/895,072
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: US 09/635,872
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 502
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-895-072-13

Query Match          93.9%; Score 31; DB 9; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDWSAL 6
Db      372 LDWSAM 377

RESULT 9
US-09-986-552-13
; Sequence 13, Application US/09986552
; Patent No. US20020150981A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 215089US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-986-552-13

Query Match          93.9%; Score 31; DB 10; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDWSAL 6
Db      372 LDWSAM 377

RESULT 10
US-10-023-894-16
; Sequence 16, Application US/10023894
; Publication No. US20030143669A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; APPLICANT: KORNFELD, Stuart
; TITLE OF INVENTION: EXPRESSION OF LYSOSOMAL HYDROLASE IN CELLS EXPRESSING PRO-N-
; TITLE OF INVENTION: ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSAMINIDA
; FILE REFERENCE: 217139US77
; CURRENT APPLICATION NUMBER: US/10/023,894
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-894-16

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDWSAL 6
Db      372 LDWSAM 377
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RESULT 11
US-10-024-197-16
; Sequence 16, Application US/10024197
; Publication No. US20030133924A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBSIDASE AND METHODS OF
; TREATING GAUCHER'S DISEASE
; FILE REFERENCE: 209794US0
; CURRENT APPLICATION NUMBER: US/10/024,197
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-024-197-16

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
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Db      372 LDWSAM 377

RESULT 12
US-10-306-686-13
; Sequence 13, Application US/10306686
; Publication No. US20030148460A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNACASE OF THE LYSOSOMAL TARGETING PATHWAY
; FILE REFERENCE: 230397US77D1V
; CURRENT APPLICATION NUMBER: US/10/306,686
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: 09/636,596
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-08-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-306-686-13

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
        |||||:
Db      372 LDWSAM 377

RESULT 13
US-10-023-888-16
; Sequence 16, Application US/10023888
; Publication No. US20030119088A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: SOLUBLE GLCNAC PHOSPHOTRANSFERASE
; FILE REFERENCE: 203515US77
; CURRENT APPLICATION NUMBER: US/10/023,888
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-888-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
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Db      372 LDWSAM 377

RESULT 14
US-10-023-889-16
; Sequence 16, Application US/10023889
; Publication No. US20030124652A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: DEFICIENT CELLS
; FILE REFERENCE: 203512US77
; CURRENT APPLICATION NUMBER: US/10/023,889
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-889-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
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Db      372 LDWSAM 377

RESULT 15
US-10-023-890-16
; Sequence 16, Application US/10023890
; Publication No. US20030124653A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHOD OF PRODUCING GLYCOPROTEINS HAVING REDUCED COMPLEX CARBOHY
; FILE REFERENCE: 203510US77
; CURRENT APPLICATION NUMBER: US/10/023,890
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-890-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
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Db      372 LDWSAM 377

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LWSAL 6

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	33	100.0	6	24	ABU08428
4	33	100.0	756	23	AB077299
5	31	93.9	53	21	AA094732
6	31	93.9	53	22	AA099802
7	31	93.9	77	22	AA099793
8	31	93.9	315	22	AA099835
9	31	93.9	345	22	AB063738

10	31	93.9	385	22	AA099822	AGC protein kinase
11	31	93.9	652	22	AB059094	Drosophila melanog
12	31	93.9	984	21	AA094736	Protein kinase C r
13	31	93.9	984	23	AA015489	Human aerin-threon
14	30	90.9	53	21	AA056197	Arabidopsis thalia
15	30	90.9	57	21	AA056196	Arabidopsis thalia
16	30	90.9	124	22	AB067643	Drosophila melanog
17	30	90.9	516	23	AB079577	Human proline dehy
18	30	90.9	536	22	AB022095	Novel human diagno
19	30	90.9	631	22	AB022094	Novel human diagno
20	30	90.9	1293	24	AB076703	Streptomyces virid
21	30	90.9	1891	18	AA023720	Platenolide syntha
22	30	90.9	1891	18	AA022610	Platenolide syntha
23	30	90.9	19938	24	AB076678	Streptomyces virid
24	29	87.9	35	22	AA008947	Human polypeptide
25	29	87.9	98	21	AA000108	Human secreted pro
26	29	87.9	129	22	AA043320	Propionibacterium
27	29	87.9	134	22	AA048444	Propionibacterium
28	29	87.9	204	16	AA074763	Serum amyloid P c
29	29	87.9	210	16	AA074769	Female hamster pro
30	29	87.9	223	13	AA029923	SAP. Homo sapiens
31	29	87.9	228	24	AB076686	Streptomyces virid
32	29	87.9	254	21	AA052497	Arabidopsis thalia
33	29	87.9	255	21	AA052496	Arabidopsis thalia
34	29	87.9	292	21	AA052495	Arabidopsis thalia
35	29	87.9	292	22	AB052479	Escherichia coli p
36	29	87.9	300	24	ABU11350	Protein encoded by
37	29	87.9	302	23	AB049167	Listeria monocytog
38	29	87.9	345	20	AA087715	An active acyltran
39	29	87.9	345	21	AA012927	Protein sequence o
40	29	87.9	352	20	AA035284	Chlamydia pneumoni
41	29	87.9	361	22	AA049927	Propionibacterium
42	29	87.9	382	19	AA023969	Connexin protein C
43	29	87.9	382	23	AB061480	Human NF-kB activa
44	29	87.9	382	23	AB061481	Human NF-kB activa
45	29	87.9	394	22	AB062389	Drosophila melanog

ALIGNMENTS

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AC AB080735;

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DT 14-JUN-2002 (first entry)

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Key Location/Qualifiers

Misc-difference 5

/note= "Wildtype Trp substituted by Ala"

WO200183547-A2.

08-NOV-2001.

PF 02-MAY-2001; 2001WO-US40654.
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 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 DR
 XX
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 PT
 XX
 XX Claim 23; Page 45; 82pp; English.
 PS
 XX
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB077313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 33; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 1 LDWSAL 6
 |||||
 RESULT 2
 ID AAM48518
 XX AAM48518 standard; Peptide; 6 AA.
 AC AAM48518;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 13.
 DE

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX Example 6; Page 48; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-NMMA8627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 33; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 Db 1 LDWSAL 6
 |||||
 RESULT 3
 ID ABU08428
 ABU08428 standard; peptide; 6 AA.

XX AC ABU08428;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #11.
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW KappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neutropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX US2002156000-A1.
 XX 24-OCT-2002.
 XX 02-MAY-2001; 2001US-0847940.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX May MJ, Ghosh S;
 XX WPI; 2003-209142/20.
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX Claim 22; Page 17; 47pp; English.
 XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 33; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWSAL 6
 Db 1 LDWSAL 6
 RESULT 4
 ABU08428
 ID ABU08428 standard; protein; 756 AA.
 XX

AC ABB77299;
 XX 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant W741A.
 XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neutropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antipsoriatic; antirheumatic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 741 /note= "Wildtype Trp substituted by Ala"
 FT WO200183547-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US40654.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYA) UNIV YALE.
 XX May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX Example 11; Page -; 82pp; English.
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. 014920 (ABE77294).

XX Sequence 756 AA;

Query Match 100.0%; Score 33; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;

OY 1 LWSAL 6
 Db 737 LWSAL 742
 :|||||

RESULT 5
 AAY94732
 ID AAY94732 standard; peptide; 53 AA.

XX

AC AAY94732;

XX 29-JAN-2001 (first entry)

DE Region A of protein kinase C related protein kinase 2.

XX Substrate specificity; phosphoinositide-dependent protein kinase 1;
 KW PDK1; protein kinase C related protein kinase 2; PRK2; cancer; apoptosis;
 KW mechanical tissue damage; ischemic disease; stroke;
 KW myocardial infarction; antigenic peptide.

XX Unidentified.

XX WO200056864-A2.

XX 28-SEP-2000.

XX 17-MAR-2000; 2000WO-GB01004.

XX 19-MAR-1999; 99GB-0006245.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;

XX WPI; 2000-647155/62.

XX Altering substrate specificity of phosphoinositide-dependent protein
 PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
 PT interacting polypeptide -

XX Disclosure; Page 12; 103pp; English.

XX This invention relates to a method for altering the substrate
 CC specificity of phosphoinositide-dependent protein kinase 1 (PDK1), by
 CC exposing it to an interacting polypeptide. Included in the invention are
 CC a preparation comprising PDK1 and an interacting polypeptide, PDK1 with
 CC altered specificity is useful for phosphorylating a residue corresponding
 CC to the Ser/Thr residue of a substrate with the following peptide
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for
 CC phosphorylating protein kinase C related protein kinase 2 (PRK2). The
 CC compound identified by methods of the invention that are capable of
 CC altering the substrate specificity of PDK1 are useful for manufacturing a
 CC medicament for treating a patient who is in need of modulation of the
 CC insulin signalling pathway and/or PDK1, PDK2 or PRK2 signalling. A
 CC compound that is capable of reducing the activity (i.e. the PDK1 and/or
 CC the PDK2 activity) of PDK1 may be useful in treating cancer. PDK1,
 CC e.g. via protein kinase B and/or SGK, may be capable of providing a

CC survival signal that protects cells from apoptosis induced in a variety
 CC of ways. Reduction of the activity of PDK1 may promote apoptosis and may
 CC be useful in treating cancer. Conditions in which aiding apoptosis may be
 CC of benefit may also include resolution of inflammation. A compound
 CC capable of increasing the activity of PDK1 may be useful in treating
 CC diabetes or obesity, or may be useful in inhibiting apoptosis. Increased
 CC activity of PDK1 may lead to increased levels of leptin, which may lead
 CC to weight loss. The compounds may suppress apoptosis, which may aid cell
 CC survival during or following cell damaging processes and in treating
 CC disease in which apoptosis is involved. Examples of the diseases include,
 CC mechanical (including heat) tissue injury or ischemic disease, for
 CC example stroke and myocardial infarction, or neural injury. The present
 CC sequence represents a region of protein kinase C related protein kinase
 CC 2 (PRK2) which interacts with PDK1.

XX Sequence 53 AA;

Query Match 93.9%; Score 31; DB 21; Length 53;
 Best Local Similarity 83.3%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LWSAL 6
 Db 12 IDWSAL 17
 :|||||

RESULT 6

AAB99802

ID AAB99802 standard; Peptide; 53 AA.

XX

AC AAB99802;

DT 20-SEP-2001 (first entry)

XX Protein kinase derived interacting peptide #4.

XX Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.

XX Homo sapiens.

OS Synthetic.

XX WO200144497-A2.

XX 21-JUN-2001.

XX 04-DEC-2000; 2000WO-GB04598.

XX 02-DEC-1999; 99US-0168559.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Biondi R;

XX WPI; 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -

XX Disclosure; Page 25; 180pp; English.

XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,

CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 53 AA;
 Query Match 93.9%; Score 31; DB 22; Length 53;
 Best Local Similarity 83.3%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 :|||||
 Db 12 IDWSAL 17

RESULT 7
 AAB99793
 ID AAB99793 standard; Peptide; 77 AA.

XX AAB99793;
 XX 20-SEP-2001 (first entry)
 XX 3-phosphoinositide-dependent protein kinase 1 binding peptide PIF.
 XX Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.

XX Homo sapiens.
 OS Synthetic.
 XX WO200144497-A2.
 XX 21-JUN-2001.
 XX 04-DEC-2000; 2000WO-GB04598.
 XX 02-DEC-1999; 99US-0168559.
 XX (UYDU-) UNIV DUNDEE.
 XX Alessi D, Biondi R;
 XX WPI; 2001-390252/41.
 XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -

XX Disclosure; Page 22; 180pp; English.
 PS
 XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing

CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 77 AA;
 Query Match 93.9%; Score 31; DB 22; Length 77;
 Best Local Similarity 83.3%; Pred. No. 14e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSAL 6
 :|||||
 Db 12 IDWSAL 17

RESULT 8
 AAB99835
 ID AAB99835 standard; Protein; 315 AA.

XX AAB99835;
 XX 20-SEP-2001 (first entry)
 XX AGC protein kinase family member PRK2 protein sequence.
 XX Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.

XX Homo sapiens.
 OS Synthetic.
 XX WO200144497-A2.
 XX 21-JUN-2001.
 XX 04-DEC-2000; 2000WO-GB04598.
 XX 02-DEC-1999; 99US-0168559.
 XX (UYDU-) UNIV DUNDEE.
 XX Alessi D, Biondi R;
 XX WPI; 2001-390252/41.

XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with
 PT interacting polypeptides -

XX Disclosure; Fig 16; 180pp; English.
 PS
 XX The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue

CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

SQ Sequence 315 AA;

Query Match 93.9%; Score 31; DB 22; Length 315;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
 Db 250 IDWSAL 255

RESULT 9

ABB63738
 ID ABB63738 standard; Protein; 345 AA.

XX

AC ABB63738;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 18006.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US09231.

XX

PR 23-MAR-2000; 2000US-191637P.

XX

PR 11-JUL-2000; 2000US-0614150.

XX

PA (PEKE) PE CORP NY.

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

DR WPI; 2001-656860/75.

XX

DR N-PSDB; ABL07841.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -

XX

PS Disclosure; SEQ ID NO 18006; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511); expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 345 AA;

Query Match 93.9%; Score 31; DB 22; Length 345;
 Best Local Similarity 83.3%; Pred. No. 6.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6

Db 136 LDWSAI 141

|||||

RESULT 10

AAB99822

ID AAB99822 standard; Protein; 385 AA.

XX

AC AAB99822;

XX

DT 20-SEP-2001 (first entry)

XX

DE AGC protein kinase family member PRK2 protein sequence.

XX

KW Protein kinase; identification; hydrophobic pocket; interacting;

KW cancer; diabetes; inhibition; apoptosis; tissue injury;

KW ischaemic injury; stroke.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200144497-A2.

XX

PD 21-JUN-2001.

XX

PF 04-DEC-2000; 2000WO-GB04598.

XX

PR 02-DEC-1999; 99US-0168559.

XX

PA (UYDU-) UNIV DUNDEE.

XX

PI Alessi D, Biondi R;

XX

DR WPI; 2001-390252/41.

XX

PT Identifying modulators of protein kinase (PK) activity, useful in

PT developing drugs for treating cancer or diabetes, by measuring the

PT ability of the compound to modulate or mimic the interaction of PK with

PT interacting polypeptides -

XX

PS Disclosure; Fig 15; 180pp; English.

XX

CC The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX

SQ Sequence 385 AA;

Query Match 93.9%; Score 31; DB 22; Length 385;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
:|||||
Db 320 IDWSAL 325

RESULT 11
ID ABB59094 standard; Protein; 652 AA.
XX
AC ABB59094;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 4074.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PS 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL03197.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 4074; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 652 AA;
Query Match 93.9%; Score 31; DB 22; Length 652;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
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Db 447 LDWSAM 452

RESULT 12
ID AAY94736 standard; Protein; 984 AA.
XX
AC AAY94736;
XX
DT 29-JAN-2001 (first entry)
XX

DE Protein kinase C related protein kinase 2.
XX
KW Substrate specificity; phosphoinositide-dependent protein kinase 1;
KW PDK1; protein kinase C related protein kinase 2; PKK2; cancer; apoptosis;
KW mechanical tissue damage; ischaemic disease; stroke;
KW myocardial infarction; antigenic peptide.
XX
OS Unidentified.
XX
PN WO200056864-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB01004.
XX
PR 19-MAR-1999; 99GB-0006245.
XX
PS (UYDU-) UNIV DUNDEE.
XX
PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;
XX
DR WPI; 2000-647155/62.
XX
PT Altering substrate specificity of phosphoinositide-dependent protein
PT kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
PT interacting polypeptide -
XX
PS Disclosure; Fig 11; 103pp; English.
XX
CC This invention relates to a method for altering the substrate
CC specificity of phosphoinositide-dependent protein kinase 1 (PDK1), by
CC exposing it to an interacting polypeptide. Included in the invention are
CC a preparation comprising PDK1 and an interacting polypeptide, PDK1 with
CC altered specificity is useful for phosphorylating a residue corresponding
CC to the Ser/Thr residue of a substrate with the following peptide
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for
CC phosphorylating protein kinase C related protein kinase 2 (PRK2). The
CC compound identified by methods of the invention that are capable of
CC altering the substrate specificity of PDK1 are useful for manufacturing a
CC medicament for treating a patient who is in need of modulation of the
CC insulin signalling pathway and/or PDK1, PDK2 or PKK2 signalling. A
CC compound that is capable of reducing the activity (i.e. the PDK1 and/or
CC the PDK2 activity) of PDK1 may be useful in treating cancer. PDK1, e.g.
CC via protein kinase B and/or SGK, may be capable of providing a survival
CC signal that protects cells from apoptosis induced in a variety of ways.
CC Reduction of the activity of PDK1 may promote apoptosis and may be useful
CC in treating cancer. Conditions in which aiding apoptosis may be benefit
CC may also include resolution of inflammation. A compound capable of
CC increasing the activity of PDK1 may be useful in treating diabetes or
CC obesity, or may be useful in inhibiting apoptosis. Increased activity of
CC PDK1 may lead to increased levels of leptin, which may lead to weight
CC loss. The compounds may suppress apoptosis, which may aid cell survival
CC during or following cell damaging processes and in treating disease in
CC which apoptosis is involved. Examples of the diseases include, mechanical
CC (including heat) tissue injury or ischaemic disease, for example stroke
CC and myocardial infarction, or neural injury. The present sequence
CC represents a protein kinase C related protein kinase 2 amino acid
CC sequence, used in the course of the invention.
XX
SQ Sequence 984 AA;

Query Match 93.9%; Score 31; DB 21; Length 984;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
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Db 919 IDWSAL 924

RESULT 13
ID AAO15489 standard; Protein; 984 AA.

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Query Match 90.9%; Score 30; DB 21; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 30 VDMSAL 35

RESULT 15
AAG56196
ID AAG56196 standard; Protein; 57 AA.

XX AAG56196;
XX
XX DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 72195.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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Query Match 90.9%; Score 30; DB 21; Length 57;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 34 VDMSAL 39

Search completed: February 18, 2004, 14:26:24
Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
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Title: US-09-643-260-12
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Scoring table: BLOSUM62
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Searched: 801455 seqs, 209382283 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	36	100.0	8	11	US-09-847-946A-92
6	36	100.0	8	11	US-09-847-946A-100
7	36	100.0	9	11	US-09-847-946A-91
8	36	100.0	9	11	US-09-847-946A-94
9	36	100.0	9	11	US-09-847-946A-97
10	36	100.0	9	11	US-09-847-946A-98
11	36	100.0	10	11	US-09-847-946A-93
12	36	100.0	10	11	US-09-847-946A-96
13	36	100.0	11	11	US-09-847-946A-90
14	33	91.7	73	12	US-10-074-978A-310
15	33	91.7	314	12	US-10-074-978A-66

16	33	91.7	320	12	US-10-074-978A-68	Sequence 68, Appl
17	33	91.7	404	12	US-10-074-978A-64	Sequence 64, Appl
18	33	91.7	404	12	US-10-074-978A-304	Sequence 304, Appl
19	33	91.7	404	15	US-10-225-567A-480	Sequence 480, Appl
20	32	88.9	6	10	US-09-847-940B-11	Sequence 11, Appl
21	32	88.9	6	11	US-09-847-946A-11	Sequence 11, Appl
22	32	88.9	6	11	US-09-847-946A-42	Sequence 42, Appl
23	32	88.9	6	11	US-09-847-946A-84	Sequence 84, Appl
24	32	88.9	7	11	US-09-847-946A-88	Sequence 88, Appl
25	32	88.9	8	11	US-09-847-946A-81	Sequence 81, Appl
26	32	88.9	8	11	US-09-847-946A-89	Sequence 89, Appl
27	32	88.9	9	11	US-09-847-946A-80	Sequence 80, Appl
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29	32	88.9	9	11	US-09-847-946A-86	Sequence 86, Appl
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33	32	88.9	10	11	US-09-847-946A-79	Sequence 79, Appl
34	32	88.9	69	9	US-09-864-761-36612	Sequence 36612, A
35	32	88.9	71	11	US-09-969-730-172	Sequence 172, Appl
36	32	88.9	72	11	US-09-774-639-171	Sequence 171, Appl
37	32	88.9	278	12	US-10-220-511-11	Sequence 11, Appl
38	32	88.9	404	12	US-10-307-234-8	Sequence 8, Appl
39	32	88.9	547	12	US-10-369-493-11197	Sequence 11197, A
40	32	88.9	766	12	US-10-104-047-2545	Sequence 2545, Ap
41	32	88.9	830	12	US-10-264-237-1879	Sequence 1879, Ap
42	32	88.9	1232	12	US-10-369-493-21495	Sequence 21495, A
43	31	86.1	6	10	US-09-847-940B-2	Sequence 2, Appl
44	31	86.1	6	11	US-09-847-946A-2	Sequence 2, Appl
45	31	86.1	6	11	US-09-847-946A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-12
; Sequence 12, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-12

Query Match 100.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 2
US-09-847-946A-12
; Sequence 12, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-12

Query Match 100.0%; Score 36; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 3

US-09-847-946A-95
; Sequence 95, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-95

Query Match 100.0%; Score 36; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 4

US-09-847-946A-99
; Sequence 99, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-99

Query Match 100.0%; Score 36; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 1 LDYSWL 6

RESULT 5

US-09-847-946A-92
; Sequence 92, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-92

Query Match 100.0%; Score 36; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 3 LDYSWL 8

RESULT 6

US-09-847-946A-100
; Sequence 100, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar A
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-100

Query Match 100.0%; Score 36; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||||
Db 1 LDYSWL 6

RESULT 7

US-09-847-946A-91
; Sequence 91, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar A
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-91

Query Match 100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||||
Db 1 LDYSWL 6

RESULT 8

US-09-847-946A-94
; Sequence 94, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar A
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-94

Query Match 100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||||
Db 1 LDYSWL 6

RESULT 9

US-09-847-946A-97
; Sequence 97, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar A
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-97

Query Match 100.0%; Score 36; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 3 LDYSWL 8

RESULT 10

US-09-847-946A-98
 ; Sequence 98, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 98
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-98

Query Match 100.0%; Score 36; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 2 LDYSWL 7

RESULT 11

US-09-847-946A-93
 ; Sequence 93, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 93
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-93

Query Match 100.0%; Score 36; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 2 LDYSWL 7

RESULT 12

US-09-847-946A-96
 ; Sequence 96, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 96
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-96

Query Match 100.0%; Score 36; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 3 LDYSWL 8

RESULT 13

US-09-847-946A-90
 ; Sequence 90, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 90
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-90

US-09-847-946A-90

Query Match 100.0%; Score 36; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
Db 3 LDYSWL 8

RESULT 14

US-10-074-978A-310
; Sequence 310, Application US/10074978A
; Publication No. US20040010119A1

; GENERAL INFORMATION:

; APPLICANT: Leite, Mario

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Fernandes, Elma

; APPLICANT: Li, Li

; APPLICANT: Kekuda, Rameesh

; APPLICANT: Liu, Xiahong

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Patturajan, Meera

; APPLICANT: Blalock, Angela

; APPLICANT: Ballinger, Robert

; APPLICANT: Vernet, Corine

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Gusev, Vladimir

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter S

; APPLICANT: Ellerman, Karen

; APPLICANT: Heyes, Melvin P

; APPLICANT: Herrman, John

; APPLICANT: Pena, Carol E A

; APPLICANT: Shimkets, Richard A

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Moore, No. US20040010119A1lle

; APPLICANT: Shenoy, Suresh

; APPLICANT: Edinger, Shlomit

; APPLICANT: Gunther, Erik

; APPLICANT: Stone, Dave

; APPLICANT: Millet, Isabelle

; APPLICANT: Peyman, John

; APPLICANT: Smithson, Glenda

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-269

; CURRENT APPLICATION NUMBER: US/10/074,978A

; CURRENT FILING DATE: 2003-01-07

; PRIOR APPLICATION NUMBER: 60/268,221

; PRIOR FILING DATE: 2001-02-12

; PRIOR APPLICATION NUMBER: 60/335,109

; PRIOR FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: 60/312,284

; PRIOR FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: 60/268,496

; PRIOR FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: 60/276,703

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/330,293

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/322,127

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/280,899

; PRIOR FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 60/310,797

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/268,646

; PRIOR FILING DATE: 2001-02-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 310
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-310

Query Match 91.7%; Score 33; DB 12; Length 73;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
Db 46 LDYTWL 51

RESULT 15

US-10-074-978A-66

; Sequence 66, Application US/10074978A

; Publication No. US20040010119A1

; GENERAL INFORMATION:

; APPLICANT: Leite, Mario

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Fernandes, Elma

; APPLICANT: Li, Li

; APPLICANT: Kekuda, Rameesh

; APPLICANT: Liu, Xiahong

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Patturajan, Meera

; APPLICANT: Blalock, Angela

; APPLICANT: Ballinger, Robert

; APPLICANT: Vernet, Corine

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Gusev, Vladimir

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter S

; APPLICANT: Ellerman, Karen

; APPLICANT: Heyes, Melvin P

; APPLICANT: Herrman, John

; APPLICANT: Pena, Carol E A

; APPLICANT: Shimkets, Richard A

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Moore, No. US20040010119A1lle

; APPLICANT: Shenoy, Suresh

; APPLICANT: Edinger, Shlomit

; APPLICANT: Gunther, Erik

; APPLICANT: Stone, Dave

; APPLICANT: Millet, Isabelle

; APPLICANT: Peyman, John

; APPLICANT: Smithson, Glenda

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-269

; CURRENT APPLICATION NUMBER: US/10/074,978A

; CURRENT FILING DATE: 2003-01-07

; PRIOR APPLICATION NUMBER: 60/268,221

; PRIOR FILING DATE: 2001-02-12

; PRIOR APPLICATION NUMBER: 60/335,109

; PRIOR FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: 60/312,284

; PRIOR FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: 60/268,496

; PRIOR FILING DATE: 2001-02-13

; PRIOR APPLICATION NUMBER: 60/276,703

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/330,293

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/322,127

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/280,899

; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-66

Query Match 91.7%; Score 33; DB 12; Length 314;
Best Local Similarity 83.3%; Pred.No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||:
Db 116 LDYTWL 121

Search completed: February 18, 2004, 15:41:59
Job time : 17.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSLW 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	6	ABB08734	Mutated IKKbeta NE
2	36	100.0	6	AAW48517	NBD mutant peptide
3	36	100.0	6	AAW48540	Anti-inflammatory
4	36	100.0	6	AAW48592	Anti-inflammatory
5	36	100.0	6	ABU08427	Human NEMO binding
6	36	100.0	7	AAW48596	Anti-inflammatory
7	36	100.0	8	AAW48589	Anti-inflammatory
8	36	100.0	8	AAW48597	Anti-inflammatory
9	36	100.0	9	AAW48588	Anti-inflammatory

10	36	100.0	9	23	AAW48591	Anti-inflammatory
11	36	100.0	9	23	AAW48594	Anti-inflammatory
12	36	100.0	9	23	AAW48595	Anti-inflammatory
13	36	100.0	10	23	AAW48590	Anti-inflammatory
14	36	100.0	10	23	AAW48593	Anti-inflammatory
15	36	100.0	11	23	AAW48587	Anti-inflammatory
16	36	100.0	156	23	ABG00789	Human IKKbeta muta
17	33	91.7	390	22	ABG00789	Novel human diaga
18	33	91.7	404	19	AAW59035	Human G-protein co
19	33	91.7	404	19	AAW31344	Human G-protein co
20	33	91.7	404	19	AAW34984	Human G-protein co
21	33	91.7	404	20	AAW28463	Polypeptide encodi
22	33	91.7	404	22	AAW78632	Human protein SEQ
23	33	91.7	404	23	AAU79260	Human ADMR protein
24	33	91.7	404	23	AAU79261	Human ADMR variant
25	33	91.7	404	24	ABP81996	Human adrenomedull
26	33	91.7	448	22	ABW12312	Human GPCR homolog
27	33	91.7	448	22	AAW79616	Human protein SEQ
28	32	88.9	6	23	ABB08733	Mutated IKKbeta NE
29	32	88.9	6	23	AAW48516	NBD mutant peptide
30	32	88.9	6	23	AAW48539	Anti-inflammatory
31	32	88.9	6	23	AAW48581	Anti-inflammatory
32	32	88.9	6	24	ABU08426	Human NEMO binding
33	32	88.9	7	23	AAW48585	Anti-inflammatory
34	32	88.9	8	23	AAW48578	Anti-inflammatory
35	32	88.9	8	23	AAW48586	Anti-inflammatory
36	32	88.9	9	23	AAW48577	Anti-inflammatory
37	32	88.9	9	23	AAW48580	Anti-inflammatory
38	32	88.9	9	23	AAW48583	Anti-inflammatory
39	32	88.9	9	23	AAW48584	Anti-inflammatory
40	32	88.9	10	23	AAW48579	Anti-inflammatory
41	32	88.9	10	23	AAW48582	Anti-inflammatory
42	32	88.9	11	23	AAW48576	Anti-inflammatory
43	32	88.9	69	22	ABG30764	Human liver peptid
44	32	88.9	69	22	ABG30729	Peptide #3380 enco
45	32	88.9	69	22	ABB35904	Peptide #3410 enco

ALIGNMENTS

RESULT 1

ABB08734

ID ABB08734 standard; peptide; 6 AA.

XX

AC ABB08734;

XX

DT 14-JUN-2002 (first entry)

XX

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 12.

XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiaesthetic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antitumor; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT Misc-difference 3

FT /note= "Wildtype Trp substituted by Tyr"

XX

XX WO200183547-A2.

XX

XX 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 XX WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 45; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-KB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 1 LDYSWL 6
 |||||
 |||||
 RESULT 2
 AAM48517
 ID AAM48517 standard; Peptide; 6 AA.
 XX
 AC AAM48517;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 12.
 DE

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 XX Example 6; Page 48; 88pp; English.
 PS
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-NM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 1 LDYSWL 6
 |||||
 |||||
 RESULT 3
 AAM48540
 ID AAM48540 standard; Peptide; 6 AA.

XX AAM48540;
 XX 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 43.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 XX antiarthritis; osteopathic; antibacterial; virucide;
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 XX autoimmune disorder; multiple sclerosis; transplant rejection;
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 XX factor kappaB activation, and for treating asthma, lung inflammation,
 XX psoriasis -
 XX Claim 6; Page 61; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 XX AAM48628-AAM48645), comprising a membrane translocation domain
 XX (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 XX amino acid residues, fused to a NEMO binding sequence
 XX (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 XX cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 XX antibacterial, immunosuppressive, virucide and antiallergic activity. The
 XX compounds act as selective inhibitors of cytokine-mediated NFkappaB
 XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 XX the NEMO binding domain that results in inhibition of IKKbeta kinase
 XX activation and subsequent decreased phosphorylation of IkappaB. The
 XX compounds are useful for treating inflammatory disorders, e.g. asthma,
 XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 XX bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 XX telangiectasia. The compounds are also useful for treating
 XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 XX arthritis.
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 36; DB 23; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 LDYSWL 6
 XX |||||

Db 1 LDYSWL 6
 RESULT 4
 AAM48592
 ID AAM48592 standard; Peptide; 6 AA.
 XX AC AAM48592;
 XX 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 95.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 XX antiarthritis; osteopathic; antibacterial; virucide;
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 XX autoimmune disorder; multiple sclerosis; transplant rejection;
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 XX factor kappaB activation, and for treating asthma, lung inflammation,
 XX psoriasis -
 XX Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 XX AAM48628-AAM48645), comprising a membrane translocation domain
 XX (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 XX amino acid residues, fused to a NEMO binding sequence
 XX (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 XX cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 XX antibacterial, immunosuppressive, virucide and antiallergic activity. The
 XX compounds act as selective inhibitors of cytokine-mediated NFkappaB
 XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 XX the NEMO binding domain that results in inhibition of IKKbeta kinase
 XX activation and subsequent decreased phosphorylation of IkappaB. The
 XX compounds are useful for treating inflammatory disorders, e.g. asthma,
 XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 XX bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 XX telangiectasia. The compounds are also useful for treating
 XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 XX arthritis.
 XX Sequence 6 AA;

Query Match 100.0%; Score 36; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 1 LDYSWL 6

RESULT 5
 ABU08427
 ID ABU08427 standard; peptide; 6 AA.
 XX
 AC ABU08427;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #10.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antiirreumatic; antiarthritic; mutant; muten.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX
 XX 24-OCT-2002.
 PD
 PF 02-MAY-2001; 2001US-0847940.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 XX May MJ, Ghosh S;
 PI
 XX
 DR WPI; 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.

The present invention relates to antiinflammatory compounds comprising
 NEMO binding domain (NBD) peptides. The NEMO binding domains are
 found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 (IKKalpha) proteins. The antiinflammatory compounds of the invention
 are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 in a cell, where the compounds are capable of blocking the interaction
 between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 antiinflammatory compound further comprises at least one membrane
 translocation domain. The compounds are useful for treating
 inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 telangiectasia, and for transplantation detection. The compounds of
 the invention block NF-kappaB induction by IKK but do not inhibit
 the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 NBD mutant peptides.

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 36; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 1 LDYSWL 6

RESULT 6
 AAM48596
 ID AAM48596 standard; Peptide; 7 AA.
 XX
 AC AAM48596;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 99.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antiirreumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially
 AAM48628-AAM48645), comprising a membrane translocation domain
 (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 amino acid residues, fused to a NEMO binding sequence
 (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 cytostatic, antipsoriatic, antiirreumatic, antiarthritic, osteopathic,
 antibacterial, immunosuppressive, dermatological, neuroprotective,
 nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 compounds act as selective inhibitors of cytokine-mediated NFkappaB
 activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 the NEMO binding domain that results in inhibition of IKKbeta kinase
 activation and subsequent decreased phosphorylation of IkappaB. The
 compounds are useful for treating inflammatory disorders, e.g. asthma,
 lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 36; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 1 LDYSWL 6

RESULT 7
 AAM48589
 ID AAM48589 standard; Peptide; 8 AA.
 XX AAM48589;
 XX

20-MAR-2002 (first entry)
 Anti-inflammatory peptide SEQ ID NO 92.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 36; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 3 LDYSWL 8

RESULT 8
 AAM48597
 ID AAM48597 standard; Peptide; 8 AA.
 XX AAM48597;
 XX

20-MAR-2002 (first entry)
 Anti-inflammatory peptide SEQ ID NO 100.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antiatherosclerotic, dermatological, neuroprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 8 AA;
 SQ Query Match 100.0%; Score 36; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 Db 1 LDYSWL 6
 |||||

RESULT 9
 AAM48588
 ID AAM48588 standard; Peptide; 9 AA.
 XX
 AC AAM48588;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 91.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 XX WO200183554-A2.
 PN
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
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 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
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 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
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 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 Db 1 LDYSWL 6
 |||||

RESULT 10
 AAM48591
 ID AAM48591 standard; Peptide; 9 AA.
 XX
 AC AAM48591;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 94.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 XX WO200183554-A2.
 PN
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
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 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
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PT psoriasis -
 XX
 PS
 XX
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 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 DB 1 LDYSWL 6
 RESULT 11
 AAM48594
 ID AAM48594 standard; Peptide; 9 AA.
 AC AAM48594;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 97.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYUA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
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 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 36; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 DB 1 LDYSWL 6
 RESULT 12
 AAM48595
 ID AAM48595 standard; Peptide; 9 AA.
 AC AAM48595;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 98.
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYUA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI

```

PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
XX (UYA ) UNIV YALE.
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PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
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XX
XX Sequence 9 AA;
XX
Query Match 100.0%; Score 36; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 2 LDYSWL 7

RESULT 13
AAM48590
ID AAM48590 standard; Peptide; 10 AA.
XX
XX AAM48590;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 93.
XX
XX Antiinflammatory; antiasthmatic; cytotstatic; antipsoriatic; nontropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.

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XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
XX (UYA ) UNIV YALE.
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CC arthritis.
XX
XX Sequence 10 AA;
XX
Query Match 100.0%; Score 36; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 2 LDYSWL 7

RESULT 14
AAM48593
ID AAM48593 standard; Peptide; 10 AA.
XX
XX AAM48593;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 96.
XX
XX Antiinflammatory; antiasthmatic; cytotstatic; antipsoriatic; nontropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.

```


KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
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 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 36; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 RESULT 15
 AAM48587
 ID AAM48587 standard; Peptide; 11 AA.
 AC AAM48587;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 90.
 DE
 XX Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nontropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
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 XX WO200183554-A2.
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 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 36; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 3 LDYSWL 8
 Search completed: February 18, 2004, 14:26:23
 Job time : 23.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDFS WL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	179	11 Q8BZU5	Q8BZU5 mus musculus
2	35	100.0	315	13 Q91838	Q91838 coturnix co
3	35	100.0	391	16 P95247	P95247 mycobacteri
4	35	100.0	407	2 Q55047	Q55047 shigella so
5	35	100.0	414	2 Q9S0Y1	Q9S0Y1 plesiomonas
6	35	100.0	414	2 Q9F738	Q9F738 shigella so
7	35	100.0	415	16 Q8VJK7	Q8VJK7 mycobacteri
8	35	100.0	1115	10 Q942A0	Q942A0 oryza sativ
9	33	94.3	61	16 Q9PEJ5	Q9PEJ5 xyfella fas
10	33	94.3	144	16 Q8Z6L9	Q8Z6L9 salmonella
11	33	94.3	144	16 Q84950	Q84950 salmonella
12	33	94.3	233	16 Q24927	Q24927 helicobacte
13	33	94.3	253	16 Q9ZMX2	Q9ZMX2 helicobacte
14	33	94.3	518	16 Q9JYP7	Q9JYP7 neisseria m
15	33	94.3	518	16 Q9JTN9	Q9JTN9 neisseria m
16	33	94.3	1227	5 Q20129	Q20129 caenorhabdi

17	32	91.4	208	17	Q28570	Q28570 archaeoglob
18	32	91.4	355	10	Q8RWE1	Q8RWE1 arabidopsis
19	32	91.4	371	10	Q81871	Q81871 arabidopsis
20	32	91.4	449	16	Q910V1	Q910V1 pseudomonas
21	32	91.4	467	16	Q92X93	Q92X93 rhizobium m
22	32	91.4	490	16	P96442	P96442 rhizobium m
23	31	88.6	44	4	Q96PA0	Q96PA0 homo sapien
24	31	88.6	54	16	Q8E977	Q8E977 shewanella
25	31	88.6	56	8	Q8WFN8	Q8WFN8 diadema pau
26	31	88.6	56	8	Q8WFS5	Q8WFS5 diadema pau
27	31	88.6	56	8	Q8WFS5	Q8WFS5 diadema sec
28	31	88.6	56	8	Q8WFR7	Q8WFR7 diadema pal
29	31	88.6	56	8	Q8W7C7	Q8W7C7 diadema set
30	31	88.6	56	8	Q8WFM2	Q8WFM2 diadema sav
31	31	88.6	56	8	Q8WFM2	Q8WFM2 diadema set
32	31	88.6	56	8	Q8WFM2	Q8WFM2 diadema sav
33	31	88.6	56	8	Q8W7G2	Q8W7G2 echinotrix
34	31	88.6	56	8	Q8W8G9	Q8W8G9 diadema pal
35	31	88.6	56	8	Q8W7C8	Q8W7C8 diadema sav
36	31	88.6	56	8	Q8WFO4	Q8WFO4 diadema pau
37	31	88.6	56	8	Q8WFO1	Q8WFO1 diadema pau
38	31	88.6	56	8	Q94P45	Q94P45 diadema ant
39	31	88.6	56	8	Q952P4	Q952P4 diadema ant
40	31	88.6	56	8	Q8W7L6	Q8W7L6 diadema sav
41	31	88.6	56	8	Q8W7U9	Q8W7U9 diadema ant
42	31	88.6	56	8	Q8WFS5	Q8WFS5 diadema mex
43	31	88.6	56	8	Q8WFP2	Q8WFP2 diadema pau
44	31	88.6	56	8	Q8W8D4	Q8W8D4 diadema set
45	31	88.6	56	8	Q952H7	Q952H7 diadema ant

ALIGNMENTS

RESULT 1

Q8BZU5 PRELIMINARY; PRT; 179 AA.

AC Q8BZU5; TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical membrane all-alpha structure containing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK033531; BAC28343.1; -
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 21321 MW; CBF710227B0CDB18 CRC64;

Query Match 100.0%; Score 35; DB 11; Length 179;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
Db 5 LDFS WL 10

RESULT 2

Q91838 PRELIMINARY; PRT; 315 AA.

ID Q91838
AC Q91838;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Interferon regulatory factor 1 (Interferon regulatory factor-1).
 GN IRF-1.
 OS Coturnix coturnix (Common quail), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TaxID=9091, 93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Coturnix;
 RA Zoeller B., Mueller I., Nanda I., Guttenbach M., Dosch E., Schmid M.,
 RA Jungwirth C.;
 RT "Sequence analysis of avian interferon regulatory factors (IRF)
 RT reveals close relation of the chicken and quail interferon induced
 RT transcriptional apparatus. Cytogenetic studies and sequence comparison
 RT of the avian IRF-1, ICSBP and a MHC class II gene reveals that the
 RT avian cell line C-32 is derived from quail";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Coturnix japonica; STRAIN=BREED:FRANZOESISCHE MASTWACHTEL;
 RA Zoeller B., Ingrid R.M., Nanda I., Guttenbach M.;
 RT "Sequence comparison of avian interferon regulatory factors and
 RT identification of the avian CEC-32 cell as a quail cell line.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ271052; CAC01088.1; -;
 DR EMBL; AJ277745; CAB91630.1; -;
 DR HSP; P15314; IIF1.
 DR InterPro; IPR001346; IRF.
 DR Pfam; PF00605; IRF; 1.
 DR PRINTS; PR00267; INTERREGFCT.
 DR ProDom; PD002355; IRF; 1.
 DR SMART; SM00348; IRF; 1.
 DR PROSITE; PS00601; IRF; 1.
 SQ SEQUENCE 315 AA; 36257 MW; 7E32521A2D2D62D0 CRC64;
 Query Match 100.0%; Score 35; DB 13; Length 315;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 297 LDFSWL 302
 RESULT 3
 P95247 ID P95247 PRELIMINARY; PRT; 391 AA.
 AC P95247;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical 37.4 kDa protein (PPE family protein).
 GN RV252C OR MTC198.21C OR MT2419.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Winn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z83860; CAB06149.1; -;
 DR TIGR; MT2419; -;
 DR Tuberculist; RV2352c; -;
 DR InterPro; IPR000030; Microbac_PPE.
 DR Pfam; PF00823; PPE; 1. Complete proteome.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 391 AA; 37355 MW; 360B67EEBF6CE46A CRC64;
 Query Match 100.0%; Score 35; DB 16; Length 391;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 3 LDFSWL 8
 RESULT 4
 Q55047 ID Q55047 PRELIMINARY; PRT; 407 AA.
 AC Q55047;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Form I operon ORF protein genes, insertion sequence IS630
 DE protein.
 OS Shigella sonnei.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=53G;
 RA Hough H-S.;
 RT "Genetic analysis and identification of an IS630 element in the form I
 RT operon of Shigella sonnei 53G.";
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34305; AAA84874.1; -;
 SQ SEQUENCE 407 AA; 47980 MW; 23BFAF09EEBD55D7 CRC64;
 Query Match 100.0%; Score 35; DB 2; Length 407;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 175 LDFSWL 180
 RESULT 5
 Q9S0V1 ID Q9S0V1 PRELIMINARY; PRT; 414 AA.
 AC Q9S0V1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF5P (WBGV) (ORF5G).
 GN WBGV OR ORF5G.

OS Plesiomonas shigelloides (Aeromonas shigelloides), and
 OS Shigella sonnei.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Plesiomonas.
 OX NCBI_TaxID=703, 624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.shigelloides; STRAIN=SEROTYPE O17;
 RA Chida T., Okamura N., Yoshida Y., Ohtani K., Arakawa E., Watanabe H.;
 RT "Complete DNA sequence of the O-antigen (rfb) gene cluster in
 RT Plesiomonas shigelloides serotype O17 having the same O-antigen as
 RT Shigella sonnei: comparison with that of S. sonnei."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.shigelloides; STRAIN=SEROTYPE O17;
 RX MEDLINE=99036814; PubMed=98117819;
 RA Hough H.H., Venkatesan M.M.;
 RT "Genetic analysis of Shigella sonnei form I antigen: identification of
 RT novel IS630 as an essential element for the form I expression."
 RL Microb. Pathog. 25:165-173(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.shigelloides; STRAIN=C27;
 RX PubMed=10992522;
 RA Shepherd J., Wang L., Reeves P.R.;
 RT "Comparison of the O antigen gene clusters of Escherichia coli
 RT (Shigella) Sonnei and Plesiomonas shigelloides O17: Sonnei gained its
 RT current plasmid borne O antigen genes from Plesiomonas shigelloides in
 RT a recent event."
 RL Infect. Immun. 68:6056-6061(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.sonnei;
 RA Xu D.Q., Cisar J.O., Ambulos N. Jr., Burr D., Kopecko D.J.;
 RT "Molecular cloning and characterization of the O-antigen gene cluster
 RT of Shigella sonnei: genetic stability, proposed biosynthetic pathway
 RT and essential genes for expression of form I O polysaccharide in
 RT Salmonella vaccine vector strain."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB025970; BAA85010.1; -
 DR EMBL; AF285970; AAG17412.1; -
 DR EMBL; AF294823; AAK85169.1; -
 SQ SEQUENCE 414 AA; 49038 MW; E92985FE7F19D953 CRC64;
 Query Match 100.0%; Score 35; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFS WL 6
 Db 175 LDFS WL 180
 RESULT 6
 Q9F738 PRELIMINARY; PRT; 414 AA.
 AC Q9F738
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Wbgv.
 GN Wbgv.
 OS Shigella sonnei.
 OG Plasmid Pinv.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=53G1;
 RX MEDLINE=20448976; PubMed=10992522;
 RA Shepherd J., Wang L., Reeves P.R.;

RT "Comparison of the O antigen gene clusters of Escherichia coli
 RT (Shigella) Sonnei and Plesiomonas shigelloides O17: Sonnei gained its
 RT current plasmid borne O antigen genes from Plesiomonas shigelloides in
 RT a recent event."
 RL Infect. Immun. 68:6056-6061(2000).
 DR EMBL; AF285971; AAG17422.1; -
 KW Plasmid.
 SQ SEQUENCE 414 AA; 49034 MW; EA6CA44A19ACD8CD CRC64;
 Query Match 100.0%; Score 35; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFS WL 6
 Db 175 LDFS WL 180
 RESULT 7
 Q8VJK7 PRELIMINARY; PRT; 415 AA.
 AC Q8VJK7
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE PPE family protein.
 GN MT2422.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB007082; AAK46715.1; -
 DR TIGR; MT2422; -
 DR InterPro: IPR000030; Microbac_PPE.
 DR Pfam: PF00823; PPE; 1.
 SQ SEQUENCE 415 AA; 40093 MW; 8B48C7671EBF4521 CRC64;
 Query Match 100.0%; Score 35; DB 16; Length 415;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFS WL 6
 Db 34 LDFS WL 39
 RESULT 8
 Q942A0 PRELIMINARY; PRT; 1115 AA.
 AC Q942A0
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Beta galactosidase-like protein.
 GN P0431G06.9.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
   clone: P0431G06.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003683; BAB64698.1; -
DR Gramene; O942A0; -
DR InterPro; IPR006101; Glyco_hydro_2.
DR InterPro; IPR006102; Glyco_hydro_2ig.
DR InterPro; IPR006104; Glyco_hydro_2SB.
DR InterPro; IPR006103; Glyco_hydro_2TIM.
DR InterPro; IPR004200; Glyco_hydro_42C.
DR InterPro; IPR004199; Glyco_hydro_42N.
DR Pfam; PF02930; Bgal_small_C; 1.
DR Pfam; PF02929; Bgal_small_N; 1.
DR Pfam; PF00703; Glyco_hydro_2; 1.
DR Pfam; PF02836; Glyco_hydro_2_C; 1.
DR Pfam; PF02837; Glyco_hydro_2_N; 1.
DR PRINTS; PR00132; GHYDRLASE2.
DR PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
DR PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
SQ SEQUENCE 1115 AA; 126078 MW; 1AABF6AA305CA8C5 CRC64;

Query Match 100.0%; Score 35; DB 10; Length 1115;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 697 LDFSWL 702

RESULT 9
Q9PEJ5 PRELIMINARY; PRT; 61 AA.
AC Q9PEJ5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Xf1033.
GN Xf1033.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Pacinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA de Oliveira M.C., de Oliveira F.G., Nunes L.R., Oliveira M.A.,
RA Nhani A. Jr., Nobrega F.G., Palmieri D.A., Paris A.,
RA Peixoto B.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,

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RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159 (2000).
DR EMBL; AF003940; AAF83843.1; -
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 61 AA; 6849 MW; 6CD080BD7BAE107 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 61;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 2 MDPSWL 7

RESULT 10
Q8Z6L9 PRELIMINARY; PRT; 144 AA.
ID Q8Z6L9;
AC Q8Z6L9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative pathogenicity island protein.
GN SSCB OR STY1717.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jajais K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
DR EMBL; AL627271; CAD01962.1; -
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 2.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 144 AA; 16390 MW; ECE0DA7F0E325B08 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 45 IDPSWL 50

RESULT 11
Q84950 PRELIMINARY; PRT; 144 AA.
ID Q84950;
AC Q84950;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SSCB (Secretion system chaparone).
GN SSCB OR STM1403.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=SL1344;
RA Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;
RT "Macrophage-dependent induction of the Salmonella pathogenicity island
RL 2 type III secretion system and its role in intracellular survival.";
RM Mol. Microbiol. 0:0-0(1998).
RN RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=9900132; PubMed=9786193;
RA Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G.,
RA Vazquez-Torres A., Gleeson C., Fang F.C., Holden D.W.;
RT "Genes encoding putative effector proteins of the type III secretion
RL system of Salmonella pathogenicity island 2 are required for bacterial
RM virulence and proliferation in macrophages.";
RN Mol. Microbiol. 30:163-174(1998).
RN RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=2153498; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL LT2.";
RM Nature 413:852-856(2001).
RN RP EMBL; AF020808; AAC28884.1; -
DR EMBL; AJ224892; CA12190.1; -
DR EMBL; AE008761; AAL20327.1; -
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 2.
KM Complete proteome.
SQ SEQUENCE 144 AA; 16375 MW; B60EDA7F0E325B0B CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;
Best Local Similarity 83.3%; Pred. NO. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDPSWL 6
Db 45 IDPSWL 50

RESULT 12
O24927 PRELIMINARY; PRT; 253 AA.
AC O24927;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein HP0101.
GN HP0101.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
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pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000532; AAD07180.1; -
DR TIGR; HP0101; -
DR InterPro; IPR002718; HP_OMP.
DR Pfam; PF01856; HP_OMP; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 29463 MW; C9A6BBE2C5A90003 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;
Best Local Similarity 83.3%; Pred. NO. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDPSWL 6
Db 149 LDPSWI 154

RESULT 13
Q9ZMX2 PRELIMINARY; PRT; 253 AA.
AC Q9ZMX2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Putative.
GN JHP0093.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RL gastric pathogen Helicobacter pylori.";
RM Nature 397:176-180(1999).
DR EMBL; AE001448; AAD05674.1; -
KM Complete proteome.
SQ SEQUENCE 253 AA; 29526 MW; 5C5F5239737E90AE CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;
Best Local Similarity 83.3%; Pred. NO. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDPSWL 6
Db 149 LDPSWI 154

RESULT 14
Q9JYP7 PRELIMINARY; PRT; 518 AA.
AC Q9JYP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein NMB1485.
GN NMB1485.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
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RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.P., Dodson R.J.,
RA Nelson W.C., Winn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parkey D.S., Blair E., Cifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Piza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AE002498; AAF41841.1; -.
DR TIGR; NME1485; -.
DR InterPro; IPR000644; CBS domain.
DR InterPro; IPR005170; CorC_HlyC.
DR InterPro; IPR005496; TerC.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF03471; CorC_HlyC; 1.
DR Pfam; PF03741; TerC; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 518 AA; 57342 MW; CFE9324DA672DC96 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
DB :|||||
1 MDFS WL 6

RESULT 15

Q9JTN9 PRELIMINARY; PRT; 518 AA.
AC Q9JTN9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Conserved hypothetical integral membrane protein.
GN NMA1694.
OS *Neisseria meningitidis* (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jegelis K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of *Neisseria*
meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162756; CAB84922.1; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR005170; CorC_HlyC.
DR InterPro; IPR005496; TerC.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF03471; CorC_HlyC; 1.
DR Pfam; PF03741; TerC; 1.
DR SMART; SM00116; CBS; 2.
KW Complete proteome.
SQ SEQUENCE 518 AA; 57358 MW; 47FBC652664E38E0 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6

Db :|||||
1 MDFS WL 6

Search completed: February 18, 2004, 14:35:50
Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDPSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	313	1 IRF1_CHICK	Q90876 gallus gall
2	33	94.3	868	1 NI80_YEAST	P33420 saccharomyc
3	31	88.6	121	1 YGD4_YEAST	P53186 saccharomyc
4	31	88.6	224	1 PDXH_MYCTU	O06207 mycobacteri
5	31	88.6	229	1 BCL2_BOVIN	O02718 bos taurus
6	31	88.6	236	1 BCL2_CRILLO	Q9JJW8 cricetus
7	31	88.6	236	1 BCL2_MOUSE	P10417 mus musculus
8	31	88.6	236	1 BCL2_RAT	P49950 rattus norv
9	31	88.6	239	1 BCL2_HUMAN	P10415 homo sapien
10	31	88.6	444	1 GLGA_DEIRA	O9RW61 deinococcus
11	31	88.6	495	1 SYC_AQUAE	O67153 aquifex aeo
12	31	88.6	612	1 YNB8_YEAST	P53976 saccharomyc
13	31	88.6	612	1 YND4_YEAST	P53963 saccharomyc
14	31	88.6	678	1 VID3_AGRRH	P13463 agrobacteri
15	31	88.6	1343	1 VGR2_RAT	O08775 rattus norv
16	30	85.7	438	1 E1BL_ADECT	P14266 canine aden
17	30	85.7	745	1 IKKA_HUMAN	O15111 h inhibitor
18	30	85.7	745	1 IKKA_MOUSE	Q06880 m inhibitor
19	30	85.7	756	1 IKKB_HUMAN	O14920 homo sapien
20	30	85.7	757	1 IKKB_MOUSE	O08351 mus musculus
21	30	85.7	757	1 IKKB_RAT	O9QY78 rattus norv
22	30	85.7	926	1 MAY3_SCHCO	P37934 schizophyll
23	29	82.9	233	1 BCL2_CHICK	Q00709 gallus gall
24	29	82.9	263	1 TRUA_BUCAP	Q8K9U4 buchnera ap
25	29	82.9	304	1 YG78_PSEAE	Q91347 pseudomonas
26	29	82.9	308	1 CITR_BACSU	P39127 bacillus su
27	29	82.9	328	1 YCDU_ECOLI	P75910 escherichia
28	29	82.9	362	1 SIA9_HUMAN	O8UNP4 homo sapien
29	29	82.9	397	1 ARG1_STAP	Q8C8E9 s arginine
30	29	82.9	401	1 HIS2_SYNY3	P74592 synochocyst
31	29	82.9	404	1 ADMR_HUMAN	O15218 homo sapien
32	29	82.9	477	1 GLGA_ECOLI	P08323 escherichia
33	29	82.9	477	1 GLGA_SALTI	Q8Z232 salmonella

34	29	82.9	477	1 GLGA_SALTY	P05416 salmonella
35	29	82.9	494	1 DPOW_HUMAN	Q9NP87 homo sapien
36	29	82.9	506	1 TDT_CHICK	P36195 gallus gall
37	29	82.9	518	1 TDT_MONDO	O02789 monodelphis
38	29	82.9	522	1 CPE4_RAT	P51869 rattus norv
39	29	82.9	529	1 T1MK_ECOLI	P08957 escherichia
40	29	82.9	529	1 T1M_SALPO	P07989 salmonella
41	29	82.9	529	1 T1M_SALTY	P40813 salmonella
42	29	82.9	530	1 TDT_MOUSE	P09838 mus musculus
43	29	82.9	561	1 Y423_MYCGE	P47662 mycoplasma
44	29	82.9	561	1 Y423_MYCPN	P75174 mycoplasma
45	29	82.9	630	1 Y242_MYCGE	P47484 mycoplasma

ALIGNMENTS

RESULT 1
ID IRF1_CHICK STANDARD; PRT; 313 AA.
AC Q90876;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interferon regulatory factor 1 (IRF-1) ..
GN IRF1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95241453; PubMed=7536924;
RA Jungwirth C., Rebbert M., Ozato K., Degen H.J., Schultz U.,
RA David I.B.;
RT "Chicken interferon consensus sequence-binding protein (ICSBP) and
RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
RT conservation in the IRF gene family."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).
CC -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the IRF family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L39766; AAA62160.1; ..
CC HSSP: P15314; IIF1.
CC InterPro: IPR001346; IRF.
CC Pfam: PF00605; IRF; 1.
CC PRINTS: PR00267; INTERREGCT.
CC PRODOM: PD002355; IRF; 1.
CC SMART: SM00348; IRF; 1.
CC PROSITE: PS00601; IRF; 1.
CC Transcription regulation; DNA-binding; Activator; Nuclear protein.
CC DNA BIND 7 109 TRYPTOPHAN PENTAD REPEAT.
CC SQ SEQUENCE 313 AA; 36009 MW; 0895FA3736FA7463 CRC64;
Query Match 100.0%; Score 35; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 LDPSWL 6
|||||

Query Match 94.3%; Score 33; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSXL 6
Db 782 IDFSWL 787

RESULT 3
YGD4_YEAST
ID YGD4_YEAST STANDARD; PRT; 121 AA.
AC Y53186;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 13.6 kDa protein in MIG1-AGA2 intergenic region.
GN YGL034C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
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DR EMBL; 272556; CAA96735.1; -;
DR PIR; S64036; S64036.
DR SGD; S0003002; YGL034C.
KW Hypothetical protein; ATP-binding.
FT NP_BIND 77 84
SQ SEQUENCE 121 AA; 13573 MW; 88D46FF50B67000F CRC64;
Query Match 88.6%; Score 31; DB 1; Length 121;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSXL 6
Db 40 LEFSWL 45

RESULT 4
PDH MYCTU
ID PDH MYCTU STANDARD; PRT; 224 AA.
AC Q06207;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase) (PNFOX).
GN PDH OR RV2607 OR MT2682 OR MTCV1A10.26C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=H37Rv;
RX MEDLINE=98295987; Pubmed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

295 LDFSXL 300
Db 868 AA.
PRT; 868 AA.
STANDARD;
Q08917;
01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NIP80 protein (NIP100 protein).
NIP80 OR NIP100 OR YPL114C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Schlenstedt G., Silver P.A.;
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RA Silver P.A.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
MEDLINE=97313271; Pubmed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoerge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R., Johnston M., Kalman S., Klein K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petal F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scherrens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H., Ureterazu L.A., Uehinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
Nature 387;103-105(1997).
-!- SIMILARITY: Contains 1 CAP-Gly domain.
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DR EMBL; X72237; CAA51030.1; -;
DR EMBL; 273530; CAA97881.1; -;
DR PIR; S65186; S65186.
DR SGD; S0006095; NIP100.
DR GO; GO:0005869; C:dynactin complex; IDA.
DR GO; GO:0000092; P:mitotic anaphase B; IGI.
DR InterPro: IPR000938; CAP-Gly.
DR Pfam; PF01302; CAP_GLY; 1.
DR PROSITE; PS00845; CAP_GLY_1; 1.
DR PROSITE; PS0245; CAP_GLY_2; 1.
KW Cytoskeleton; Coiled coil.
DOMAIN 34 84 CAP-GLY.
FT DOMAIN 101 175 COILED COIL (POTENTIAL).
FT DOMAIN 207 375 COILED COIL (POTENTIAL).
FT DOMAIN 645 776 COILED COIL (POTENTIAL).
SEQUENCE 868 AA; 100289 MW; A72EA9E938945081 CRC64;

RA Hornaby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: OXIDIZE PNP AND PMP INTO PYRIDOXAL 5'-PHOSPHATE (PLP)
 CC (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Pyridoxamine 5'-phosphate + H(2)O + O(2) =
 CC Pyridoxal 5'-phosphate + NH(3) + H(2)O(2).
 CC -!- COFACTOR: FMN (BY SIMILARITY).
 CC -!- PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and
 CC pyridoxal phosphate.
 CC -!- SIMILARITY: BELONGS TO THE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z95387; CAB08613.1; -.
 DR EMBL; AE007101; AAK46998.1; -.
 DR PIR; F70570; F70570.
 DR HSSP; P28225; 1DNL.
 DR TIGR; MT2682; -.
 DR TubercuList; RV2607; -.
 DR InterPro; IPR000659; Pyridox oxidase.
 DR Pfam; PF01243; Pyridox oxidase; 1.
 DR ProDom; PD006312; Pyridox oxidase; 1.
 DR TIGRFAMs; TIGR00558; pdxH; 1.
 DR PROSITE; PS01064; PYRIDOX OXIDASE; 1.
 KW Pyridoxine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
 KW Complete proteome.
 SQ SEQUENCE 224 AA; 25186 MW; 66ABC0AAACE90DC1 CRC64;

 Query Match 88.6%; Score 31; DB 1; Length 224;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LDPSWL 6
 DQ |||||
 Db 32 LDFDNL 37

 RESULT 5
 ID BCL2_BOVIN STANDARD; PRT; 229 AA.
 AC Q02718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN Apoptosis regulator Bcl-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Holstein; TISSUE=Thymus;
 RA Reyes R.A., Cockerell G.L.;
 RT "Bovine leukemia virus associated-leukemogenesis is correlated
 RT with suppression of programmed cell death and increased expression
 RT of Bcl-2.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
 CC including factor-dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane
 CC permeability. Appears to function in a feedback loop system with
 CC caspases. Inhibits caspase activity either by preventing the
 CC release of cytochrome c from the mitochondria and/or by binding to
 CC the apoptosis-activating factor (APAF-1) (By similarity).
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By
 CC similarity).
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
 CC for interaction with RAF-1 (By similarity).
 CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and
 CC occurs during the G2/M phase of the cell cycle (By similarity). In
 CC the absence of growth factors, Bcl2 appears to be phosphorylated
 CC by other protein kinases such as ERKs and stress-activated
 CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
 CC activity, causes the release of cytochrome c into the cytosol
 CC promoting further caspase activity (By similarity).
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U92434; AAB53319.1; -.
 DR HSSP; Q07817; 1MAZ.
 DR InterPro; IPR000712; Bcl2 BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR002475; Bcl2_family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2; 1.
 DR Pfam; PF02180; BH4; 1.
 DR SMART; SM00337; BCL; 1.
 DR SMART; SM00265; BH4; 1.
 DR TIGRFAMs; TIGR00865; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1; 1.
 DR PROSITE; PS50063; BH4_2; 1.
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
 FT DOMAIN 10 30
 FT DOMAIN 64 68 POLY-PRO.
 FT DOMAIN 69 72 POLY-ALA.
 FT DOMAIN 83 97 BH3.

```

FT DOMAIN 126 145 BH1.
FT DOMAIN 177 192 BH2.
FT TRANSMEM 202 223 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25099 MW; AD1DD0AF98FF11D CRC64;

Query Match 88.6%; Score 31; DB 1; Length 229;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
DB 201 DFSWL 205

RESULT 6
BCL2 CRILLO STANDARD; PRT; 236 AA.
AC Q9JVV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T., Christmann M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein."
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN (2)
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11181062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9 and caspase-3."
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

```

RX MEDLINE=92375724; PubMed=15087112;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=92727291; PubMed=9115213;
RA Ito T., Deng X., Carr B., May W.S. Jr.;
RT "Bcl-2 phosphorylation required for anti-apoptosis function.";
RL J. Biol. Chem. 272:11671-11673(1997).
RN [4]
RP DEPHOSPHORYLATION BY PP2A.
RX MEDLINE=99069407; PubMed=9852076;
RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
RT "Reversible phosphorylation of Bcl2 following interleukin 3 or
RT bryostatins 1 is mediated by direct interaction with protein
RT phosphatase 2A.";
RL J. Biol. Chem. 273:34157-34163(1998).
RN [5]
CC -/- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -/- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1.
CC -/- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -/- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=PI0417-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=PI0417-2; Sequence=VSP_000513;
CC -/- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -/- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1.
CC -/- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC -/- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC Promoting further caspase activity.
CC -/- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -/- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -/- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -/- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -/- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; L31532; AAA37282.1;
DR ENBL; M16506; AAA37282.1; JOINED.
DR ENBL; M16506; AAA37281.1;
DR PIR; B25960; TWMSB1.
DR HSSP; Q07817; 1MAZ.
DR MGD; MGI:88138; Bcl2.

DR GO; GO:0008189; F:Apoptosis inhibitor activity; IDA.
DR GO; GO:0005515; P:protein binding activity; IDA.
DR GO; GO:0006915; P:apoptosis; IDA.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;
KW Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC).
FT VARSPPLIC 193 236 DAPVELYGPSMRPLDFSWLSUKLLSLALVGACITLGAYL
FT GHK -> VGACIVE (in isoform Beta).
FT /FTId=VSP_000513.
SQ SEQUENCE 236 AA; 26425 MW; AA85EF6B0766BE0A CRC64;
Query Match 88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DFSWL 6
DB 208 DFSWL 212
|||||
BCL2_RAT STANDARD; PRT; 236 AA.
AC P4950; Q62837; Q64032;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94193015; PubMed=8144041;
RA Sato T., Irie S., Krajewski S., Reed J.C.;
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL Gene 140:291-292(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [3]
RP SEQUENCE OF 19-172 FROM N.A.

RX MEDLINE=95059917; PubMed=7969891;
RA Castren E., Ohga Y., Berraghi M.P., Trimigiorgis G., Thoenen H.,
RA Lindholm D.;
RT "bcl-2 messenger RNA is localized in neurons of the developing and
RT adult rat brain.";
RL Neuroscience 61:165-177(1994).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
CC highest levels in reproductive tissues. In the adult brain,
CC expression is localized in mitral cells of the olfactory bulb,
CC granule and pyramidal neurons of hippocampus, pontine nuclei,
CC cerebellar granule neurons, and in ependymal cells. In prenatal
CC brain, expression is higher and localized in the neuroepithelium
CC and in the cortical plate.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC -!- PTM: Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: L14680; AAA53662.1; -;
CC EMBL: U34964; AA77687.1; -;
CC EMBL: S74122; -; NOT_ANNOTATED_CDS.
CC PIR: I53744; I53744.
CC PIR: I67432; I67432.
CC HSP: Q07817; IMAZ.
CC InterPro: IPR000712; Bcl2 BH.
CC InterPro: IPR003093; Bcl2 BH4.
CC InterPro: IPR002475; Bcl2 family.
CC InterPro: IPR004725; Bcl2_reg.
CC Pfam: PF00452; Bcl-2; 1.
CC Pfam: PF02180; BH4; 1.
CC SMART: SM00337; BCL; 1.
CC SMART: SM00265; BH4; 1.
CC TIGRfam: TIGR00865; bcl-2; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS01260; BH4_1; 1.

DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT CONFLICT 42 42 A -> R (IN REF. 2).
FT CONFLICT 157 157 E -> G (IN REF. 1).
FT CONFLICT 164 164 S -> Y (IN REF. 2).
FT CONFLICT 212 212 L -> Q (IN REF. 2).
SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;
Query Match 88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DFSWL 6
Db 208 DFSWL 212
RESULT 9
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q13842; Q16197;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=86196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-Ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., [7]
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.
RX MEDLINE=92096610; PubMed=133299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas.";
RL Blood 79:229-237(1992).
RN [7]
RN SUBCELLULAR LOCATION.
RP MEDLINE=91066924; PubMed=2250705;
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death.";
RL Nature 348:334-336(1990).
RN [8]
RN MUTAGENESIS.
RP MEDLINE=94239528; PubMed=8183370;
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT apoptosis and heterodimerization with Bax.";
RL Nature 369:321-323(1994).
RN [9]
RN CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RP MEDLINE=98057466; PubMed=9395403;
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA Uno K., Hardwick J.M.;
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL Science 278:1966-1968(1997).
RN [10]
RN REVIEW ON PHOSPHORYLATION.
RP MEDLINE=21260650; PubMed=11368354;
RA Ruvoilo P.P., Deng X., May W.S.;
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL Leukemia 15:515-522(2001).
RN [11]
RN PHOSPHORYLATION BY ASK1/JNK1.
RX MEDLINE=20036804; PubMed=10567572;
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
RT protein kinase pathway normally activated at G(2)/M.";
RL Mol. Cell. Biol. 19:8469-8478(1999).
CC CC
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1.
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=PI0415-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=PI0415-2; Sequence=VSP 000512;
CC TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1.
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type
CC II chronic lymphatic leukemia) by a chromosomal translocation
CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying
CC the chromosomal translocation could be attributed to the Ig
CC somatic hypermutation mechanism resulting in nucleotide
CC transitions.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromancer/Genes/BCL2ID49.html".
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M13994; AA51813.1; ALT_SEQ.
CC EMBL; M13995; AA51814.1; ALT_SEQ.
CC EMBL; M14745; AA35591.1; -.
CC EMBL; X06487; CAA29778.1; -.
CC EMBL; BC027258; AAH27258.1; -.
CC EMBL; S72602; AAD14111.1; ALT_SEQ.
CC FIR; C37332; TVHUAL.
CC PDB; 1GSM; 21-WAR-01.
CC PDB; 1GUH; 13-JUN-01.
CC Genew; HGNC:990; BCL2.
CC MIM; 151430; -.
CC GO; GO:0005743; C-mitochondrial inner membrane; TAS.
CC GO; GO:0008189; Frapoptosis inhibitor activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; TAS.
CC GO; GO:0006959; P:humoral immune response; TAS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
CC GO; GO:0007048; P:oncogenesis; TAS.
CC GO; GO:0000074; P:regulation of cell cycle; TAS.
CC InterPro; IPR000712; Bcl2_BH.
CC InterPro; IPR003093; Bcl2_BH4.
CC InterPro; IPR002475; BCL2 family.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC SMART; SM00337; BCL; 1.
CC SMART; SM00265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS50062; BCL2 FAMILY; 1.
CC PROSITE; PS01080; BHL; 1.

DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1; 1.
 DR PROSITE; PS00063; BH2; 1.
 KW Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
 KW Mitochondrion; Phosphorylation; Chromosomal translocation;
 KW Polymorphism; Disease mutation; 3D-structure.

Query Match 88.6%; Score 31; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFWL 6
 |||||
 DB 211 DFWL 215

RESULT 10
 ID GLGA DEIRA STANDARD; PRT; 444 AA.
 AC Q9RW51;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen] synthase).
 DE synthase).
 GN GLGA OR DR0594.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RL / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans RL.";
 RL Science 286:1571-1577(1999).
 CC -!- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
 CC -!- CATALYTIC ACTIVITY: ADP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 CC ADP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -!- PATHWAY: Glycogen biosynthesis; second step.
 CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.

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 CC -----
 DR EMBL; AF001917; AAF10170.1; ALT_INIT.
 DR TIGR; DR0594; -.
 DR HAMAP; MF 00484; -.
 DR InterPro; IPR001296; Glyco trans 1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KW Complete proteome.
 FT BINDING 15 15 ADP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 444 AA; 48457 MW; 767605781A915302 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSW 5
 |||||
 DB 426 LDFSW 430

RESULT 11
 ID SYNC AQUAE STANDARD; PRT; 495 AA.
 AC O67163;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cysteine-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase)
 DE (CysRS).
 DE CysRS).
 GN CYSS OR AQ_1068.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OC NCBI_TaxID=63363;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VFS;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
 RT Nature 392:353-358(1998).
 RL Nature 392:353-358(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
 CC diphosphate + L-cysteinylyl-tRNA(Cys).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC Strong, to methionyl-tRNA synthetase.

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 CC -----
 DR EMBL; AE000721; AAC07125.1; -.
 DR PIR; H70391; H70391.
 DR HAMAP; MF 00041; -.
 DR InterPro; IPR002308; Cys tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt 1.
 DR Pfam; PF01406; tRNA-synt 1e; 1.
 DR PRINTS; PR00983; TRNASYNTHCYS.
 DR TIGRFAMs; TIGR00435; CysRS; 1.
 DR PROSITE; PS00178; AA TRNA_LIGASE_I; FALSE NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 31 41 "HIGH" REGION.
 FT SITE 266 270 "KMSKS" REGION.
 FT BINDING 269 269 ATP (BY SIMILARITY).
 SQ SEQUENCE 495 AA; 57135 MW; A454658B2BBAE8A4 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 495;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSW 5
 |||||
 DB 302 LDFSW 306

RESULT 12
 YNB8_YEAST
 ID YNB8_YEAST STANDARD; PRT; 612 AA.
 AC P53976;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 69.6 kDa protein in HDAL-PUB1 intergenic region.
GN YNL018C OR N2831.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Andre B., Iraqui Housseini I., Urrestarazu L.A., Vissers S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YNL034W.
CC -----
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CC -----
DR EMBL; Z71294; CAA95880.1; -.
DR PIR; S62930; S62930.
DR SGD; S0004963; YNL018C.
KW Hypothetical protein.
SQ SEQUENCE 612 AA; 69551 MW; E655B2D96317FC62 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 612;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 17 LDFQWL 22

RESULT 13
YND4 YEAST STANDARD; PRT; 612 AA.
ID YND4 YEAST
AC P33963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 69.4 kDa protein in NCE3-HHT2 intergenic region.
GN YNL034W OR N2740.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YNL018C.
CC -----
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CC -----
DR EMBL; Z71310; CAA95897.1; -.
DR PIR; S62956; S62956.
DR SGD; S0004979; YNL034W.
KW Hypothetical protein.
SQ SEQUENCE 612 AA; 69373 MW; E39B7080B8DBE0285 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 612;

Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 17 LDFQWL 22

RESULT 14
VID3 AGRRH STANDARD; PRT; 678 AA.
ID VID3 AGRRH
AC P13463;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein virD3.
GN VirD3.
OS Agrobacterium rhizogenes.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A4;
RX MEDLINE=89039712; PubMed=3185501;
RA Hirayama T., Muranaka T., Ohkawa H., Oka A.;
RT "Organization and characterization of the virCD genes from
RT Agrobacterium rhizogenes.";
RL Mol. Gen. Genet. 213:229-237(1988).
CC -----
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CC -----
DR EMBL; X12867; CAA31352.1; -.
DR PIR; S12456; S12456.
KW Crown gall tumor; Plasmid.
SQ SEQUENCE 678 AA; 72777 MW; A5BCEBA58AC26532 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFSWL 6
Db 418 DFSWL 422

RESULT 15
VGR2 RAT STANDARD; PRT; 1343 AA.
ID VGR2 RAT
AC O08775;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1).
GN KDR OR FLK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSWM 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	35	100.0	391	2 A70663	probable PPE prote
2	35	100.0	414	2 T44513	hypothetical prote
3	33	94.3	61	2 D82732	hypothetical prote
4	33	94.3	144	2 A10698	probable pathogeni
5	33	94.3	253	2 D71975	hypothetical prote
6	33	94.3	253	2 E64532	hypothetical prote
7	33	94.3	518	2 A81865	conserved hypotet
8	33	94.3	518	2 C81077	conserved hypotet
9	33	94.3	868	2 S65186	NIP80 protein - ye
10	33	94.3	1214	2 T21915	hypothetical prote
11	32	91.4	208	1 F69462	hypothetical prote
12	32	91.4	371	2 T04971	hypothetical prote
13	32	91.4	449	2 F83328	probable sodium/al
14	32	91.4	467	2 E95850	probable amino aci
15	32	91.4	490	2 G95953	probable membrane
16	31	88.6	121	2 S64036	hypothetical prote
17	31	88.6	150	2 S74754	hypothetical prote
18	31	88.6	199	2 F82836	hypothetical prote
19	31	88.6	219	2 T30439	hypothetical prote
20	31	88.6	224	2 F70570	probable ptdH prot
21	31	88.6	236	1 TVMSA1	transforming protei
22	31	88.6	236	2 I53744	gene bcl-2 protein
23	31	88.6	236	2 JC7383	B-cell lymphoma 2
24	31	88.6	239	1 TVHUA1	transforming prote
25	31	88.6	247	2 C96594	unknown protein, 7
26	31	88.6	253	2 S65170	hypothetical prote
27	31	88.6	262	2 G72694	hypothetical prote
28	31	88.6	266	2 T31582	hypothetical prote
29	31	88.6	331	2 B95880	conserved hypotet

30	31	88.6	338	2 A82890	hypothetical prote
31	31	88.6	387	2 D88968	protein T27B7.3 [i
32	31	88.6	401	2 T44831	probable emulcan r
33	31	88.6	440	2 B71153	hypothetical prote
34	31	88.6	461	2 B83601	probable transport
35	31	88.6	467	2 AE1892	hypothetical prote
36	31	88.6	472	2 B75501	glycogen synthase
37	31	88.6	484	2 T33504	hypothetical prote
38	31	88.6	495	2 H70391	cysteine-trna liga
39	31	88.6	516	2 AC1892	hypothetical prote
40	31	88.6	544	2 T45498	hypothetical prote
41	31	88.6	611	2 G83177	probable sodium/hy
42	31	88.6	612	2 S62930	hypothetical prote
43	31	88.6	612	2 S62956	hypothetical prote
44	31	88.6	641	2 AG2794	hypothetical prote
45	31	88.6	641	2 F97573	hypothetical prote

ALIGNMENTS

RESULT 1

A70663

probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: A70663

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70663

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-391 <COL>

A:Cross-references: GB:Z83860; GB:AL123456; NID:G3261681; PIDN:CAB06149.1; PID:G290759;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: PPE

Query Match 100.0%; Score 35; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWM 6

|||||

DB 3 LDFSWM 8

RESULT 2

T44513

hypothetical protein SP [imported] - Plesiomonas shigelloides

C:Species: Plesiomonas shigelloides

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T44513

R:Chida, T.; Okamura, N.; Yoshida, Y.; Ohtani, K.; Arakawa, E.; Watanabe, H.

A:Description: Complete DNA sequence of the O-antigen (rfb) gene cluster in Plesiomonas

A:Reference number: Z22786

A:Accession: T44513

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-414 <CHI>

A:Cross-references: EMBL:AB025970; PIDN:BAA85010.1

A:Experimental source: ATCC 14029

Query Match 100.0%; Score 35; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 175 LDFSWL 180

RESULT 3
D82732
hypothetical protein XF1033 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82732
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: AB8515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82732
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <STM>
A:Cross-references: GB:AE003940; GB:AE003849; NID:g9105966; PIDN:RAF03843.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1033

Query Match 94.3%; Score 33; DB 2; Length 61;
Best Local Similarity 83.3%; Pred. No. 6.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 2 MDPSWL 7

RESULT 4
AI0698
probable pathogenicity island protein scb [imported] - Salmonella enterica subsp. enter C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AI0698
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AI0698
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01962.1; PID:g16502804; GSPDB:GN00176
C:Genetics:
A:Gene: scb

Query Match 94.3%; Score 33; DB 2; Length 144;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 45 LDFSWL 50

RESULT 5
D71975
hypothetical protein jhp0093 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: D71975
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: D71975
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <ARN>
A:Cross-references: GB:AE001448; GB:AE001439; NID:g4154594; PIDN:AAD05674.1; PID:g415460 A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0093

Query Match 94.3%; Score 33; DB 2; Length 253;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 149 LDFSWI 154

RESULT 6
E64532
hypothetical protein HP0101 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: E64532
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: E64532
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-253 <TOM>
A:Cross-references: GB:AE000532; GB:AE000511; NID:g2313184; PIDN:AAD07180.1; PID:g231313 C:Genetics:
A:Start codon: TTG

Query Match 94.3%; Score 33; DB 2; Length 253;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
Db 149 LDFSWI 154

RESULT 7
AB1865
conserved hypothetical integral membrane protein NMA1694 [imported] - Neisseria meningit C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: AB1865
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

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; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81865
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-518 <PAR>
A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84922.1; PID:g738033
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1694

Query Match          94.3%; Score 33; DB 2; Length 518;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWSL 6
Db 1 MDFSWSL 6

RESULT 8
C81077
conserved hypothetical protein NMB1485 [imported] - Neisseria meningitidis (strain MC58)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: C81077
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-518 <TET>
A;Cross-references: GB:AE002499; GB:AE002098; NID:g7226724; PIDN:AAF41841.1; PID:g722672
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1485

Query Match          94.3%; Score 33; DB 2; Length 518;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWSL 6
Db 1 MDFSWSL 6

RESULT 9
S65186
NIP80 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein P2279; protein YPL174c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 05-Dec-1997
C;Accession: S65186; S34343
R;Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65183
A;Accession: S65186
A;Molecule type: DNA
A;Residues: 1-868 <BEN>
A;Cross-references: EMBL:Z73530; NID:q1370366; PID:e246907; PID:gl370367; MIPS:YPL174c
R;Schlenstedt, G.; Silver, P.A.
submitted to the EMBL Data Library, May 1993
A;Reference number: S34342
A;Accession: S34343
A;Molecule type: DNA

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A;Residues: 169-429, 'V', 431-868 <SCH>
A;Cross-references: EMBL:X72227
C;Genetics:
A;Gene: SGD:NIP100; NIP80
A;Cross-references: MIPS:YPL174c; SGD:S0006095
A;Map position: 16L
C;Keywords: transmembrane protein
F:574-590/Domain: transmembrane #status predicted <TMM>

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Query Match          94.3%; Score 33; DB 2; Length 868;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDFSWSL 6
Db 782 IDFSWSL 787

```

RESULT 10

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T21915
hypothetical protein F37D6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21915
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19487
A;Accession: T21915
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-1214 <WIL>
A;Cross-references: EMBL:Z75540; PIDN:CAA99847.1; GSPDB:GN00019; CBSP:F37D6.1
A;Experimental source: clone F37D6
C;Genetics:
A;Gene: CBSP:F37D6.1
A;Map position: 1
A;Introns: 43/1; 59/3; 103/3; 149/2; 230/3; 278/3; 313/1; 439/2; 489/3; 571/1; 625/2; 6

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Query Match          94.3%; Score 33; DB 2; Length 1214;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 LDFSWSL 6
Db 772 LDFSWI 777

```

RESULT 11

```

F69462
hypothetical protein AF1703 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: F69462
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69462
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <KLE>
A;Cross-references: GB:AE000986; GB:AE000782; NID:g2689309; PIDN:AAB89558.1; PID:g26488
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH1

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Query Match          91.4%; Score 32; DB 1; Length 208;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDFSWSL 6

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Db          155 LDFAWL 160
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RESULT 12
T04971
hypothetical protein T16L1.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C:Accession: T04971
R;Bevan, M.; Obermaier, B.; Deutschenbauer, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15393
A:Accession: T04971
A:Molecule type: DNA
A:Residues: 1-371 <BEV>
A:Cross-references: EMBL:AL031394
A:Experimental source: cultivar Columbia, BAC clone T16L1
C:Genetics:
A:Map position: 4
A:Introns: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1
A>Note: T16L1.30
C:Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30
Query Match          91.4%; Score 32; DB 2; Length 371;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
||||:|
Db          325 LDFNWL 330
||||:|
RESULT 13
F83328
probable sodium/alanine symporter PA2533 [imported] - Pseudomonas aeruginosa (strain PAO)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83328
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho-
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83328
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: GB:AE004681; GB:AE004091; MID:g9948587; PIDN:AAG05921.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA2533
C:Superfamily: sodium-dependent D-alanine/glycine transport protein
Query Match          91.4%; Score 32; DB 2; Length 449;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
||||:|
Db          407 LDFAWL 412
||||:|
RESULT 14
E95850
probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) ma
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: E95850
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo

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A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: E95850
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A:Molecule type: DNA
A:Residues: 1-467 <KUR>
A:Cross-references: PIDN:CAC48469.1; PID:g15139941; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMB20069
A:Genome: plasmid
C:Superfamily: sodium-dependent D-alanine/glycine transport protein
Query Match          91.4%; Score 32; DB 2; Length 467;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
||||:|
Db          407 LDFAWL 412
||||:|
RESULT 15
G95953
probable membrane-anchored protein [imported] - Sinorhizobium meliloti (strain 1021) mas
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: G95953
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95953
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <KUR>
A:Cross-references: PIDN:CAC49295.1; PID:g15140781; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: expal; SMB21319
A:Genome: plasmid
Query Match          91.4%; Score 32; DB 2; Length 490;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
||||:|
Db          466 VDFSWL 471
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Search completed: February 18, 2004, 14:38:46
Job time : 8.5921 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDFSWM 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	10	US-09-847-940B-11
2	35	100.0	6	11	US-09-847-946A-11
3	35	100.0	6	11	US-09-847-946A-42
4	35	100.0	6	11	US-09-847-946A-84
5	35	100.0	7	11	US-09-847-946A-88
6	35	100.0	8	11	US-09-847-946A-81
7	35	100.0	8	11	US-09-847-946A-89
8	35	100.0	9	11	US-09-847-946A-80
9	35	100.0	9	11	US-09-847-946A-83
10	35	100.0	9	11	US-09-847-946A-86
11	35	100.0	9	11	US-09-847-946A-87
12	35	100.0	10	11	US-09-847-946A-82
13	35	100.0	10	11	US-09-847-946A-85
14	35	100.0	11	11	US-09-847-946A-79
15	33	94.3	265	10	US-09-881-752A-368

16	33	94.3	868	12	US-10-369-493-22465	Sequence 22465, A
17	32	91.4	6	10	US-09-847-940B-12	Sequence 12, Appl
18	32	91.4	6	11	US-09-847-946A-12	Sequence 12, Appl
19	32	91.4	6	11	US-09-847-946A-95	Sequence 95, Appl
20	32	91.4	7	11	US-09-847-946A-99	Sequence 99, Appl
21	32	91.4	8	11	US-09-847-946A-100	Sequence 100, Appl
22	32	91.4	8	11	US-09-847-946A-91	Sequence 91, Appl
23	32	91.4	9	11	US-09-847-946A-94	Sequence 94, Appl
24	32	91.4	9	11	US-09-847-946A-97	Sequence 97, Appl
25	32	91.4	9	11	US-09-847-946A-98	Sequence 98, Appl
26	32	91.4	10	11	US-09-847-946A-93	Sequence 93, Appl
27	32	91.4	10	11	US-09-847-946A-96	Sequence 96, Appl
28	32	91.4	11	11	US-09-847-946A-90	Sequence 90, Appl
29	32	91.4	106	12	US-09-864-408A-5624	Sequence 5624, Ap
30	31	88.6	236	15	US-10-277-693A-11	Sequence 11, Appl
31	31	88.6	239	8	US-08-726-211-5	Sequence 5, Appl
32	31	88.6	239	12	US-10-141-618-12	Sequence 12, Appl
33	31	88.6	239	12	US-10-053-645A-21	Sequence 21, Appl
34	31	88.6	239	12	US-10-387-961A-5	Sequence 5, Appl
35	31	88.6	239	15	US-10-101-482-12	Sequence 12, Appl
36	31	88.6	239	15	US-10-277-693A-10	Sequence 10, Appl
37	31	88.6	239	15	US-10-072-830-2	Sequence 2, Appl
38	31	88.6	472	12	US-10-369-493-23432	Sequence 23432, A
39	31	88.6	662	10	US-09-924-358-11	Sequence 11, Appl
40	31	88.6	662	12	US-10-410-764-11	Sequence 11, Appl
41	31	88.6	1398	12	US-10-021-571-6	Sequence 6, Appl
42	31	88.6	6	10	US-09-847-940B-2	Sequence 2, Appl
43	30	85.7	6	11	US-09-847-946A-2	Sequence 2, Appl
44	30	85.7	6	11	US-09-847-946A-33	Sequence 33, Appl
45	30	85.7				

ALIGNMENTS

RESULT 1
US-09-847-940B-11
; Sequence 11, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-11

Query Match 100.0%; Score 35; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWM 6
Db 1 LDFSWM 6

RESULT 2
US-09-847-946A-11
; Sequence 11, Application US/09847946A
; Publication NO. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-11

Query Match 100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
Db 1 LDFS WL 6

RESULT 3

US-09-847-946A-42
; Sequence 42, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-42

Query Match 100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
Db 1 LDFS WL 6

RESULT 4

US-09-847-946A-84
; Sequence 84, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-84

Query Match 100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
Db 1 LDFS WL 6

RESULT 5

US-09-847-946A-88
; Sequence 88, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-88

Query Match 100.0%; Score 35; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
Db 1 LDFS WL 6

RESULT 6

US-09-847-946A-81
; Sequence 81, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-81

Query Match 100.0%; Score 35; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 3 LDFSWL 8

RESULT 7
US-09-847-946A-89
; Sequence 89, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-89

Query Match 100.0%; Score 35; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 1 LDFSWL 6

RESULT 8
US-09-847-946A-80
; Sequence 80, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-80

Query Match 100.0%; Score 35; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6
Db 1 LDFSWL 6

RESULT 9
US-09-847-946A-83
; Sequence 83, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-83

Query Match 100.0%; Score 35; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
|||||
Db 1 LDFS WL 6

RESULT 10

US-09-847-946A-86
; Sequence 86, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-86

Query Match 100.0%; Score 35; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
|||||
Db 3 LDFS WL 8

RESULT 11

US-09-847-946A-87
; Sequence 87, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-87

Query Match 100.0%; Score 35; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
|||||
Db 2 LDFS WL 7

RESULT 12

US-09-847-946A-82
; Sequence 82, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-82

Query Match 100.0%; Score 35; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
|||||
Db 2 LDFS WL 7

RESULT 13

US-09-847-946A-85
; Sequence 85, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-85

US-09-847-946A-85

Query Match 100.0%; Score 35; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
Db 3 LDFSWL 8

RESULT 14

US-09-847-946A-79
; Sequence 79, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-79

Query Match 100.0%; Score 35; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
Db 3 LDFSWL 8

RESULT 15

US-09-881-752A-368
; Sequence 368, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter pylori

US-09-881-752A-368

Query Match 94.3%; Score 33; DB 10; Length 265;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
|||||
Db 161 LDFSWI 166

Search completed: February 18, 2004, 15:41:58
Job time : 16.7529 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDFS WL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query #	Score	Match	Length	DB	ID	Description
1	35	100.0	6	23	ABB08733		Mutated IKKbeta NE
2	35	100.0	6	23	AA048516		NBD mutant peptide
3	35	100.0	6	23	AA048519		Anti-inflammatory
4	35	100.0	6	23	AA048581		Anti-inflammatory
5	35	100.0	6	24	AB008446		Human NEMO binding
6	35	100.0	7	23	AA048595		Anti-inflammatory
7	35	100.0	8	23	AA048578		Anti-inflammatory
8	35	100.0	8	23	AA048586		Anti-inflammatory
9	35	100.0	9	23	AA048577		Anti-inflammatory

ALIGNMENTS

RESULT 1

ABB08733

ABB08733
ID ABB08733 standard; peptide: 6 AA.

AC ABB08733:

14-JUN-2002 (first entry)

DE Mutated TKKbat = NEMO bind

XX

KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive
KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
KW antitartarostylerotic; viricide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antarthritic; osteopathic; antulcer; mutant; mutagen.

OS Homo sapiens.

OS Homo sapiens

XX	Key	Location/Qualifiers
EH		

key
Misc-difference 3

ET	MISC-DIFFERENCE	/note=	Wildtype	Trp substituted by phe"
ET				

XX PN WO200183547-A2

XX
PD
08-NOV-2001

XX FD

10	35	100.0	9	23	AAW48580	Anti-inflammatory
11	35	100.0	9	23	AAW48583	Anti-inflammatory
12	35	100.0	9	23	AAW48584	Anti-inflammatory
13	35	100.0	10	23	AAW48579	Anti-inflammatory
14	35	100.0	10	23	AAW48582	Anti-inflammatory
15	35	100.0	11	23	AAW48576	Anti-inflammatory
16	35	100.0	756	23	ABW77296	Human IKKbeta muta
17	33	94.3	144	21	AAW70582	Salmonella Pachogee
18	33	94.3	253	19	AAW1039	H. pylori ORF 06a6
19	33	94.3	265	19	AAW98384	H. pylori GPFO 128
20	33	94.3	528	24	ABP79808	N. gonorrhoeae ami
21	32	91.4	6	23	ABB08734	Mutated IKKbeta AM
22	32	91.4	6	23	AAW48517	NBD mutant peptide
23	32	91.4	6	23	AAW48540	Anti-inflammatory
24	32	91.4	6	23	AAW48540	Anti-inflammatory
25	32	91.4	6	24	ABU08427	Human NEMO binding
26	32	91.4	7	23	AAW48596	Anti-inflammatory
27	32	91.4	8	23	AAW48589	Anti-inflammatory
28	32	91.4	8	23	AAW48597	Anti-inflammatory
29	32	91.4	9	23	AAW48588	Anti-inflammatory
30	32	91.4	9	23	AAW48591	Anti-inflammatory
31	32	91.4	9	23	AAW48594	Anti-inflammatory
32	32	91.4	9	23	AAW48595	Anti-inflammatory
33	32	91.4	10	23	AAW48590	Anti-inflammatory
34	32	91.4	10	23	AAW48593	Anti-inflammatory
35	32	91.4	11	23	AAW48587	Anti-inflammatory
36	32	91.4	756	23	ABW77297	Human IKKbeta muta
37	31	88.6	23	20	AAW7823	Epitope of a Bcl-2
38	31	88.6	23	22	AAW874140	Bax epitope #10.
39	31	88.6	25	20	AAW87829	Epitope of a Bcl-2
40	31	88.6	25	22	AAW74146	Bax epitope #16
41	31	88.6	42	21	AAW34347	Human secreted pro
42	31	88.6	46	24	ABU07212	Maize SSIII C-term
43	31	88.6	46	24	ABU07218	Maize SSIII C-term
44	31	88.6	87	22	ABG10985	Novel human diagno
45	31	88.6	106	22	AAW83837	Human immune/baema

PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (UYVA) UNIV YALE.
 PA
 PI May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 DR
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 44; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammation
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 1 LDFSWL 6
 |||||
 RESULT 2
 ID AAM48516
 XX AAM48516 standard; Peptide; 6 AA.
 AC AAM48516;
 XX
 DT 20-MAR-2002 (first entry)
 XX NBD mutant peptide SEQ ID NO 11.
 DE

XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; neutropenic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 Example 6; Page 47; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antibacterial, immunosuppressive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 Db 1 LDFSWL 6
 |||||
 RESULT 3
 ID AAM48539
 AAM48539 standard; Peptide; 6 AA.

XX AC AAM48539;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 42.
 XX
 KW Antinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 61; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWL 6
 |||||

Db 1 LDFSWL 6
 RESULT 4
 AAM48581
 ID AAM48581 standard; Peptide; 6 AA.
 XX
 XX AAM48581;
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 84.
 XX
 KW Antinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
 |||||
 Db 1 LDFS WL 6

RESULT 5
 ABU08426
 ID ABU08426 standard; peptide; 6 AA.

XX AC ABU08426;

DT 12-JUN-2003 (first entry)

DE Human NEMO binding site (NBD) mutant peptide #9.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; muten.

XX OS Homo sapiens.

OS Synthetic.

PN US2002156000-A1.

XX PD 24-OCT-2002.

PF 02-MAY-2001; 2001US-0847940.

XX PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX PA (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

XX PI May MJ, Ghosh S;

XX DR WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -

XX PS Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFS WL 6
 |||||
 Db 1 LDFS WL 6

RESULT 6

AAW48585
 ID AAW48585 standard; Peptide; 7 AA.

XX AC AAW48585;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 88.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAW48628-AAW48645), comprising a membrane translocation domain
 CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
 |||||
 Db 1 LDFSWL 6

RESULT 7
 AAM48578
 ID AAM48578 standard; Peptide; 8 AA.

XX AC AAM48578;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 81.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX PS Claim 6; Page 62; 88pp; English.

XX CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 35; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
 |||||
 Db 3 LDFSWL 8

RESULT 8
 AAM48586

ID AAM48586 standard; Peptide; 8 AA.

XX AC AAM48586;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 89.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX PS Claim 6; Page 62; 88pp; English.

XX CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

SQ Sequence 8 AA;

Query Match 100.0%; Score 35; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
 Db 1 LDFSWL 6
 |||||

RESULT 9

AAW48577
 ID AAW48577 standard; Peptide; 9 AA.

AC AAW48577;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 80.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAW48628-AAW48645), comprising a membrane translocation domain

CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
 CC amino acid residues; fused to a NEMO binding sequence
 CC (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutropic, antiatherosclerotic, virucide and antiallergic activity. The
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
 Db 1 LDFSWL 6
 |||||

RESULT 10

AAW48580

ID AAW48580 standard; Peptide; 9 AA.

AC AAW48580;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 83.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

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 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -
 XX
 PS
 XX
 CC Claim 6; Page 62; 88pp; English.
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 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
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 CC telangiectasia. The compounds are also useful for treating
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 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
 |||||
 Db 1 LDFSWL 6

RESULT 11
 AAM48583
 ID AAM48583 standard; Peptide; 9 AA.
 AC AAM48583;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 DE Anti-inflammatory peptide SEQ ID NO 86.

XX Antinflammatory; antiasthmatic; cytotatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRACIS PHARM INC.

XX (UYTA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.
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 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
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 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6
 |||||
 Db 3 LDFSWL 8

RESULT 12
 AAM48584
 ID AAM48584 standard; Peptide; 9 AA.
 AC AAM48584;
 XX
 XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 87.

XX Antinflammatory; antiasthmatic; cytotatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

```

PR 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA ) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Claim 6; Page 62; 89pp; English.
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CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 35; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
DB 2 LDFSWL 7
RESULT 13
AAM48579
ID AAM48579 standard; Peptide; 10 AA.
XX
XX AAM48579;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 82.
XX
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.

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XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14346.
XX
XX 02-MAY-2000; 2000US-201261P.
XX 22-AUG-2000; 2000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA ) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
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PT domain fused to NEMO binding sequence, useful for blocking nuclear
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 35; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSWL 6
DB 2 LDFSWL 7
RESULT 14
AAM48582
ID AAM48582 standard; Peptide; 10 AA.
XX
XX AAM48582;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 85.
XX
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.

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KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX
 PS Claim 6; Page 62; 88pp; English.
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 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 35; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWSL 6
 Db 3 LDFSWSL 8
 RESULT 15
 AAM48576
 ID AAM48576 standard; Peptide; 11 AA.
 XX AC
 XX AAM48576;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 79.
 XX
 KW Antiinflammatory; antiasthmatic; cytotatic; antipsoriatic; nontropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFKappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
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 PF 02-MAY-2001; 2001WO-US14346.
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 PA (UYA) UNIV YALE.
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 35; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDFSWSL 6
 Db 3 LDFSWSL 8
 Search completed: February 18, 2004, 14:26:22
 Job time : 22.7763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17,3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	518	5 Q968Y8	Q968Y8 caenorhabdi
2	33	100.0	521	11 Q8C4D5	Q8C4D5 mus musculus
3	33	100.0	535	5 Q968Y7	Q968Y7 caenorhabdi
4	31	93.9	908	16 Q8ZAJ4	Q8ZAJ4 yersinia pe
5	31	93.9	535	17 Q27987	Q27987 archaeoglob
6	31	93.9	763	10 Q9SUZ5	Q9SUZ5 arabidopsis
7	30	90.9	187	2 Q9JRL8	Q9JRL8 xanthomonas
8	30	90.9	187	2 Q9JRL9	Q9JRL9 xanthomonas
9	30	90.9	187	2 Q9JRL5	Q9JRL5 xanthomonas
10	30	90.9	187	2 Q9JRM0	Q9JRM0 xanthomonas
11	30	90.9	187	2 Q9JRL7	Q9JRL7 xanthomonas
12	30	90.9	205	16 Q8EBG1	Q8EBG1 shewanella
13	30	90.9	221	16 Q9A120	Q9A120 streptococc
14	30	90.9	221	16 Q8P239	Q8P239 streptococc
15	30	90.9	225	17 Q8TR10	Q8TR10 methanosarc
16	30	90.9	245	2 Q68096	Q68096 rhodobacter

17	30	90.9	261	4 Q9P012	Q9P012 homo sapien
18	30	90.9	261	11 Q99K13	Q99K13 mus musculus
19	30	90.9	290	2 Q9F238	Q9F238 xanthomonas
20	30	90.9	290	2 Q9RBQ2	Q9RBQ2 xanthomonas
21	30	90.9	290	2 Q9RBQ3	Q9RBQ3 xanthomonas
22	30	90.9	290	2 Q9RBQ3	Q9RBQ3 xanthomonas
23	30	90.9	293	16 Q8PFB8	Q8PFB8 xanthomonas
24	30	90.9	307	11 Q9CXJ5	Q9CXJ5 mus musculus
25	30	90.9	316	16 Q98IR6	Q98IR6 rhizobium 1
26	30	90.9	317	4 Q9BRA3	Q9BRA3 homo sapien
27	30	90.9	332	2 Q9RA30	Q9RA30 vibrio mari
28	30	90.9	344	11 Q9R306	Q9R306 mus musculus
29	30	90.9	442	10 Q9SZ32	Q9SZ32 arabidopsis
30	30	90.9	461	10 Q9M0J8	Q9M0J8 arabidopsis
31	30	90.9	500	11 Q8CHX7	Q8CHX7 mus musculus
32	30	90.9	563	4 Q8NS10	Q8NS10 homo sapien
33	30	90.9	688	9 Q9FZR2	Q9FZR2 mycoplasma
34	30	90.9	810	16 Q8ZKN4	Q8ZKN4 salmonella
35	30	90.9	810	16 Q8Z226	Q8Z226 salmonella
36	30	90.9	906	16 Q8YXK2	Q8YXK2 anabaena sp
37	30	90.9	997	2 Q68533	Q68533 pseudomonas
38	29	87.9	69	10 Q43289	Q43289 arabidopsis
39	29	87.9	125	16 Q8DUU9	Q8DUU9 streptococc
40	29	87.9	150	16 Q9HTX9	Q9HTX9 pseudomonas
41	29	87.9	151	5 Q77003	Q77003 biomphalari
42	29	87.9	156	4 Q96G14	Q96G14 homo sapien
43	29	87.9	162	8 Q94Z49	Q94Z49 neolepidape
44	29	87.9	162	8 Q94Z27	Q94Z27 profundiver
45	29	87.9	175	16 Q8PQ04	Q8PQ04 xanthomonas

ALIGNMENTS

RESULT 1

Q968Y8	PRELIMINARY;	PRT;	518 AA.
ID	Q968Y8;		
AC	Q968Y8;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Hypothetical protein T28B4.1b.		
GN	T28B4.1 OR T28B4.1B.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RX	MEDLINE=99069613; PubMed=9851916;		
RA	None;		
RT	"Genome sequence of the nematode C. elegans: a platform for		
RT	investigating biology. The C. elegans Sequencing Consortium."		
RL	Science 282:2012-2018(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Wilson R., Greco T., Sansone J.;		
RT	"The sequence of C. elegans cosmid T28B4.";		
RL	Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Bristol N2;		
RA	Waterston R.;		
RT	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AF026206; AAK39308.1; -		
DR	WormPep; T28B4.1b; CE27216.		
DR	InterPro; IPR001810; F-box.		
DR	Pfam; PF00846; F-box; 1.		
DR	SMART; SM00256; FBOX; 1.		
DR	PROSITE; PS50181; FBOX; 1.		
SQ	SEQUENCE 518 AA; 60125 MW; A8A30C911618ED47 CRC64;		

Query Match 100.0%; Score 33; DB 5; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 Db 323 LDASWL 328
 |||||

RESULT 2
 Q8C4D5 PRELIMINARY; PRT; 521 AA.
 AC Q8C4D5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK082517; BAC38515.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 521 AA; 57719 MW; D4C2F39CB25122D5 CRC64;

Query Match 100.0%; Score 33; DB 11; Length 521;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 Db 283 LDASWL 288
 |||||

RESULT 3
 Q968Y7 PRELIMINARY; PRT; 535 AA.
 AC Q968Y7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE T28B4.1a protein.
 GN T28B4.1 OR T28B4.1A.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R., Greco T., Sansone J.;
 RT "The sequence of C. elegans cosmid T28B4.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026206; AAK39309.1; -.
 DR WormPep; T28B4.1a; CE27215.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SMO0256; FBOX; 1.
 DR PROSITE; PS50181; FBOX; 1.
 SQ SEQUENCE 535 AA; 62557 MW; CFEA8794E188C104 CRC64;

Query Match 100.0%; Score 33; DB 5; Length 535;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 Db 340 LDASWL 345
 |||||

RESULT 4
 Q8ZAJ4 PRELIMINARY; PRT; 308 AA.
 ID Q8ZAJ4;
 AC Q8ZAJ4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)
 DE High-affinity branched-chain amino acid transport system, permease
 DE protein (High-affinity branched-chain amino acid ABC transport system
 DE membrane permease).
 GN LIVH OR YPO3807 OR Y0423.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jageis K., Kariyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AJ414159; CAC93274.1; -.
 DR EMBL; AE013643; AAM84012.1; -.
 DR InterPro; IPR001851; Bac_inmem_transp.
 DR Pfam; PF02653; BPD_transp_2; 1.
 SQ Complete proteome.
 KW SEQUENCE 308 AA; 33042 MW; 9C25277B553063A7 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 308;
 Best Local Similarity 83.3%; Pred. No. 4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 :|||||

Db 66 IDASWL 71

RESULT 5

O27987 PRELIMINARY; PRT; 535 AA.

AC O27987; 535 AA.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Cytochrome oxidase, subunit I (CYDA-2).

GN AF2297.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI_TaxID=2234;

RP [1]

SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kierulff A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RA "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";

RT Nature 390:364-370 (1997).

RL EMBL; AB000946; AAB88960.1; -.

DR TIGR; AF2297; -.

DR InterPro; IPR002585; Bac_Ubq_Cox.

DR InterPro; IPR000515; BPD_transp.

DR Pfam; PF01654; Bac_Ubq_Cox; 1.

DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.

QX Hypothetical protein; Complete proteome.

SK SEQUENCE 535 AA; 57605 MW; 68C821D58A11EE96 CRC64;

Query Match 93.9%; Score 31; DB 17; Length 535;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 8 IDASWL 13

RESULT 6

Q9SUZ5 PRELIMINARY; PRT; 763 AA.

AC Q9SUZ5; 763 AA.

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical 85.2 kDa protein.

GN F4F15.210.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC euroside II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RP [1]

SEQUENCE FROM N.A.

RA Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL049711; CAB41330.1; -.

DR InterPro; IPR001965; Znf_PHD.

DR InterPro; IPR001841; Znf_Ring.

DR SMART; SM00249; PHD; 2.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS0016; ZF_PHD 2; 1.

DR PROSITE; PS0089; ZF_RING_2; 1.

KW Hypothetical protein.

SK SEQUENCE 763 AA; 85199 MW; 92BB47843D5314F9 CRC64;

Query Match 93.9%; Score 31; DB 10; Length 763;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 613 LDASWL 618

RESULT 7

Q9JRL8 PRELIMINARY; PRT; 187 AA.

AC Q9JRL8; 187 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Metallo-beta-lactamase 3 (fragment).

GN MBL3.

OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Stenotrophomonas.

OX NCBI_TaxID=40324;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=U152;

RA Walker R.A., Higgins P., Payne D.J., Amves S.G.;

RT "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia isolates.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ289083; CAB94702.1; -.

DR HSP; P52700; ISML.

DR InterPro; IPR001018; Beta_lactamase_B.

DR InterPro; IPR001279; Blactmase-like.

DR Pfam; PF00753; lactamase B; 1.

DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.

FT NON_TER 1

FT NON_TER 187

SK SEQUENCE 187 AA; 19931 MW; F07D49E4B4C88043 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;

Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 12 VDASWL 17

RESULT 8

Q9JRL9 PRELIMINARY; PRT; 187 AA.

AC Q9JRL9; 187 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Metallo-beta-lactamase 2 (fragment).

GN MBL2.

OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=0062;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289082; CAB94701.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta lactamase B.
DR Pfam; PF00753; lactamase B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19960 MW; 877D49E4B4C898F4 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 12 VDASWL 17

RESULT 9
Q9JRL5
ID Q9JRL5 PRELIMINARY; PRT; 187 AA.
AC Q9JRL5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Metallo-beta-lactamase 511 (Fragment).
GN MBL511 OR MBL5.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=511, and 37;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289086; CAB94705.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta lactamase B.
DR Pfam; PF00753; lactamase B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19811 MW; 7A2B11372028E5FE CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 12 VDASWL 17

RESULT 10
Q9JRM0
ID Q9JRM0 PRELIMINARY; PRT; 187 AA.
AC Q9JRM0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Metallo-beta-lactamase 1 (Fragment).
GN MBL1.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=GEL;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289081; CAB94700.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta lactamase B.
DR Pfam; PF00753; lactamase B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19901 MW; 72B8515412892A08 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 12 VDASWL 17

RESULT 11
Q9JRL7
ID Q9JRL7 PRELIMINARY; PRT; 187 AA.
AC Q9JRL7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Metallo-beta-lactamase 4 (Fragment).
GN MBL4.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=J2323;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289084; CAB94703.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta lactamase B.
DR Pfam; PF00753; lactamase B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19900 MW; D3C749E4B60C3F18 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;

```

OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=J1192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic K., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

RP SEQUENCE FROM N.A.
RC SPECIES=S.Pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=2213808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.Y., Smoot J.C., Porcella S.F., Park
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Strepto-
RT phage-encoded toxins, the high-virulence phenotype, and clo-
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RL EMBL; AA009993; AAL97264.1; --
DR EMBL; AE014143; AAM78967.1; --
DR InterPro: IPR000415; Nitroreductase.
DR Pfam: PF00881; Nitroreductase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 221 AA: 25369 MW: A929A147BEE0027D6 CRC64:

```

Query Match      90.9%;      Score 30;  DB 16;  Length 221;
Best Local Similarity 83.3%;      Pred. No. 4.4e+02;
Matches 5;  Conservative 1;  Mismatches 0;  Indels

Qy      1  LDAQWL 6
        |||:|
Db      36  LDAAWL 41

RESULT 15
Q8TR10      Q8TR10      PRELIMINARY;
ID      Q8TR10
AC      Q8TR10;
PRT;      225 AA.

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein MA1374.
 GN MA1374.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.D., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AF010807; AM04790.1; -.
 DR InterPro; IPR005237; Cons_hypoth289.
 DR InterPro; IPR002761; DUF71.
 DR Pfam; PF01902; DUF71; 1.
 DR TIGRFAMs; TIGR00290; MJ0570 dom; 1.
 DR TIGRFAMs; TIGR00289; TIGR00289; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 225 AA; 25146 MW; A573D46D1DDFB9D1 CRC64;

Query Match 90.9%; Score 30; DB 17; Length 225;
 Best Local Similarity 83.3%; Pred. No. 4.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 Db 149 LDSSWL 154

Search completed: February 18, 2004, 14:35:48
 Job time : 19.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	419	T32441	hypothetical prote
2	31	93.9	308	AF0463	high-affinity bran
3	31	93.9	535	A69537	cytochrome oxidase
4	31	93.9	763	T49089	hypothetical prote
5	30	90.9	245	T03533	probable precorrin
6	30	90.9	290	T48880	beta-lactamase (EC
7	30	90.9	290	S45349	L1 metallo-beta-la
8	30	90.9	332	T44437	aminodeoxychorism
9	30	90.9	442	T04815	hypothetical prote
10	30	90.9	461	D85312	probable homeodoma
11	30	90.9	810	AG0937	bifunctional aspar
12	30	90.9	906	AG1957	hypothetical prote
13	30	90.9	919	QYFKG	phosphoenolpyruvat
14	29	87.9	150	C82594	conserved hypothet
15	29	87.9	177	B41377	cytochrome c-L pre
16	29	87.9	243	G83450	hypothetical prote
17	29	87.9	252	C83837	hypothetical prote
18	29	87.9	255	G75626	probable 3-alpha-h
19	29	87.9	256	F84612	hypothetical prote
20	29	87.9	284	D84504	probable VSR-1-like
21	29	87.9	269	A75397	probable signal pe
22	29	87.9	274	E83444	probable transcrip
23	29	87.9	277	T29979	hypothetical prote
24	29	87.9	278	H82759	cell division prot
25	29	87.9	282	E70890	hypothetical prote
26	29	87.9	286	A48399	probable oxidoredu
27	29	87.9	286	A85739	probable dehydroge
28	29	87.9	286	H90879	probable dehydroge
29	29	87.9	289	A37209	thiosulfate sulfur

30	29	87.9	295	2	S15081	thiosulfate sulfur
31	29	87.9	296	1	ROHU	thiosulfate sulfur
32	29	87.9	296	2	AH2327	hypothetical prote
33	29	87.9	297	1	ROBO	thiosulfate sulfur
34	29	87.9	297	2	JC4398	thiosulfate sulfur
35	29	87.9	297	2	JC5286	thiosulfate sulfur
36	29	87.9	301	2	G83182	hypothetical prote
37	29	87.9	316	2	F89791	peptidoglycan hydr
38	29	87.9	318	2	T52663	thiosulfate sulfur
39	29	87.9	326	2	B99790	hypothetical prote
40	29	87.9	329	2	A86300	hypothetical prote
41	29	87.9	333	2	F70678	probable transposa
42	29	87.9	359	2	S15305	rfbG protein - Sal
43	29	87.9	359	2	AH0766	CDPglucose 4,6-deh
44	29	87.9	360	2	T26037	hypothetical prote
45	29	87.9	360	2	S32695	wnt-2 protein - Ca

ALIGNMENTS

RESULT 1

T32441
Hypothetical protein T28B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T32441
R:Wilson, R.; Greco, T.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T28B4.
A:Reference number: Z21168
A:Accession: T32441
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-419 <WIL>
A:Cross-references: EMBL:AF026206; PIDN:AAB71262.1; GSPDB:GNO00028; CESP:T28B4.1
A:Experimental source: strain Bristol N2; clone T28B4
C:Genetics:
A:Gene: CESP:T28B4.1
A:Map position: X
A:introns: 47/3; 68/3; 102/3; 153/1; 207/1; 296/1

Query Match 100.0%; Score 33; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
|||||
DB 340 LDASWL 345

RESULT 2

AF0463
high-affinity branched-chain amino acid transport system, permease protein livH [import:
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AF0463
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whithead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0463
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC93274.1; PID:gi5981721; GSPDB:GNO0175
C:Genetics:
A:Gene: livH
C:Superfamily: leucine transport protein livH
Query Match 93.9%; Score 31; DB 2; Length 308;

Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 66 IDASWL 71

RESULT 3
A69537
cytochrome oxidase, subunit I (cydA-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
C:Accession: A69537
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69537
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-535 <KLE>
A:Cross-references: GB:AE000946; GB:AE000782; NID:92689269; PIDN:AB88960.1; PID:9264822
C:Superfamily: cytochrome d complex terminal oxidase chain I

Query Match 93.9%; Score 31; DB 2; Length 535;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 8 IDASWL 13

RESULT 4
T49089
hypothetical protein F4F15.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49089
R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25015
A:Accession: T49089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-763 <ALC>
A:Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.210
A:Experimental source: cultivar Columbia; BAC clone F4F15
C:Genetics:
A:Gene: ATSP:F4F15.210
A:Map position: 3
A:Introns: 11/2; 124/3; 183/1; 199/3; 230/3; 274/1; 297/3; 325/2; 351/3; 478/1; 641/2; 6

Query Match 93.9%; Score 31; DB 2; Length 763;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 613 LDASWI 618

RESULT 5
T03533
probable precorrin-2 methyltransferase (EC 2.1.1.-) - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 18-Feb-2000
C:Accession: T03533

R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A:Reference number: Z14955; MUID:9740404; PMID:9256491
A:Accession: T03533
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-245 <VLC>
A:Cross-references: EMBL:AF010496; NID:93128256; PIDN:AAC16186.1; PID:93128334
C:Genetics:
A:Map position: 1
C:Superfamily: precorrin-3 methylase
C:Keywords: methyltransferase

Query Match 90.9%; Score 30; DB 2; Length 245;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 197 LDAAWL 202

RESULT 6
T4880
beta-lactamase (EC 3.5.2.6) L-1 precursor [validated] - Pseudomonas maltophilia
N:Alternate names: L-1 metallo-beta-lactamase
C:Species: Pseudomonas maltophilia
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T48880
R:Sanschagrin, F.; Dufresne, J.; Levesque, R.C.
Antimicrob. Agents Chemother. 42, 1245-1248, 1998
A:Title: Molecular heterogeneity of the L-1 metallo-beta-lactamase family from Stenotrop
A:Reference number: Z24841; MUID:98253990; PMID:9593158
A:Accession: T48880
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-290 <SAN>
A:Cross-references: EMBL:AF010282; PIDN:AAC21590.1
A:Experimental source: strain GNI2873
C:Genetics:
A:Gene: blas
C:Function:
A:Description: catalyzes the hydrolysis of an amide bond in the beta-lactam ring of the
C:Keywords: antibiotic resistance; hydrolase
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-290/Product: L-1 metallo-beta-lactamase #status predicted <MAT>

Query Match 90.9%; Score 30; DB 2; Length 290;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
:|||||
Db 34 VDASWL 39

RESULT 7
S45349
L1 metallo-beta-lactamase - Xanthomonas maltophilia
C:Species: Xanthomonas maltophilia
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S45349
R:Walsh, T.R.; Hall, L.; Assinder, S.J.; Nichols, W.W.; Cartwright, S.J.; MacGowan, A.P.
Biochim. Biophys. Acta 1218, 199-201, 1994
A:Title: Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophilia
A:Reference number: S45349; MUID:94289479; PMID:8018721
A:Accession: S45349
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <WAL>

Query Match 90.9%; Score 30; DB 2; Length 290;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 34 VDASWL 39

RESULT 8
T4437
aminodoxochromate lyase homolog [imported] - Moritella marina
C:Species: Moritella marina
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T4437
R:Morita, N.; Ueno, A.; Tanaka, M.; Ohgiya, S.; Hoshino, T.; Kawasaki, K.; Yumoto, I.; I
Biotechnol. Lett. 21, 641-646, 1999
A>Title: Cloning and sequencing of clustered genes involved in fatty acid biosynthesis
A:Reference number: 222768
A:Accession: T4437
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-332 <WOR>
A:Cross-references: EMBL:AB021978; PIDN:BA085259.1
A:Experimental source: ATCC 15381
C:Genetics:
A>Note: pabC
C:Superfamily: yceG protein

Query Match 90.9%; Score 30; DB 2; Length 332;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 187 LDAWL 192

RESULT 9
T04815
hypothetical protein F10M23.260 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04815
R:Bevan, M.; Lechamy, A.; Chedid, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H
submitted to the Protein Sequence Database, February 1999
A:Reference number: 215385
A:Accession: T04815
A:Molecule type: DNA
A:Residues: 1-442 <BEV>
A:Cross-references: EMBL:AL035440
A:Experimental source: cultivar Columbia; BAC clone F10M23
C:Genetics:
A:Map position: 4
A:introns: 140/3; 165/3; 236/1; 358/3
A>Note: F10M23.260

Query Match 90.9%; Score 30; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 128 VDASWL 133

RESULT 10
D85312
probable homeodomain protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: D85312
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85312
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-461 <STO>
A:Cross-references: GB:NC_001268; NID:g7269545; PIDN:CA879547.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4G26920
A:Map position: 4

Query Match 90.9%; Score 30; DB 2; Length 461;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 128 VDASWL 133

RESULT 11
AH0937
bifunctional aspartokinase II/homoserine dehydrogenase Iican I write [imported] - Salm
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0937
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0937
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-810 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09522.1; PID:g16504639; GSPDB:GN00176
C:Genetics:
A:Superfamily: thrA bifunctional enzyme; aspartate kinase homology; homoserine dehydrog.

Query Match 90.9%; Score 30; DB 2; Length 810;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 146 LDAWL 151

RESULT 12
AG1957
hypothetical protein all1210 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1957
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1957
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-906 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873167.1; PID:g17130557; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1210

Query Match 90.9%; Score 30; DB 2; Length 906;
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 DB 225 LDSSWL 230
 |||
 |||

RESULT 13
 QYFKG
 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Corynebacterium glutamicum
 C:Species: Corynebacterium glutamicum
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
 C:Accession: S05512; J50183
 R:Bikmann, B.J.; Follettie, M.T.; Griot, M.U.; Sinskey, A.J.
 Mol. Gen. Genet. 218, 330-339, 1989
 A:Title: The phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: molecular
 A:Reference number: S05511; MUID:89384460; PMID:2779518
 A:Accession: S05512
 A:Molecule type: DNA
 A:Residues: 1-919 <EIK>
 A:Cross-references: GB:X14234; NID:948688; PIDN:CAA32450.1; PID:948689
 A:Note: the authors translated the codon ATT for residue 387 as Glu, AAA for residue 553
 R:O'Regan, M.; Thierbach, G.; Bachmann, B.; Villeval, D.; Lepage, P.; Viret, J.F.; Lemol
 Gene 77, 237-251, 1989
 A:Title: Cloning and nucleotide sequence of the phosphoenolpyruvate carboxylase-coding g
 A:Reference number: J50183; MUID:89326141; PMID:2666264
 A:Accession: J50183
 A:Molecule type: DNA
 A:Residues: 1-606, 'KL', 609-799, 'FT', 802-914, 'L', 916-919 <ORE>
 A:Cross-references: GB:M25819; NID:9144984; PIDN:AAA83537.1; PID:9144985
 A:Experimental source: ATCC 13032
 A:Note: residues 2-15 were confirmed by protein sequencing
 C:Comment: This enzyme catalyzes the carboxylation (by carbon dioxide) of phosphoenolpyr
 C:Comment: The activity of this protein is not stimulated by acetyl-CoA in the absence o
 C:Genetics:
 A:Gene: ppc
 A:Superfamily: phosphoenolpyruvate carboxylase
 C:Keywords: allosteric regulation; carbon dioxide fixation; carbon-carbon lyase; carboxy
 F:2-919/Product: phosphoenolpyruvate carboxylase #status predicted <MAT>
 F:611-624/Region: substrate binding #status predicted

Query Match 90.9%; Score 30; DB 1; Length 919;
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 DB 105 LDATWL 110
 |||
 |||

RESULT 14
 C82994
 conserved hypothetical protein PA5211 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: C82994
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bu
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: C82994
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <STO>
 A:Cross-references: GB:AE004934; GB:AE004091; NID:99951515; PIDN:AAG08596.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA5211

Query Match 87.9%; Score 29; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6
 DB 117 DASWL 121
 |||
 |||

RESULT 15
 B41377
 cytochrome c-L precursor [validated] - Paracoccus denitrificans
 N:Alternate names: cytochrome c551; cytochrome c552; moxG protein
 C:Species: Paracoccus denitrificans
 C:Date: 28-May-1992 #sequence_revision 02-Jul-1996 #text_change 15-Sep-2000
 C:Accession: B41377
 R:Van Spanning, R.J.M.; Wansell, C.W.; De Boer, T.; Hazelaar, M.J.; Anazawa, H.; Harms,
 J. Bacteriol. 173, 6948-6961, 1991
 A:Title: Isolation and characterization of the moxJ, moxG, moxI, and moxR genes of Para
 A:Reference number: A41377; MUID:92041581; PMID:1657871
 A:Accession: B41377
 A:Molecule type: DNA
 A:Residues: 1-177 <VAN>
 A:Cross-references: GB:M57684; NID:9150589; PIDN:AAA25583.1; PID:9150591
 R:Chen, L.; Durlay, R.C.E.; Matthews, F.S.; Davidson, V.L.
 Science 264, 86-90, 1994
 A:Title: Structure of an electron transfer complex: methylamine dehydrogenase, amicyanin
 A:Reference number: A57985; MUID:94188715; PMID:8140419
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 23-177
 R:Chen, L.; Mathews, F.S.
 submitted to the Brookhaven Protein Data Bank, October 1993
 A:Reference number: A52094; PDB:2MTA
 A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 23-169
 C:Genetics:
 A:Gene: moxG
 C:Complex: associates in a heterotetramer with methylamine dehydrogenase large and small
 C:Function:
 A:Description: electron acceptor for methanol dehydrogenase; can also accept an electron
 A:Pathway: methanol oxidation; methylamine oxidation
 C:Superfamily: cytochrome c-L; cytochrome c6 homology
 C:Keywords: chromoprotein; electron transfer; heme; heterotetramer; iron; metalloprotein
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:23-177/Product: cytochrome c-L #status experimental <MAT>
 F:69-142/Domain: cytochrome c6 homology <CY6>
 F:79,82/Binding site: heme (Cys) (covalent) #status experimental
 F:83,123/Binding site: heme iron (His, Met) (axial ligands) #status experimental

Query Match 87.9%; Score 29; DB 1; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6
 DB 152 DASWL 156
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 |||

Search completed: February 18, 2004, 14:38:44
 Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	33	100.0	6	10	US-09-847-940B-10
2	33	100.0	6	11	US-09-847-946A-10
3	33	100.0	105	10	US-09-738-626-6278
4	30	90.9	191	12	US-10-291-265-310
5	30	90.9	221	15	US-10-169-048-2
6	30	90.9	261	9	US-09-765-205-14
7	30	90.9	261	12	US-10-360-849A-12
8	30	90.9	261	12	US-10-360-849A-15
9	30	90.9	261	12	US-10-360-849A-18
10	30	90.9	277	12	US-10-291-265-310
11	30	90.9	919	10	US-09-738-626-6970
12	30	90.9	935	9	US-09-784-208-3
13	30	90.9	935	12	US-10-077-745-1
14	30	90.9	935	12	US-10-338-915-1
15	30	90.9	935	14	US-10-078-107-1

16	30	90.9	935	14	US-10-077-751-1	Sequence 1, Appli
17	30	90.9	935	15	US-10-315-023-3	Sequence 3, Appli
18	30	90.9	935	15	US-10-315-023-8	Sequence 8, Appli
19	29	87.9	136	10	US-09-738-973-123	Sequence 123, App
20	29	87.9	136	10	US-09-854-133-123	Sequence 123, App
21	29	87.9	136	15	US-10-144-649A-123	Sequence 3740, Ap
22	29	87.9	238	12	US-10-108-260A-3740	Sequence 592, App
23	29	87.9	269	12	US-10-369-493-592	Sequence 5377, Ap
24	29	87.9	277	12	US-10-369-493-5377	Sequence 7867, Ap
25	29	87.9	278	12	US-10-369-493-7867	Sequence 11783, A
26	29	87.9	279	12	US-10-369-493-11783	Sequence 14664, A
27	29	87.9	279	12	US-10-369-493-14664	Sequence 15142, A
28	29	87.9	279	12	US-10-369-493-15142	Sequence 7936, Ap
29	29	87.9	285	12	US-10-369-493-7936	Sequence 821, App
30	29	87.9	286	12	US-10-369-493-821	Sequence 21834, A
31	29	87.9	293	12	US-10-369-493-21834	Sequence 90, Appl
32	29	87.9	297	10	US-09-981-353-90	Sequence 12482, A
33	29	87.9	305	9	US-09-815-242-12482	Sequence 6011, Ap
34	29	87.9	314	10	US-09-738-626-6011	Sequence 5327, Ap
35	29	87.9	322	9	US-09-815-242-5327	Sequence 40, Appl
36	29	87.9	397	14	US-10-029-180-40	Sequence 101, App
37	29	87.9	437	15	US-10-145-415-101	Sequence 10355, A
38	29	87.9	465	15	US-10-156-761-10355	Sequence 23656, A
39	29	87.9	491	12	US-10-369-493-23656	Sequence 1887, Ap
40	29	87.9	501	12	US-10-094-749-1887	Sequence 3205, Ap
41	29	87.9	512	12	US-10-320-797-3205	Sequence 3747, Ap
42	29	87.9	571	12	US-10-369-493-3747	Sequence 2, Appli
43	29	87.9	854	11	US-09-770-107-2	Sequence 17, Appl
44	29	87.9	865	12	US-10-347-470A-17	Sequence 3190, Ap
45	29	87.9	1066	15	US-10-128-714-3190	

ALIGNMENTS

RESULT 1
US-09-847-940B-10
; Sequence 10, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-10

Query Match 100.0%; Score 33; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 1 LDASWL 6

RESULT 2
US-09-847-946A-10
; Sequence 10, Application US/09847946A
; Publication NO. US2003005499A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide

US-09-847-946A-10

Query Match 100.0%; Score 33; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 1 LDASWL 6

RESULT 3

US-09-738-626-6278
; Sequence 6278, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6278
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

US-09-738-626-6278

Query Match 100.0%; Score 33; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 48 LDASWL 53

RESULT 4

US-10-291-265-782
; Sequence 782, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 782
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-291-265-782

Query Match 90.9%; Score 30; DB 12; Length 191;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 161 LDASWL 166

RESULT 5

US-10-169-048-2
; Sequence 2, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes

US-10-169-048-2

Query Match 90.9%; Score 30; DB 15; Length 221;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 36 LDASWL 41

RESULT 6

US-09-765-205-14
; Sequence 14, Application US/09765205
; Patent No. US20020034800A1

; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 261
; TYPE: PRT
; ORGANISM: human
US-09-765-205-14

Query Match 90.9%; Score 30; DB 9; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 161 LDASWV 166
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RESULT 7
US-10-360-849A-12
; Sequence 12, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc..
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aidas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 261
; TYPE: PRT
; ORGANISM: danio rerio
US-10-360-849A-12

Query Match 90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 161 LDASWV 166
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RESULT 8
US-10-360-849A-15
; Sequence 15, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc..
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aidas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl

; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 261
; TYPE: PRT
; ORGANISM: mus musculus
US-10-360-849A-15

Query Match 90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 161 LDASWV 166
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RESULT 9
US-10-360-849A-18
; Sequence 18, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc..
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aidas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: home sapiens
US-10-360-849A-18

Query Match 90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 161 LDASWV 166
|||||

RESULT 10
US-10-291-265-310
; Sequence 310, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al

```
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 310
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-310

Query Match          90.9%; Score 30; DB 12; Length 277;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDASWL 6
Db      161 LDASWL 166

RESULT 11
US-09-738-626-6970
; Sequence 6970, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6970
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6970

Query Match          90.9%; Score 30; DB 10; Length 919;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDASWL 6
Db      105 LDATWL 110

RESULT 12
US-09-784-208-3
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; Sequence 3, Application US/09784208
; Patent No. US20010019836A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, Hiroshi
; APPLICANT: ONO, Eiiji
; APPLICANT: MATSUI, Kazuhiko
; APPLICANT: MORIYA, Mika
; APPLICANT: ITO, Hisao
; APPLICANT: HARA, Yoshihiko
; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR
; FILE REFERENCE: 0010-0989-0
; CURRENT APPLICATION NUMBER: US/09/784,208
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/271,438
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: JP 10-69068
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: JP 10-297129
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-09-784-208-3

Query Match          90.9%; Score 30; DB 9; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDASWL 6
Db      10 LDSSWL 15

RESULT 13
US-10-077-745-1
; Sequence 1, Application US/10077745
; Publication No. US20030172698A1
; GENERAL INFORMATION:
; APPLICANT: KODA, TAKAYUKI
; APPLICANT: SATO, KAZUHIRO
; TITLE OF INVENTION: ORGANIC NITROGEN-CONTAINING COMPOSITION AND FERTILIZER COMPRISING
; FILE REFERENCE: 219843USO
; CURRENT APPLICATION NUMBER: US/10/077,745
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: JP 2001-044137
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-077-745-1

Query Match          90.9%; Score 30; DB 12; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDASWL 6
Db      10 LDSSWL 15

RESULT 14
US-10-338-915-1
; Sequence 1, Application US/10338915
; Publication No. US20030190713A1
; GENERAL INFORMATION:
```

Wed Feb 18 17:21:01 2004

; APPLICANT: Ueda, Hiroshi
; APPLICANT: Koda, Takayuki
; APPLICANT: Sato, Masakazu
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 232696US0CONT
; CURRENT APPLICATION NUMBER: US/10/338,915
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 10/077,999
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: JP 2001-044136
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-338-915-1

Query Match 90.9%; Score 30; DB 12; Length 935;
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 10 LDSSWL 15

RESULT 15
US-10-078-107-1
; Sequence 1, Application US/10078107
; Publication No. US20020182688A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: HARA, YOSHIHIKO
; APPLICANT: SATO, MASAKAZU
; APPLICANT: AKIYOSHI, NAOKI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 219846US0
; CURRENT APPLICATION NUMBER: US/10/078,107
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: JP 2001-044134
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-078-107-1

Query Match 90.9%; Score 30; DB 14; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 10 LDSSWL 15

Search completed: February 18, 2004, 15:41:58
Job time : 17.7529 secs

No art

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDPASWL 6

Scoring table: BLOSUM62

Scoring cards: [Scoring cards](#)
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	6	23	AAM48515	NBD mutant peptide
3	33	100.0	6	24	ABU08425	Human NEMO binding
4	33	100.0	105	22	AAG32524	C glutamicam prote
5	33	100.0	756	23	ABW77295	Human IKKbeta muta
6	31	93.9	618	21	AAG32182	Arabidopsis thalia
7	31	93.9	676	21	AAG32181	Arabidopsis thalia
8	31	93.9	763	21	AAG32180	Arabidopsis thalia
9	30	90.9	117	22	ABG30551	Novel human diagno

PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYUA) UNIV YALE.
 PI May MJ, Ghosh S;
 XX WPI; 2002-179350/23.
 DR
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 44; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprising contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of Ikbappab. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 33; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 Db 1 LDASWL 6
 |||||
 |||||
 RESULT 2
 AAM48515
 ID AAM48515 standard; Peptide; 6 AA.
 XX
 AC AAM48515;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SRQ ID NO 10.

XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; Ikbappab kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAB-) PRACIS PHARM INC.
 PA (UYUA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX
 PT Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 PS Example 6; Page 47; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antithrombotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of Ikbappab kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of Ikbappab kinase
 CC activation and subsequent decreased phosphorylation of Ikbappab. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 33; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 Db 1 LDASWL 6
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 RESULT 3
 ABU08425
 ID ABU08425 standard; peptide; 6 AA.

XX ABU08425;
 XX 12-JUN-2003 (first entry)
 XX Human NEMO binding site (NBD) mutant peptide #8.
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neurotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; muten.
 XX Homo sapiens.
 OS Synthetic.
 XX US2002156000-A1.
 XX 24-OCT-2002.
 XX 02-MAY-2001; 2001US-0847940.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX May MJ, Ghosh S;
 XX WPI: 2003-209142/20.
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX Claim 22; Page 17; 47pp; English.
 XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 33; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 |||||
 DB 1 LDASWL 6
 RESULT 4
 AAG92524
 ID AAG92524 standard; Protein; 105 AA.
 XX

AC AAG92524;
 XX 26-SEP-2001 (first entry)
 XX C glutamicum protein fragment SEQ ID NO: 6278.
 DE Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX Corynebacterium glutamicum.
 OS EP1108790-A2.
 PN 20-JUN-2001.
 PD 18-DEC-2000; 2000EP-0127688.
 PF 16-DEC-1999; 99JP-0377484.
 PR 07-APR-2000; 2000JP-0159162.
 PR 03-AUG-2000; 2000JP-0280988.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI: 2001-376931/40.
 DR N-PSDB; AAH67743.
 XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT -
 XX Claim 17; SEQ ID NO: 6278; 246pp + Sequence Listing; English.
 PS The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX Sequence 105 AA;
 SQ Query Match 100.0%; Score 33; DB 22; Length 105;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 |||||
 DB 48 LDASWL 53
 RESULT 5
 ABB77295
 ID ABB77295 standard; protein; 756 AA.
 XX ABB77295;
 XX 14-JUN-2002 (first entry)
 XX Human IKKbeta mutant W739A.
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

OY 1 LDASWL 6
Db 468 LDASWI 473

RESULT 7
AAG32181
ID AAG32181 standard; Protein; 676 AA.
XX AC AAG32181;
XX 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 38773.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
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XX 19-APR-1999; 99US-0130077.
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XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
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XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 07-MAY-1999; 99US-0132487.
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XX 27-MAY-1999; 99US-0136392.
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PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161320.
PR 28-OCT-1999; 99US-0161392.
PR 28-OCT-1999; 99US-0161393.
PR 29-OCT-1999; 99US-0162142.

Query Match 93.8%; Score 31; DB 21; Length 676;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6
Db 526 LDASWI 531

RESULT 8
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AAG32180
ID AAG32180 standard; Protein; 763 AA.
XX
AC AAG32180;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38772.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144633.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
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PR 22-JUL-1999; 99US-0145088.
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PR 22-JUL-1999; 99US-0145087.
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PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.

PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 93.9%; Score 31; DB 21; Length 763;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 613 LDASWI 618

RESULT 9
ABG20551
ID ABG20551 standard; Protein; 117 AA.
XX
AC ABG20551;
XX
DT 18-FEB-2002 (first entry)
XX

DE Novel human diagnostic protein #20542.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS84738.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 XX Claim 20; SEQ ID No 50910; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (III). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 117 AA;
 SQ
 Query Match 90.9%; Score 30; DB 22; Length 117;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 DB 38 LDANWL 43
 RESULT 10
 AAB42606
 ID AAB42606 standard; Protein; 119 AA.
 XX
 AC AAB42606;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 XX Human ORFX ORF2370 polypeptide sequence SEQ ID NO:4740.
 DE
 XX

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX WO200058473-A2.
 XX 05-OCT-2000.
 XX 31-MAR-2000; 2000WO-US08621.
 XX 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Shimkets RA, Leach M;
 PI WPI; 2000-602362/57.
 DR N-PSDB; AAC76815.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 XX Claim 11; Page 3920; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; antirheumatic;
 CC antinflammatory; antibacterial; antiviral; antifungal; antithyroid;
 CC antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 XX Sequence 119 AA;
 SQ
 Query Match 90.9%; Score 30; DB 21; Length 119;
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASWL 6
 DB 29 LDAWL 34

RESULT 11
AAE03936
ID AAE03936 standard; Protein; 156 AA.
XX
AC AAE03936;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human gene 39 encoded secreted protein HEMDM08, SEQ ID NO:99.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery;
KW cell culture; chemotaxis; food additive; gene therapy;
KW binding partner identification.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT Protein /label= signal_peptide
FT 29..156
FT /note= "Mature secreted protein"
XX
XX WO200077022-A1.
PN
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US15136.
XX
XX 11-JUN-1999; 99US-0138629.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI; 2001-367020/38.
XX
XX N-PSDB; AAD08383.
XX
XX Nucleic acids encoding 50 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
PT disease, botulism, cancers and Scimitar syndrome -
XX
XX Claim 11; Page 547; 614pp; English.
XX
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 50 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell

CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein of the invention.
XX
SQ Sequence 156 AA;
Query Match 90.9%; Score 30; DB 22; Length 156;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDASWL 6
Db 56 LDASWV 61
|||||
56 LDASWV 61
RESULT 12
AAE03978
ID AAE03978 standard; Protein; 189 AA.
XX
AC AAE03978;
XX
DT 09-AUG-2001 (first entry)
XX
XX Human gene 39 encoded secreted protein fragment, SEQ ID NO:172.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnery;
KW cell culture; chemotaxis; food additive; gene therapy;
KW binding partner identification.
XX
XX Homo sapiens.
XX
XX WO200077022-A1.
PN
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US15136.
XX
XX 11-JUN-1999; 99US-0138629.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI; 2001-367020/38.
XX
XX Nucleic acids encoding 50 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's
PT disease, botulism, cancers and Scimitar syndrome -
XX
XX Claim 11; Page 547; 614pp; English.
XX
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
CC protein genes and AAE03898-AAE03947 represent the proteins they encode.
CC AAE03948-AAE03996 represent human secreted protein fragments or variants.
CC The genes and their secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 50 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell

CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplant, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis. and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.

SQ Sequence 189 AA;
 Query Match 90.9%; Score 30; DB 22; Length 189;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 DB 164 LDASWV 169
 |||||:
 164 LDASWV 169

RESULT 13
 AAU14439
 ID AAU14439 standard; Protein; 191 AA.
 AC AAU14439;
 XX
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human novel protein #310.
 XX
 KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antiaschmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200155437-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US02623.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 XX
 PA (HYSE-) HYSSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI; 2001-451939/48.
 DR N-PSDB; AAS22744.
 XX
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 PT
 XX Example 4; Page 816; 894pp; English.
 PS
 XX The invention relates to polynucleotides encoding novel human

CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicite an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

XX
 SQ Sequence 191 AA;

Query Match 90.9%; Score 30; DB 22; Length 191;
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 DB 161 LDASWV 166
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 161 LDASWV 166

RESULT 14
 AAU03119
 ID AAU03119 standard; Protein; 221 AA.
 XX
 AC AAU03119;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Streptococcus pyogenes virulence protein #1.
 DE
 XX Virulence; attenuated microorganism; Streptococcal infection;
 KW Gram-positive bacteria; antimicrobial; impetigo; pneumonia.
 KW
 XX Streptococcus pyogenes.
 OS
 XX
 XX WO200148208-A2.
 PN
 XX
 PD 05-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-GB04997.
 XX
 PR 23-DEC-1999; 99GB-0030462.
 PR 23-DEC-1999; 99GB-0030463.
 PR 23-DEC-1999; 99GB-0030464.
 PR 23-DEC-1999; 99GB-0030466.
 PR 23-DEC-1999; 99GB-0030467.
 PR 23-DEC-1999; 99GB-0030469.
 PR 23-DEC-1999; 99GB-0030471.
 PR 23-DEC-1999; 99GB-0030472.
 PR 23-DEC-1999; 99GB-0030473.
 PR 23-DEC-1999; 99GB-0030474.
 PR 17-FEB-2000; 2000GB-0003725.
 PR 17-FEB-2000; 2000GB-0003726.
 PR 17-FEB-2000; 2000GB-0003727.
 PR 17-FEB-2000; 2000GB-0003728.
 PR 17-FEB-2000; 2000GB-0003729.
 PR 17-FEB-2000; 2000GB-0003730.

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PR 17-FEB-2000; 2000GB-0003731.
PR 17-FEB-2000; 2000GB-0003732.
PR 17-FEB-2000; 2000GB-0003733.
PR 02-MAY-2000; 2000GB-0010585.
PR 02-MAY-2000; 2000GB-0010587.
XX (MICK-) MICROSCIENCE LTD.
XX
XX Clarke EE, Zhou L, Shea JE, Feldman RG, Holden DW;
XX
XX WPI; 2001-418285/44.
XX N-PSDB; AA06351.
XX
XX Novel peptide obtained from Streptococcus pyogenes useful for treating
XX or preventing a condition associated with infection by Streptococcal or
XX Gram-positive bacteria, preferably pneumonia
XX
XX Claim 4; Page 26-27; 91pp; English.
XX
XX AAU03119-AAU03149 represent novel Streptococcus pyogenes virulence
XX proteins #1-31. The S. pyogenes virulence genes can be used to
XX produce attenuated microorganisms comprising a mutation that disrupt
XX the expression of the virulence protein. The virulence genes, proteins
XX or an attenuated microorganism are useful for therapeutic or diagnostic
XX purposes. DNA encoding the virulence proteins, the proteins themselves,
XX an attenuated microorganism or a vaccine comprising the virulence
XX protein are useful for the manufacture of a medicament for use in
XX the treatment or prevention of a condition associated with infection
XX by Streptococcal or Gram-positive bacteria, for veterinary treatment,
XX and in a screening assay for the identification of an antimicrobial
XX drug. Disorders which can be treated using S. pyogenes virulence
XX polynucleotide and polypeptide sequences include non-invasive infections
XX and invasive infections e.g. impetigo, pharyngitis, necrotising
XX fasciitis, bacteraemia, streptococcal toxic shock syndrome (STSS),
XX pneumonia and rheumatic fever. The virulence proteins are also useful
XX in the preparation of antibodies.
XX
XX Sequence 221 AA;
XX
XX Query Match 90.9%; Score 30; DB 22; Length 221;
XX Best Local Similarity 83.3%; Pred. No. 7.5e+02;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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XX |||:|
XX 36 LDRAWL 41
XX
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XX AC ABP27441;
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XX DT 02-JUL-2002 (first entry)
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XX DE Streptococcus polypeptide SEQ ID NO 4058.
XX
XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX group A streptococcus; Streptococcus pyogenes; antibacterial;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
XX OS Streptococcus pyogenes.
XX
XX WO200234771-A2.
XX
XX PD 02-MAY-2002.
XX
XX PF 29-OCT-2001; 2001WO-GB04789.
XX
XX PR 27-OCT-2000; 2000GB-0026333.
XX 24-NOV-2000; 2000GB-0028727.
XX 07-MAR-2001; 2001GB-0005640.
XX

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XX (CHIR-) CHIRON SPA.
XX (GENO-) INST GENOMIC RES.
XX
XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
XX Tettelin H;
XX
XX WPI; 2002-352536/38.
XX N-PSDB; ABN68072.
XX
XX New Streptococcus protein for the treatment or prevention of infection
XX or disease caused by Streptococcus bacteria, such as meningitis, and
XX for detecting a compound that binds to the protein -
XX
XX Claim 1; Page 3561; 4525pp; English.
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
XX streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX the specification. The proteins have antibacterial and antiinflammatory
XX activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
XX antibodies that bind (I) are used in the manufacture of medicaments for
XX the treatment or prevention of infection or disease caused by
XX Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX Nucleic acids encoding (I) are used to detect Streptococcus in a
XX biological sample. (I) is used to determine whether a compound binds to
XX (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX used as a vaccine or diagnostic composition. The disease caused by
XX Streptococcus that is prevented or treated may be meningitis. Nucleic
XX acid encoding (I) may be used to recombinantly produce (I) and may be
XX used in gene therapy. Antibodies to (I) are used for affinity
XX chromatography, immunoassays, and distinguishing/identifying
XX Streptococcus proteins.
XX
XX Sequence 221 AA;
XX
XX Query Match 90.9%; Score 30; DB 23; Length 221;
XX Best Local Similarity 83.3%; Pred. No. 7.5e+02;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 LDASWL 6
XX |||:|
XX 36 LDRAWL 41
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XX Search completed: February 18, 2004, 14:26:22
XX Job time : 23.7763 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
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Scoring table: BLOSUM62
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Searched: 801455 seqs, 209382283 residues
Total number of hits satisfying chosen parameters: 801455
Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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2	40	100.0	6 11	US-09-847-946A-9	Sequence 9, Appli
3	36	90.0	117 11	US-09-809-391-360	Sequence 360, App
4	36	90.0	117 12	US-09-882-171-360	Sequence 360, App
5	36	90.0	117 12	US-10-108-260A-2983	Sequence 2983, Ap
6	36	90.0	464 9	US-09-815-242-10647	Sequence 10647, A
7	36	90.0	467 9	US-09-815-242-4997	Sequence 4997, Ap
8	36	90.0	864 12	US-10-436-715-29	Sequence 29, Appl
9	36	90.0	864 12	US-10-436-715-82	Sequence 82, Appl
10	35	87.5	6 10	US-09-847-940B-2	Sequence 2, Appli
11	35	87.5	6 11	US-09-847-946A-2	Sequence 2, Appli
12	35	87.5	6 11	US-09-847-946A-33	Sequence 33, Appl
13	35	87.5	7 11	US-09-847-946A-37	Sequence 37, Appl
14	35	87.5	8 11	US-09-847-946A-30	Sequence 30, Appl
15	35	87.5	8 11	US-09-847-946A-38	Sequence 38, Appl

Sequence 29, Appl
Sequence 32, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 31, Appl
Sequence 34, Appl
Sequence 28, Appl
Sequence 132, Appl
Sequence 140, App
Sequence 143, App
Sequence 144, App
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Sequence 141, App
Sequence 142, App
Sequence 146, App
Sequence 147, App
Sequence 131, App
Sequence 135, App
Sequence 136, App
Sequence 133, App
Sequence 134, App
Sequence 137, App
Sequence 138, App
Sequence 139, App
Sequence 18, Appl
Sequence 18, Appl
Sequence 141, App
Sequence 2, Appl
Sequence 10, Appl

US-09-847-940B-9
; Sequence 9, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-9

ALIGNMENTS

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; Sequence 9, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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US-09-847-940B-9

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Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6
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DB 1 LNMSWL 6

RESULT 2
US-09-847-946A-9
; Sequence 9, Application US/09847946A
; Publication NO. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

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; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
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; PRIOR FILING DATE: 2000-08-22
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-9

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
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US-09-809-391-360

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 30 LNWSW 34

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; Sequence 360, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
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Db 30 LNWSW 34

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; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2983
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2983

Query Match 90.0%; Score 36; DB 12; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
 |||||
 Db 20 NWSWL 24

RESULT 6

US-09-815-242-10647
 ; Sequence 10647, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10647
 ; LENGTH: 464
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis

US-09-815-242-10647

Query Match 90.0%; Score 36; DB 9; Length 464;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
 |||||
 Db 422 NWSWL 426

RESULT 7

US-09-815-242-4997
 ; Sequence 4997, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4997
 ; LENGTH: 467
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis

US-09-815-242-4997

Query Match 90.0%; Score 36; DB 9; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
 |||||
 Db 425 NWSWL 429

RESULT 8

US-10-436-715-29
 ; Sequence 29, Application US/10436715
 ; Publication No. US20040018976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
 ; TITLE OF INVENTION: AND SPICE VARIANTS THEREOF
 ; FILE REFERENCE: D0262 NP
 ; CURRENT APPLICATION NUMBER: US/10/436,715
 ; CURRENT FILING DATE: 2003-05-13
 ; PRIOR APPLICATION NUMBER: U.S. 60/380,336
 ; PRIOR FILING DATE: 2002-05-14
 ; NUMBER OF SEQ ID NOS: 471
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 29
 ; LENGTH: 864
 ; TYPE: PRT
 ; ORGANISM: Fugu rubripes

US-10-436-715-29

Query Match 90.0%; Score 36; DB 12; Length 864;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 |||||
 Db 481 LNWSWL 486

RESULT 9

US-10-436-715-82
 ; Sequence 82, Application US/10436715
 ; Publication No. US20040018976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
 ; TITLE OF INVENTION: AND SPICE VARIANTS THEREOF
 ; FILE REFERENCE: D0262 NP
 ; CURRENT APPLICATION NUMBER: US/10/436,715
 ; CURRENT FILING DATE: 2003-05-13
 ; PRIOR APPLICATION NUMBER: U.S. 60/380,336

; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-436-715-82

Query Match 90.0%; Score 36; DB 12; Length 864;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 481 LNWQWL 486

RESULT 10
US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 87.5%; Score 35; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 11
US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2

Query Match 87.5%; Score 35; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 12
US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-33

Query Match 87.5%; Score 35; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 13
US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-37

Query Match 87.5%; Score 35; DB 11; Length 7;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 14
US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-30

Query Match 87.5%; Score 35; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNWSWL 6
|:||||
Db 3 LDWSWL 8

RESULT 15
US-09-847-946A-38
; Sequence 38, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-38

Query Match 87.5%; Score 35; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNWSWL 6
|:||||
Db 1 LDWSWL 6

Search completed: February 18, 2004, 15:41:57
Job time : 17.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	Mutated IKKbeta NE
2	40	100.0	6	23	NBD mutant peptide
3	40	100.0	6	24	Human NEMO binding
4	40	100.0	295	22	Drosophila melanog
5	40	100.0	756	23	Human IKKbeta muta
6	38	95.0	135	20	Human ovarian tumo
7	37	92.5	130	22	Human immune/haema
8	37	92.5	464	21	Macaca mulatta rha
9	36	90.0	117	23	Human novel secret

10	36	90.0	464	22	AAU35054	Enterococcus faeca
11	36	90.0	467	22	AAU33501	Enterococcus faeca
12	36	90.0	767	23	ABP65725	Bifidobacterium lo
13	35	87.5	6	23	ABB08725	IKKbeta NEMO bindi
14	35	87.5	6	23	AAW48530	Anti-inflammatory
15	35	87.5	6	23	AAW48655	NBD mutant peptide
16	35	87.5	6	24	ABU08418	Human NEMO binding
17	35	87.5	7	23	AAW48534	Anti-inflammatory
18	35	87.5	8	23	AAW48527	Anti-inflammatory
19	35	87.5	8	23	AAW48535	Anti-inflammatory
20	35	87.5	9	20	AAW96182	IKK-alpha polypept
21	35	87.5	9	23	AAW48526	Anti-inflammatory
22	35	87.5	9	23	AAW48529	Anti-inflammatory
23	35	87.5	9	23	AAW48532	Anti-inflammatory
24	35	87.5	9	23	AAW48533	Anti-inflammatory
25	35	87.5	10	23	ABB77313	IKKbeta NEMO bindi
26	35	87.5	10	23	AAW48528	Anti-inflammatory
27	35	87.5	10	23	AAW48531	Anti-inflammatory
28	35	87.5	11	23	ABB77311	Human NBD peptide
29	35	87.5	11	23	AAW48506	Human IKKbeta pept
30	35	87.5	11	23	AAW48525	Anti-inflammatory
31	35	87.5	11	23	AAW48653	NBD peptide. Synt
32	35	87.5	13	23	AAW48640	Anti-inflammatory
33	35	87.5	13	23	AAW48641	Anti-inflammatory
34	35	87.5	13	23	AAW48642	Anti-inflammatory
35	35	87.5	13	23	AAW48645	Anti-inflammatory
36	35	87.5	17	23	AAW48638	Anti-inflammatory
37	35	87.5	17	23	AAW48639	Anti-inflammatory
38	35	87.5	17	23	AAW48643	Anti-inflammatory
39	35	87.5	17	23	AAW48644	Anti-inflammatory
40	35	87.5	18	23	AAW48628	Anti-inflammatory
41	35	87.5	18	23	AAW48629	Anti-inflammatory
42	35	87.5	18	23	AAW48632	Anti-inflammatory
43	35	87.5	18	23	AAW48633	Anti-inflammatory
44	35	87.5	22	23	AAW48630	Anti-inflammatory
45	35	87.5	22	23	AAW48631	Anti-inflammatory

ALIGNMENTS

RESULT 1
ABB08731
ID ABB08731 standard; peptide; 6 AA.
XX
AC ABB08731;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 9.
XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neutropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiaethmatic; antiallergic;
KW dermatological; antibacterial; antipsoaritic; antirheumatic;
KW antiarthritic; osteopathic; antilucer; mutant; mutein.

OS Homo sapiens.
OS Synthetic.

XX
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "Wildtype Asp substituted by Asn"
XX
XX WO200183547-A2.
XX
XX
PD 08-NOV-2001.
XX

PF 02-MAY-2001; 2001WO-US40654.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2002-179350/23.
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 44; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 1 LNWSWL 6
 |||||
 |||||
 RESULT 2
 AAM48514
 ID AAM48514 standard; Peptide; 6 AA.
 XX
 AC AAM48514;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 9.

XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAB-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 PT
 XX Example 6; Page 47; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 1 LNWSWL 6
 |||||
 |||||
 RESULT 3
 ABU08424
 ID ABU08424 standard; peptide; 6 AA.

XX AC ABU08424;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #7.
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN US2002156000-A1.
 XX PD 24-OCT-2002.
 XX PF 02-MAY-2001; 2001US-0847940.
 XX PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX PI May MJ, Ghosh S;
 XX WI; 2003-209142/20.
 XX Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX Claim 22; Page 17; 47pp; English.
 XX The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 40; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 DB 1 LNWSWL 6
 RESULT 4
 AB062034
 ID ABB62034 standard; Protein; 295 AA.
 XX

AC ABB62034;
 XX 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 12894.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WI; 2001-656860/75.
 DR N-PSDB; ABL06137.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Disclosure; SEQ ID NO 12894; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB057737-AB072072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 295 AA;
 SQ Query Match 100.0%; Score 40; DB 22; Length 295;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 DB 286 LNWSWL 291
 RESULT 5
 ABB77304
 ID ABB77304 standard; protein; 756 AA.
 XX ABB77304;
 XX 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant D738N.
 XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;

KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antiparasitic; antirheumatic;
XX antiarthritic; osteopathic; antitumor; mutant; mitein.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 738
FT /note= "Wildtype Asp substituted by Asn"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (UYUA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
XX inflammatory disorders, osteoporosis and cancer, comprises contacting a
XX cell with an anti-inflammatory compound comprising at least one NEMO
XX binding domain -

XX Example 11; Page -; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
XX comprises contacting a cell with an anti-inflammatory compound
XX (ABB08725-ABB08742) comprising at least one NEMO binding domain
XX (ABB77313). The compound has acts through selective inhibition of
XX cytokine-mediated NF-kB activation by blocking the interaction of NEMO
XX with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
XX interaction results in inhibition of IKKbeta kinase activation and
XX subsequent decreased phosphorylation of IkbappB. The compound may also
XX act (directly or indirectly) by blocking the recruitment of leukocytes
XX into sites of acute and chronic inflammation, by down-regulating the
XX expression of E-selectin on leukocytes or by blocking osteoclast
XX differentiation. The compound is useful in treating NF-kB mediated
XX conditions, where the condition is an inflammatory disorder, an
XX autoimmune disease, transplant rejection, osteoporosis, cancer,
XX Alzheimer's disease, atherosclerosis, a viral infection or ataxia
XX telangiectasia. The inflammatory disorder is asthma, allergies,
XX urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
XX rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
XX bowel disease, chronic obstructive pulmonary disease, vasculitis and
XX bursitis. The inflammatory disorder may also be dermatitis, eczema,
XX psoriasis, osteoarthritis, psoriatic arthritis, lupus and
XX spondylarthritis. Also for Crohn's disease, ulcerative colitis,
XX polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
XX cryoglobulinemia or multiple sclerosis. For chronic viral infections
XX caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
XX diseases include HIV and influenza. The compound may also be useful for
XX treating anaphylaxis, drug and food sensitivity, contact dermatitis,
XX sunburn or aging. The compound may be used to replace corticosteroids in
XX any application in which corticosteroids are used, including
XX immunosuppression in transplants and cancer therapy. Also for identifying
XX anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
XX The compound may be administered alone or in combination with other known
XX anti-inflammatory agents. The present sequence is that of an IKKbeta
XX mutant, useful in examples of the invention.
XX Note: The present sequence is not given in the specification but is
XX derived from GenBank Accession No. Q14920 (ABB77294).

XX Sequence 756 AA;

Query Match 100.0%; Score 40; DB 23; Length 756;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
DB 737 LNWSWL 742

RESULT 6

AA76530
ID AAY76530 standard; Protein; 135 AA.

XX AC AAY76530;

XX DT 10-APR-2000 (first entry)

XX DE Human ovarian tumor EST fragment encoded protein 26.

XX EX Expressed sequence tag; EST; human; ovarian tumor; anticancer;

XX KW gene therapy; treatment.

XX OS Homo sapiens.

XX PN DE19817557-A1.

XX PD 21-OCT-1999.

XX PF 09-APR-1998; 98DE-1017557.

XX PR 09-APR-1998; 98DE-1017557.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI; 1999-591920/51.

XX N-PSDB; AAZ77461.

XX New nucleic acid sequences expressed in ovarian, and some other, cancer
XX tissues, and derived polypeptides, for treatment of ovarian cancer and
XX identification of therapeutic agents -

XX Claim 25; Page 254; 310pp; German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which
XX have anticancer activity and are highly expressed in ovarian tumor
XX tissue (and some also in testis and breast cancer tissue). The products
XX of the invention can be used for gene therapy. (A) are used (i) for
XX recombinant expression of polypeptides (B) and (ii) to isolate complete
XX genes. (B) are used (i) to identify agents suitable for treatment of
XX ovarian cancer; (ii) directly for treating this form of cancer
XX (including expression from gene therapy vectors) and (iii) for generation
XX of specific antibodies. (A) are identified by assembling ESTs (expressed
XX sequence tags) from a particular tissue type before comparison of the
XX expression patterns. This allows a significantly longer fragment of the
XX gene to be revealed, so should reduce the number of failures associated
XX with the fact that ESTs from different libraries may represent different
XX parts of the same unknown gene, distorting the estimated frequency of
XX occurrence in a particular tissue. AAY76505-Y76638 represent protein
XX fragments encoded by the human ovarian tumor cDNA library derived EST
XX fragments represented in AAZ77450-Z77572.

XX Sequence 135 AA;

Query Match 95.0%; Score 38; DB 20; Length 135;

Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6

DB 69 LNWSWL 74

RESULT 7
AAM85139
ID AAM85139 standard; Protein; 130 AA.
XX AC AAM85139;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen SEQ ID NO:12732.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225366.
PR 14-AUG-2000; 2000US-0225367.
PR 14-AUG-2000; 2000US-0225368.
PR 14-AUG-2000; 2000US-0225370.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-483426/52.
 DR N-PSDB; AAK57920.
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PT
 XX Claim 11; SEQ ID NO 12732; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 XX Sequence 130 AA;
 SQ
 Query Match 92.5%; Score 37; DB 22; Length 130;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 55 LNWTLW 60
 |||||
 RESULT 8
 AAK53151
 ID AAK53151 standard; Protein; 464 AA.
 XX
 AC AAK53151;
 XX
 XX 28-FEB-2001 (first entry)
 XX
 XX Macaca mulatta rhadinovirus 17577 RRV ORF32 protein SEQ ID NO:59.
 DE
 XX
 XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
 KW genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
 KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
 KW cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
 KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
 KW splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia.
 XX
 XX Macaca mulatta rhadinovirus 17577.
 OS
 XX

PN WO200028040-A2.
 XX
 XX 18-MAY-2000.
 XX
 XX 05-NOV-1999; 99WO-US26260.
 XX
 XX 06-NOV-1998; 98US-0107507.
 PR 20-NOV-1998; 98US-0109409.
 XX
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 XX Wong SW, Axthelm MK, Searles RP;
 XX WPI; 2000-376552/32.
 DR
 XX
 XX New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection -
 PT
 XX Claim 5; Page 128-129; 141pp; English.
 PS
 XX
 CC The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAK53123 to AAK53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune haemolytic anaemia, by
 CC administering the drug to a immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV, inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAK53205
 CC to AAK53213 represent sequence used in the exemplification of the
 CC present invention.
 XX
 XX Sequence 464 AA;
 SQ
 Query Match 92.5%; Score 37; DB 21; Length 464;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 397 VNWSWL 402
 |||||
 RESULT 9
 ABG95220
 ID ABG95220 standard; Protein; 117 AA.
 XX
 AC ABG95220;
 XX
 XX 15-JAN-2003 (first entry)
 XX
 XX Human novel secreted protein #41.
 DE
 XX
 XX Human; secreted protein; autoimmune disease; chemotaxis;
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
 KW nervous system disorders; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;
 KW epithelial cell proliferation; organ transplantation; food additive;
 KW preservative; nutritional.

XX OS Homo sapiens.
 XX PN US6420526-B1.
 XX PD 16-JUL-2002.
 XX PF 08-SEP-1998; 98US-0149476.
 XX PR 07-MAR-1997; 97US-038621P.
 XX PR 07-MAR-1997; 97US-040151P.
 XX PR 07-MAR-1997; 97US-040152P.
 XX PR 07-MAR-1997; 97US-040153P.
 XX PR 07-MAR-1997; 97US-040333P.
 XX PR 07-MAR-1997; 97US-040334P.
 XX PR 07-MAR-1997; 97US-040336P.
 XX PR 07-MAR-1997; 97US-040626P.
 XX PR 11-APR-1997; 97US-043331P.
 XX PR 11-APR-1997; 97US-043332P.
 XX PR 11-APR-1997; 97US-043333P.
 XX PR 11-APR-1997; 97US-043334P.
 XX PR 11-APR-1997; 97US-043315P.
 XX PR 11-APR-1997; 97US-043558P.
 XX PR 11-APR-1997; 97US-043559P.
 XX PR 11-APR-1997; 97US-043576P.
 XX PR 11-APR-1997; 97US-043578P.
 XX PR 11-APR-1997; 97US-043580P.
 XX PR 11-APR-1997; 97US-043659P.
 XX PR 11-APR-1997; 97US-043670P.
 XX PR 11-APR-1997; 97US-043671P.
 XX PR 11-APR-1997; 97US-043672P.
 XX PR 11-APR-1997; 97US-043674P.
 XX PR 23-MAY-1997; 97US-047492P.
 XX PR 23-MAY-1997; 97US-047500P.
 XX PR 23-MAY-1997; 97US-047501P.
 XX PR 23-MAY-1997; 97US-047502P.
 XX PR 23-MAY-1997; 97US-047503P.
 XX PR 23-MAY-1997; 97US-047581P.
 XX PR 23-MAY-1997; 97US-047582P.
 XX PR 23-MAY-1997; 97US-047583P.
 XX PR 23-MAY-1997; 97US-047584P.
 XX PR 23-MAY-1997; 97US-047585P.
 XX PR 23-MAY-1997; 97US-047586P.
 XX PR 23-MAY-1997; 97US-047587P.
 XX PR 23-MAY-1997; 97US-047588P.
 XX PR 23-MAY-1997; 97US-047589P.
 XX PR 23-MAY-1997; 97US-047590P.
 XX PR 23-MAY-1997; 97US-047592P.
 XX PR 23-MAY-1997; 97US-047593P.
 XX PR 23-MAY-1997; 97US-047594P.
 XX PR 23-MAY-1997; 97US-047595P.
 XX PR 23-MAY-1997; 97US-047596P.
 XX PR 23-MAY-1997; 97US-047597P.
 XX PR 23-MAY-1997; 97US-047598P.
 XX PR 23-MAY-1997; 97US-047599P.
 XX PR 23-MAY-1997; 97US-047600P.
 XX PR 23-MAY-1997; 97US-047601P.
 XX PR 23-MAY-1997; 97US-047612P.
 XX PR 23-MAY-1997; 97US-047613P.
 XX PR 23-MAY-1997; 97US-047614P.
 XX PR 23-MAY-1997; 97US-047615P.
 XX PR 23-MAY-1997; 97US-047617P.
 XX PR 23-MAY-1997; 97US-047618P.
 XX PR 23-MAY-1997; 97US-047619P.
 XX PR 06-JUN-1997; 97US-047633P.
 XX PR 06-JUN-1997; 97US-048964P.
 XX PR 13-JUN-1997; 97US-048974P.
 XX PR 08-JUL-1997; 97US-049610P.
 XX PR 16-JUL-1997; 97US-051926P.
 XX PR 18-AUG-1997; 97US-052874P.
 XX PR 22-AUG-1997; 97US-055724P.
 XX PR 22-AUG-1997; 97US-056630P.
 XX PR 22-AUG-1997; 97US-056631P.
 XX PR 22-AUG-1997; 97US-056632P.
 XX PR 22-AUG-1997; 97US-056636P.
 XX PR 22-AUG-1997; 97US-056637P.
 XX PR 22-AUG-1997; 97US-056662P.
 XX PR 22-AUG-1997; 97US-056664P.
 XX PR 22-AUG-1997; 97US-056845P.
 XX PR 22-AUG-1997; 97US-056862P.
 XX PR 22-AUG-1997; 97US-056864P.
 XX PR 22-AUG-1997; 97US-056872P.
 XX PR 22-AUG-1997; 97US-056874P.
 XX PR 22-AUG-1997; 97US-056875P.
 XX PR 22-AUG-1997; 97US-056876P.
 XX PR 22-AUG-1997; 97US-056877P.
 XX PR 22-AUG-1997; 97US-056878P.
 XX PR 22-AUG-1997; 97US-056879P.
 XX PR 22-AUG-1997; 97US-056880P.
 XX PR 22-AUG-1997; 97US-056881P.
 XX PR 22-AUG-1997; 97US-056882P.
 XX PR 22-AUG-1997; 97US-056884P.
 XX PR 22-AUG-1997; 97US-056886P.
 XX PR 22-AUG-1997; 97US-056887P.
 XX PR 22-AUG-1997; 97US-056888P.
 XX PR 22-AUG-1997; 97US-056889P.
 XX PR 22-AUG-1997; 97US-056892P.
 XX PR 22-AUG-1997; 97US-056893P.
 XX PR 22-AUG-1997; 97US-056894P.
 XX PR 22-AUG-1997; 97US-056903P.
 XX PR 22-AUG-1997; 97US-056908P.
 XX PR 22-AUG-1997; 97US-056909P.
 XX PR 22-AUG-1997; 97US-056910P.
 XX PR 22-AUG-1997; 97US-056911P.
 XX PR 05-SEP-1997; 97US-057761P.
 XX PR 05-SEP-1997; 97US-057650P.
 XX PR 12-SEP-1997; 97US-057669P.
 XX PR 02-OCT-1997; 97US-058785P.
 XX PR 06-MAR-1998; 97US-061060P.
 XX PR 98WO-US04493.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX WPI: 2002-634796/68.
 XX N-PSDB; ABS73538.
 XX PT New isolated human secreted protein for diagnosing, preventing,
 XX PT treating or ameliorating medical conditions and used as a food additive
 XX PT or preservative -
 XX PS Example 1; SEQ ID No 360; 129pp; English.
 XX CC The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of
 CC 309 cDNA sequences also given in the specification. The protein is used
 CC in a pharmaceutical composition used to prevent, treat or ameliorate a
 CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
 CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angioneuroma, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. The present sequence represents one of the novel human

CC secreted proteins of the invention.
CC Note: This sequence did not form part of the printed specification,
CC but was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=642052651.
XX
XX SQ Sequence 117 AA;
Query Match 90.0%; Score 36; DB 23; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 1 LNWSW 5
| | | | |
Db 30 LNWSW 34
RESULT 10
AAU35054
ID AAU35054 standard; Protein; 464 AA.
XX
AC AAU35054;
XX
DT 13-FEB-2002 (first entry)
XX
DE Enterococcus faecalis cellular proliferation protein #341.
XX
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GV;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS52913.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Example 3; Seq ID No 10647; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 464 AA;
Query Match 90.0%; Score 36; DB 22; Length 464;
Best Local Similarity 100.0%; Pred. No. 8.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 2 NWSWL 6
| | | | |
Db 422 NWSWL 426
RESULT 11
AAU33501
ID AAU33501 standard; Protein; 467 AA.
XX
AC AAU33501;
XX
DT 14-FEB-2002 (first entry)
XX
DE Enterococcus faecalis cellular proliferation protein #137.
XX
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR N-PSDB; AAS51360.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Example 3; Seq ID No 4997; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 467 AA;

Query Match 90.0%; Score 36; DB 22; Length 467;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
 |||||
 Db 425 NWSWL 429

RESULT 12

ABP65725
 ID ABP65725 standard; Protein; 767 AA.

XX AC ABP65725;

DT 19-NOV-2002 (first entry)

XX DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:469.

XX KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;
 KW antidiarrhetic; antibacterial; inhibitor of Salmonella; detection;
 KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
 KW rotavirus; food composition; pharmaceutical composition.

XX OS Bifidobacterium longum.

XX PN EP1227152-A1.

XX 31-JUL-2002.

XX 30-JAN-2001; 2001EP-0102050.

XX 30-JAN-2001; 2001EP-0102050.

XX (NEST) SOC PROD NESTLE SA.

XX WPI; 2002-668397/72.

XX Novel polynucleotide comprising Bifidobacterium genome sequence useful
 PT as a probe or primer for detecting and/or identifying Bifidobacterium
 PT longum in a biological sample -

XX Claim 3; SEQ ID 469; 80pp; English.

XX The present invention describes a polynucleotide (I) comprising a
 CC sequence of a Bifidobacterium genome selected from the nucleotide
 CC sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at
 CC least 90% identity or which hybridises with the sequences given in
 CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding
 CC a fusion protein, comprising a sequence selected from 1097 sequences
 CC given in ABP65358 to ABP63354 ligated in frame to a polynucleotide
 CC encoding a heterologous polypeptide. (I) has antidiarrhetic and
 CC antibacterial activities, and can be used as an inhibitor of Salmonella.
 CC (I) (which is a probe) is useful for the detection and/or identification
 CC of Bifidobacterium longum in a biological sample. A carrier containing
 CC the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM I-2618)
 CC can be used for preventing and/or treating diarrhoea brought about by
 CC pathogenic bacteria and/or rotavirus. The carrier is a food composition
 CC selected from milk, yogurt, curd, cheese, fermented milks, milk based
 CC fermented products, ice-creams, fermented cereal based products, milk
 CC based powders, infant formula, pet food or a pharmaceutical composition
 CC selected from tablets, liquid bacterial suspensions, dried oral
 CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
 CC (I) is useful in DNA arrays or chips to carry out analysis of the
 CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
 CC Bifidobacterium related nucleotide sequences given in the Sequence

CC Listing from the present invention but not mentioned further within the
 CC specification.
 CC N.B. The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office.

XX SQ Sequence 767 AA;

Query Match 90.0%; Score 36; DB 23; Length 767;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5
 |||||
 Db 569 LNWSW 573

RESULT 13

ABB08725

ID ABB08725 standard; peptide; 6 AA.

XX AC ABB08725;

DT 14-JUN-2002 (first entry)

XX DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.

XX KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiaethmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer.

XX OS Homo sapiens.

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -

XX Claim 23; Page 44; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast

CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC spondylarthritis, psoriatic arthritis, lupus and
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.

XX Sequence 6 AA;

Query Match 87.5%; Score 35; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. NO. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 |:||||
 Db 1 LDWSWL 6

RESULT 14

AA048530
 ID AAM48530 standard; Peptide; 6 AA.

AC AAM48530;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 33.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis

XX Claim 6; Page 61; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 6 AA;

Query Match 87.5%; Score 35; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. NO. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 |:||||
 Db 1 LDWSWL 6

RESULT 15

AA048655

ID AAM48655 standard; Peptide; 6 AA.

XX AAM48655;

XX 20-MAR-2002 (first entry)

XX NBD mutant peptide SEQ ID NO 2.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYUA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Example 6; Page 47; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteoprotective,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IkappaB kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;

Query Match 87.5%; Score 35; DB 23; Length 6;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
|:||||
Db 1 LDWSWL 6

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OM protein - protein search, using sw model

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(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62

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Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	6	10	US-09-847-940B-8
2	39	100.0	6	11	US-09-847-946A-8
3	36	92.3	6	10	US-09-847-940B-2
4	36	92.3	6	11	US-09-847-946A-2
5	36	92.3	6	11	US-09-847-946A-33
6	36	92.3	7	11	US-09-847-946A-37
7	36	92.3	8	11	US-09-847-946A-30
8	36	92.3	8	11	US-09-847-946A-38
9	36	92.3	9	11	US-09-847-946A-29
10	36	92.3	9	11	US-09-847-946A-32
11	36	92.3	9	11	US-09-847-946A-35
12	36	92.3	9	11	US-09-847-946A-36
13	36	92.3	10	11	US-09-847-946A-31
14	36	92.3	10	11	US-09-847-946A-34
15	36	92.3	11	11	US-09-847-946A-28

16	36	92.3	11	11	US-09-847-946A-132	Sequence 132, App
17	36	92.3	11	11	US-09-847-946A-140	Sequence 140, App
18	36	92.3	13	11	US-09-847-946A-143	Sequence 143, App
19	36	92.3	13	11	US-09-847-946A-144	Sequence 144, App
20	36	92.3	13	11	US-09-847-946A-145	Sequence 145, App
21	36	92.3	13	11	US-09-847-946A-148	Sequence 148, App
22	36	92.3	17	11	US-09-847-946A-141	Sequence 141, App
23	36	92.3	17	11	US-09-847-946A-142	Sequence 142, App
24	36	92.3	17	11	US-09-847-946A-146	Sequence 146, App
25	36	92.3	17	11	US-09-847-946A-147	Sequence 147, App
26	36	92.3	18	11	US-09-847-946A-131	Sequence 131, App
27	36	92.3	18	11	US-09-847-946A-135	Sequence 135, App
28	36	92.3	18	11	US-09-847-946A-136	Sequence 136, App
29	36	92.3	22	11	US-09-847-946A-133	Sequence 133, App
30	36	92.3	22	11	US-09-847-946A-134	Sequence 134, App
31	36	92.3	22	11	US-09-847-946A-137	Sequence 137, App
32	36	92.3	22	11	US-09-847-946A-138	Sequence 138, App
33	36	92.3	22	11	US-09-847-946A-139	Sequence 139, App
34	36	92.3	28	10	US-09-847-940B-18	Sequence 18, Appl
35	36	92.3	28	11	US-09-847-946A-18	Sequence 18, Appl
36	36	92.3	222	10	US-09-771-161A-141	Sequence 141, App
37	36	92.3	745	9	US-09-796-872-2	Sequence 2, Appl
38	36	92.3	745	10	US-09-844-908-10	Sequence 10, Appl
39	36	92.3	745	10	US-09-844-988-10	Sequence 10, Appl
40	36	92.3	745	12	US-10-408-636-3	Sequence 3, Appl
41	36	92.3	745	12	US-10-394-322A-32	Sequence 32, Appl
42	36	92.3	745	15	US-10-243-408-4	Sequence 4, Appl
43	36	92.3	745	15	US-10-059-585-35	Sequence 35, Appl
44	36	92.3	745	15	US-10-338-462-10	Sequence 10, Appl
45	36	92.3	756	9	US-09-796-872-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-847-940B-8
; Sequence 8, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-8

Query Match 100.0%; Score 39; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6
|||
Db 1 LEWSWL 6

RESULT 2
US-09-847-946A-8
; Sequence 8, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
 US-09-847-946A-8

Query Match 100.0%; Score 39; DB 11; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
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 Db 1 LEWSWL 6

RESULT 3

US-09-847-940B-2
 ; Sequence 2, Application US/09847940B
 ; Patent No. US20020156000A1
 ; GENERAL INFORMATION:

; APPLICANT: May, Michael J.
 ; APPLICANT: Ghosh, Sankar
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-117CP
 ; CURRENT APPLICATION NUMBER: US/09/847,940B
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
 US-09-847-940B-2

Query Match 92.3%; Score 36; DB 10; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 | : | | | |
 Db 1 LDWSWL 6

RESULT 4

US-09-847-946A-2
 ; Sequence 2, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:

; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
 US-09-847-946A-2

Query Match 92.3%; Score 36; DB 11; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 | : | | | |
 Db 1 LDWSWL 6

RESULT 5

US-09-847-946A-33
 ; Sequence 33, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:

; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 33
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 US-09-847-946A-33

Query Match 92.3%; Score 36; DB 11; Length 6;
 Best Local Similarity 83.3%; Pred. No. 7e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 | : | | | |
 Db 1 LDWSWL 6

RESULT 6

US-09-847-946A-37
 ; Sequence 37, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:

; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37

LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-37

Query Match 92.3%; Score 36; DB 11; Length 7;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 LEWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 7

US-09-847-946A-30
Sequence 30, Application US/09847946A
Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30

LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-30

Query Match 92.3%; Score 36; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 LEWSWL 6
|:||||
Db 3 LDWSWL 8

RESULT 8

US-09-847-946A-38
Sequence 38, Application US/09847946A
Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38

LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-38

Query Match 92.3%; Score 36; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 LEWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 9

US-09-847-946A-29

Sequence 29, Application US/09847946A
Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29

LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-29

Query Match 92.3%; Score 36; DB 11; Length 9;
Best Local Similarity 83.3%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 LEWSWL 6
|:||||
Db 1 LDWSWL 6

RESULT 10

US-09-847-946A-32

; Sequence 32, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-32

Query Match 92.3%; Score 36; DB 11; Length 9;

Best Local Similarity 83.3%; Pred. No. 7e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6

Db 1 LDWSWL 6

RESULT 11

US-09-847-946A-35

; Sequence 35, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 35

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-35

Query Match 92.3%; Score 36; DB 11; Length 9;

Best Local Similarity 83.3%; Pred. No. 7e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6

Db 3 LDWSWL 8

RESULT 12

US-09-847-946A-36

; Sequence 36, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-36

Query Match 92.3%; Score 36; DB 11; Length 9;

Best Local Similarity 83.3%; Pred. No. 7e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6

Db 2 LDWSWL 7

RESULT 13

US-09-847-946A-31

; Sequence 31, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 31

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-31

Query Match 92.3%; Score 36; DB 11; Length 10;

Best Local Similarity 83.3%; Pred. No. 68;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6

Db 2 LDWSWL 7
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
Db 3 LDWSWL 8

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Job time : 16.7529 secs

RESULT 14
US-09-847-946A-34
; Sequence 34, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-34

Query Match 92.3%; Score 36; DB 11; Length 10;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 3 LDWSWL 8

RESULT 15
US-09-847-946A-28
; Sequence 28, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-28

Query Match 92.3%; Score 36; DB 11; Length 11;
Best Local Similarity 83.3%; Pred. No. 73;

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

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13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	6	23	Mutated IKKbeta NE
2	39	100.0	6	23	NBD mutant peptide
3	39	100.0	6	24	Human NEMO binding
4	39	100.0	756	23	Human IKKbeta muta
5	36	92.3	6	23	IKKbeta NEMO bindi
6	36	92.3	6	23	Anti-inflammatory
7	36	92.3	6	23	NBD mutant peptide
8	36	92.3	6	24	Human NEMO binding
9	36	92.3	7	23	Anti-inflammatory

10	36	92.3	8	23	AAW48527	Anti-inflammatory
11	36	92.3	8	23	AAW48535	Anti-inflammatory
12	36	92.3	9	20	AAW96182	IKK-alpha polypept
13	36	92.3	9	23	AAW48526	Anti-inflammatory
14	36	92.3	9	23	AAW48529	Anti-inflammatory
15	36	92.3	9	23	AAW48532	Anti-inflammatory
16	36	92.3	9	23	AAW48533	Anti-inflammatory
17	36	92.3	10	23	ABB77313	IKKbeta NEMO bindi
18	36	92.3	10	23	AAW48528	Anti-inflammatory
19	36	92.3	10	23	AAW48531	Anti-inflammatory
20	36	92.3	11	23	ABB77311	Human NBD peptide
21	36	92.3	11	23	AAW48506	Human IKKbeta pept
22	36	92.3	11	23	AAW48525	Anti-inflammatory
23	36	92.3	11	23	AAW48653	NBD peptide. Synt
24	36	92.3	13	23	AAW48640	Anti-inflammatory
25	36	92.3	13	23	AAW48641	Anti-inflammatory
26	36	92.3	13	23	AAW48642	Anti-inflammatory
27	36	92.3	13	23	AAW48645	Anti-inflammatory
28	36	92.3	17	23	AAW48638	Anti-inflammatory
29	36	92.3	17	23	AAW48639	Anti-inflammatory
30	36	92.3	17	23	AAW48643	Anti-inflammatory
31	36	92.3	17	23	AAW48644	Anti-inflammatory
32	36	92.3	18	23	AAW48628	Anti-inflammatory
33	36	92.3	18	23	AAW48629	Anti-inflammatory
34	36	92.3	18	23	AAW48632	Anti-inflammatory
35	36	92.3	18	23	AAW48633	Anti-inflammatory
36	36	92.3	22	23	AAW48630	Anti-inflammatory
37	36	92.3	22	23	AAW48631	Anti-inflammatory
38	36	92.3	22	23	AAW48634	Anti-inflammatory
39	36	92.3	22	23	AAW48635	Anti-inflammatory
40	36	92.3	22	23	AAW48636	Anti-inflammatory
41	36	92.3	22	23	AAW48637	Anti-inflammatory
42	36	92.3	28	23	ABB08740	IKKbeta NEMO bindi
43	36	92.3	28	23	AAW48523	NBD peptide SEQ ID
44	36	92.3	28	24	ABU08434	Wild-type human NE
45	36	92.3	36	23	AAW48652	IKKbeta mutated pe

ALIGNMENTS

RESULT 1

ABB08730

ID ABB08730 standard; peptide; 6 AA.

XX

AC ABB08730;

XX

14-JUN-2002 (first entry)

DT

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 8.

XX

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

KW autoimmune disease; transplant rejection; osteoporosis; cancer;

KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;

KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;

KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;

KW osteopathic; cytostatic; neutropenic; neuroprotective; anti-HIV; human;

KW antiarteriosclerotic; virucide; antiaesthetic; antiallergic;

KW dermatological; antibacterial; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antidiabetic; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers

FT Misc-difference 2 /note= "Wildtype Asp substituted by Glu"

XX

WO200183547-A2.

PN

PD 08-NOV-2001.

XX

XX AC ABU08423;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human NEMO binding site (NBD) mutant peptide #6.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytostatic; neutrotropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotrophic; antirheumatic; antiarthritic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX US2002156000-A1.
 XX
 XX PD 24-OCT-2002.
 XX
 XX PF 02-MAY-2001; 2001US-0847940.
 XX
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX
 XX PI May MJ, Ghosh S;
 XX
 XX WPI; 2003-209142/20.
 XX
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 XX PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.
 XX
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 39; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 1 LEWSWL 6
 RESULT 4
 AB877305
 ID AB877305 standard; protein; 756 AA.
 XX

AC ABB77305;
 XX
 XX DT 14-JUN-2002 (first entry)
 XX DE Human IKKbeta mutant D738E.
 XX
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neutrotropic; neuroprotective; anti-HIV; human;
 KW antiatherosclerotic; virucide; antiaethmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
 XX
 XX OS Homo sapiens.
 OS Synthetic.
 XX
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 738 /note= "Wildtype Asp substituted by Glu"
 XX FT
 XX PN WO200183547-A2.
 XX
 XX PD 08-NOV-2001.
 XX
 XX PF 02-MAY-2001; 2001WO-US40654.
 XX
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX
 XX PA (UYVA) UNIV YALE.
 XX
 XX PI May MJ, Ghosh S;
 XX
 XX DR WPI; 2002-179350/23.
 XX
 XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -
 XX
 XX PS Example 11; Page -; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (AB808725-AB808742) comprising at least one NEMO binding domain
 CC (AB877313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. O14920 (ABB77294).
 CC
 XX Sequence 756 AA;

Query Match 100.0%; Score 39; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 |||||
 Db 737 LEWSWL 742

RESULT 5
 ABB08725
 ID ABB08725 standard; peptide; 6 AA.

AC ABB08725;

DT 14-JUN-2002 (first entry)

DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; anti-allergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antitumor.

XX Homo sapiens.

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain -

PS Claim 23; Page 44; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta.

XX Sequence 6 AA;

Query Match 92.3%; Score 36; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6

Db 1 LDWSWL 6

RESULT 6

AAW48530

ID AAW48530 standard; Peptide; 6 AA.

XX AC AAW48530;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 33.

XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;
 DR WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 XX Claim 6; Page 61; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 92.3%; Score 36; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 1 LDWSWL 6
 RESULT 7
 AAM48655
 ID AAM48655 standard; Peptide; 6 AA.
 AC AAM48655;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX NBD mutant peptide SEQ ID NO 2.
 DE
 XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX

PR 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV VALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 XX
 XX Example 6; Page 47; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 92.3%; Score 36; DB 23; Length 6;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 1 LDWSWL 6
 RESULT 8
 ABU08418
 ID ABU08418 standard; peptide; 6 AA.
 AC ABU08418;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 XX Human NEMO binding site (NBD) mutant peptide #1.
 DE
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cyostatic; nontropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotrophic; antirheumatic; antiarthritic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

PV	US2002156000-A1.
XX	
PD	24-OCT-2002.
XX	
PF	02-MAY-2001; 2001US-0847940.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	(MAYM/) MAY M J.
PA	(GHOS/) GHOSH S.
XX	
PI	May MJ, Ghosh S;
XX	
DR	WPI; 2003-209142/20.
DR	N-PSDB; ABX94269, ABX94270.
XX	
PT	Novel antiinflammatory peptide compounds comprising NEMO binding
PT	domain, useful for modulating NF-kappaB induction in a cell and for
PT	treating NF-kappaB-mediated inflammation disorders e.g., asthma,
PT	psoriasis, vasculitis -
XX	
PS	Claim 22; Page 17; 47pp; English.
XX	
CC	The present invention relates to antiinflammatory compounds comprising
CC	NEMO binding domain (NBD) peptides. The NEMO binding domains are
CC	found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
CC	(IKKalpha) proteins. The antiinflammatory compounds of the invention
CC	are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
CC	in a cell, where the compounds are capable of blocking the interaction
CC	between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
CC	antiinflammatory compound further comprises at least one membrane
CC	translocation domain. The compounds are useful for treating
CC	inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, viral infections, Ataxia
CC	telangiectasia, and for transplantation detection. The compounds of
CC	the invention block NF-kappaB induction by IKK but do not inhibit
CC	the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
CC	NBD mutant peptides.
XX	
SQ	Sequence 6 AA;
	Query Match. 92.3%; Score 36; DB 24; Length 6;
	Best Local Similarity 83.3%; Pred. No. 9.3e+05;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LEWSWL 6
	:
Db	1 LDWSWL 6
RESULT 9	
AAW48534	
ID	AAW48534 standard; Peptide; 7 AA.
XX	
AC	AAW48534;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 37.
XX	
KW	Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	

FN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PP	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-064326O.
XX	(PRAE-) PRAECIS PHARM INC.
PA	(UYUA) UNIV YALE.
PA	
XX	
PI	May MÜ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis -
PT	
XX	
PS	Claim 6; Page 61; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially AAM48628-AA48645), comprising a membrane translocation domain (AAM48620-AA48627 or AAM48646-AA48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AA48619). The antiinflammatory compounds have antiasthmatic, cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, neurotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of Ikappab. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
XX	
SQ	Sequence 7 AA;
	Query Match 92.3%; Score 36; DB 23; Length 7;
	Best Local Similarity 83.3%; Pred. No. 9.3e+05;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 LEWSWL 6
	:
Dd	1 LDWSWL 6
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ID	AAM48527 standard; Peptide; 8 AA.
XX	
AC	AAM48527;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 30.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 61; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 92.3%; Score 36; DB 23; Length 8;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 3 LDWSWL 8
 RESULT 11
 AAM48535
 ID AAM48535 standard; Peptide; 8 AA.
 XX
 AC AAM48535;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 38.
 DE
 XX

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW rheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 PT psoriasis -
 XX
 PS Claim 6; Page 61; 88pp; English.
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 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 92.3%; Score 36; DB 23; Length 8;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 1 LDWSWL 6
 RESULT 12
 AAM96182
 ID AAM96182 standard; peptide; 9 AA.
 XX

AC AAW96182;
 XX 27-APR-1999 (first entry)
 XX IKK-alpha polypeptide with binding activity.
 DE I-kappa-B kinase; IKK-alpha; gene expression; modulation;
 KW suppression; activation; tumour necrosis factor; TNF; interleukin-1;
 KW IL-1; TNF receptor associated factor; TRAF.
 XX Homo sapiens.
 OS
 XX WO9901541-A1.
 PN
 XX 14-JAN-1999.
 PD
 XX 01-JUL-1998; 98WO-US13782.
 PF
 XX 10-JUL-1997; 97US-0890854.
 XX
 PR 01-JUL-1997; 97US-0887115.
 XX (TULA-) TULARIK INC.
 PA
 XX Cao Z, Regnier C, Rothe M;
 PI
 XX WPI; 1999-106044/09.
 DR
 XX Newly isolated human kinase IkappaB Kinase (IKK- α) polypeptides -
 PT useful in screening for agents that modulate the interaction of an
 PT IKK polypeptide to a binding target and for modulating signal
 PT transduction involving IkappaB in a cell
 XX
 XX Disclosure; Page -: 32pp; English.
 PS
 XX I-kappa-B kinase (AAW96158), deletion mutants of it retaining
 CC I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a
 CC six residue domain of I-kappa-B containing one of Ser32 and Ser36,
 CC and a candidate agent) can be used to screen for agents that
 CC modulate the interaction of an IKK polypeptide to a binding target.
 CC The modulation of the kinase activity of IKK-alpha forms a method
 CC for modulating signal transduction involving I-kappa-B in a cell.
 CC The IKK-alpha polypeptides are useful for generating oligonucleotide
 CC primers and probes for use in the isolation of natural
 CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
 CC translatable transcripts, hybridization probes, polymerase chain
 CC reaction (PCR) probes and primers. Their diagnostic applications
 CC include IKK-alpha hybridization probes for identifying wild-type and
 CC mutant IKK-alpha alleles in clinical and laboratory samples.
 CC Therapeutic application includes the use of IKK- α nucleic acids
 CC for modulating cellular expression or intracellular
 CC concentration/availability of active IKK-alpha.
 CC Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
 CC activation induced by tissue necrosis factor (TNF), interleukin-1
 CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and
 CC NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of
 CC IKK-alpha showing exemplary binding activity are described in
 CC AAW96185-W96182. These peptides all comprise one of Cys30, Glu543,
 CC Leu604, Thr679, Ser680, Pro684, Thr686 or Ser687 of the full length
 CC IKK-alpha described in AAW96157. Deletion mutants of the invention
 CC comprise at least one of these regions.
 CC N.B. The present sequence is not given in the present specification
 CC but is derived from the sequence given in AAW96157 as specified.
 XX
 XX Sequence 9 AA;

Query Match 92.3%; Score 36; DB 20; Length 9;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6
 |:||||
 Db 2 LDWSWL 7

RESULT 13
 ID AAW48526 standard; Peptide; 9 AA.
 XX AAM48526;
 AC
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 29.
 DE
 XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX Novel antinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 61; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAW48628-AAW48645), comprising a membrane translocation domain
 CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
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 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 9 AA;

Query Match 92.3%; Score 36; DB 23; Length 9;
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:|||||
Db 1 LDWSWL 6

RESULT 14
AAM48529
ID AAM48529 standard; Peptide; 9 AA.
XX
AC AAM48529;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 32.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
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CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
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CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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CC activation and subsequent decreased phosphorylation of IkappaB. The
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CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC breastitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
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CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.
XX
SQ Sequence 9 AA;
Query Match 92.3%; Score 36; DB 23; Length 9;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:|||||
Db 1 LDWSWL 6

RESULT 15
AAM48532
ID AAM48532 standard; Peptide; 9 AA.
XX
AC AAM48532;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 35.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYA) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
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CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
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CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX

SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 23; Length 9;
Best Local Similarity 83.3%; Pred. NO. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 3 LDWSWL 8

Search completed: February 18, 2004, 14:26:20
Job time : 22.7763 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 20938283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	6	10	US-09-847-940B-7
2	38	100.0	6	11	US-09-847-946A-7
3	38	100.0	12	12	US-10-369-493-20896
4	38	100.0	1217	12	US-10-104-047-2263
5	35	92.1	196	16	US-10-080-170-120
6	35	92.1	230	16	US-10-080-170-548
7	35	92.1	1055	9	US-09-759-667A-3
8	34	89.5	56	12	US-09-933-767-359
9	34	89.5	56	15	US-10-023-282-359
10	34	89.5	64	9	US-09-864-761-39808
11	34	89.5	170	12	US-10-104-047-2210
12	34	89.5	449	15	US-10-156-761-7842
13	34	89.5	493	12	US-10-147-324-2
14	34	89.5	544	12	US-10-257-378-17
15	34	89.5	544	15	US-10-067-668-8

16	89.5	544	15	US-10-175-696-8	Sequence 8, Appli
17	89.5	659	12	US-10-369-493-12634	Sequence 12634, A
18	89.5	821	12	US-10-369-493-7850	Sequence 7850, Ap
19	86.8	6	10	US-09-847-940B-8	Sequence 8, Appli
20	86.8	6	11	US-09-847-946A-8	Sequence 8, Appli
21	86.8	186	15	US-10-106-698-8201	Sequence 74, Appl
22	86.8	288	9	US-09-820-893-74	Sequence 8201, Ap
23	86.8	323	9	US-09-820-893-131	Sequence 131, App
24	86.8	323	12	US-10-264-237-1765	Sequence 1765, Ap
25	86.8	350	9	US-09-820-893-132	Sequence 132, App
26	86.8	355	10	US-09-712-363-161	Sequence 161, App
27	86.8	355	12	US-10-084-843-79	Sequence 79, Appl
28	86.8	355	12	US-10-193-002-80	Sequence 80, Appl
29	86.8	355	12	US-10-098-732A-2	Sequence 2, Appli
30	86.8	433	16	US-10-080-170-547	Sequence 547, App
31	86.8	440	16	US-10-080-170-164	Sequence 164, App
32	86.8	828	12	US-10-369-493-20660	Sequence 20660, A
33	86.8	1053	12	US-10-369-493-22733	Sequence 22733, A
34	86.8	1569	14	US-10-108-605-303	Sequence 303, App
35	84.2	6	10	US-09-847-940B-2	Sequence 2, Appli
36	84.2	6	10	US-09-847-940B-9	Sequence 9, Appli
37	84.2	6	11	US-09-847-946A-2	Sequence 2, Appli
38	84.2	6	11	US-09-847-946A-9	Sequence 9, Appli
39	84.2	6	11	US-09-847-946A-33	Sequence 33, Appl
40	84.2	7	11	US-09-847-946A-37	Sequence 37, Appl
41	84.2	8	11	US-09-847-946A-30	Sequence 30, Appl
42	84.2	8	11	US-09-847-946A-38	Sequence 38, Appl
43	84.2	9	11	US-09-847-946A-29	Sequence 29, Appl
44	84.2	9	11	US-09-847-946A-32	Sequence 32, Appl
45	84.2	9	11	US-09-847-946A-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

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; Sequence 7, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-7

Query Match 100.0%; Score 38; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. NO. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LAWSWL 6
Db 1 LAWSWL 6

RESULT 2

US-09-847-946A-7
; Sequence 7, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Firdels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-7

Query Match 100.0%; Score 38; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 1 LAWSWL 6

RESULT 3
US-10-369-493-20896
; Sequence 20896, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20896
; LENGTH: 872
; TYPE: PRT
; ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-10-369-493-20896

Query Match 100.0%; Score 38; DB 12; Length 872;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 692 LAWSWL 697

RESULT 4
US-10-104-047-2263
; Sequence 2263, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047

; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2263
; LENGTH: 1217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2263

Query Match 100.0%; Score 38; DB 12; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 590 LAWSWL 595

RESULT 5
US-10-080-170-120
; Sequence 120, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-120

Query Match 92.1%; Score 35; DB 16; Length 196;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 109 VAWSWL 114

RESULT 6
US-10-080-170-548
; Sequence 548, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-548

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Query Match      : 92.1%; Score 35; DB 16; Length 210;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSWL 6
      123 VAMSWL 128

RESULT 7
US-09-759-667A-3
; Sequence 3, Application US/09759667A
; Patent No. US20020064777A1
; GENERAL INFORMATION:
; APPLICANT: Mengiste, Tesaye
; APPLICANT: Paszkowski, Jerzy
; TITLE OF INVENTION: Recombination Repair Gene, MIM, from Arabidopsis thaliana
; FILE REFERENCE: S-30568A
; CURRENT APPLICATION NUMBER: US/09/759,667A
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 9815485.9
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 9900760.1
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-759-667A-3

Query Match      : 92.1%; Score 35; DB 9; Length 1055;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSWL 6
      248 LAWSWV 253

RESULT 8
US-09-933-767-359
; Sequence 359, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
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;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,164
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/085,925
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,921
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,923
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,922
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/092,921
;; PRIOR FILING DATE: 1998-07-15
;; PRIOR APPLICATION NUMBER: 60/094,657
;; PRIOR FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1245
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 359
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (56)
;; OTHER INFORMATION: Xaa equals stop translation
US-09-933-767-359

Query Match 89.5%; Score 34; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
DB 9 LAWSW 13

RESULT 9
US-10-023-282-359
;; Sequence 359, Application US/10023282
;; Publication No. US20030092893A1
;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 207 Human Secreted Proteins
;; FILE REFERENCE: P2007P1
;; CURRENT APPLICATION NUMBER: US/10/023,282
;; CURRENT FILING DATE: 2001-12-20
;; EARLIER APPLICATION NUMBER: 09/205,258
;; EARLIER FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: PCT/US98/11422
;; EARLIER FILING DATE: 1998-06-04
;; EARLIER APPLICATION NUMBER: 60/048,885
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,375
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,881
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,880
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,896
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,020
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,876
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,895
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,884
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,894
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,971
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,964

;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,882
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,899
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,893
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,900
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,901
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,892
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,915
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,019
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,970
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,972
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,916
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,373
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,875
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,949
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,883
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,897
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,898
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,962
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,963
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,877
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,878
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/070,923
;; EARLIER FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: 60/092,921
;; EARLIER FILING DATE: 1998-07-15
;; EARLIER APPLICATION NUMBER: 60/094,657
;; NUMBER OF SEQ ID NOS: 1227
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 359
;; LENGTH: 56
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (56)
;; OTHER INFORMATION: Xaa equals stop translation
US-10-023-282-359

Query Match 89.5%; Score 34; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LAWSW 5
|||||

Db 9 LAWSW 13

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RESULT 10
US-09-864-761-39808
; Sequence 39808, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIORITY APPLICATION NUMBER: US/09/864,761
; PRIORITY APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIORITY APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIORITY APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIORITY APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIORITY APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIORITY APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIORITY APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIORITY APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39808
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004596.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EST HUMAN HIT: BE891286.1, EVALU6 3.00e-33
; OTHER INFORMATION: SWISSPROT HIT: P14528, EVALU6 4.50e+00
US-09-864-761-39808
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Query Match

89.5%; Score 34; DB 9; Length 64;

Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LAWSW 5
Db 33 LAWSW 37

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RESULT 11
US-10-104-047-2210
; Sequence 2210, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cdNA
; FILE REFERENCE: H1-A0105
; CURRENT FILING DATE: 2002-03-25
; PRIORITY APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2210
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2210
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Query Match 89.5%; Score 34; DB 12; Length 170;
Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAWSW 6
Db 162 LWMSW 167

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RESULT 12
US-10-156-761-7842
; Sequence 7842, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7842
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7842
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Query Match 89.5%; Score 34; DB 15; Length 449;
Best Local Similarity 83.3%; Pred. No. 2.3e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAWSW 6
Db 42 LAWDWL 47

RESULT 13
US-10-147-324-2
; Sequence 2, Application US/10147324
; Publication No. US20030215812A1
; GENERAL INFORMATION:
; APPLICANT: MA, YAN-FEN
; APPLICANT: XUE, YAN-FEN
; TITLE OF INVENTION: GENE ENCODING B-MANNANASE, ENZYME PREPARATION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 0304-0001
; CURRENT APPLICATION NUMBER: US/10/147,324
; CURRENT FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-147-324-2

Query Match 89.5%; Score 34; DB 12; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
| | | | |
Db 280 LAWSW 284

RESULT 14
US-10-257-378-17
; Sequence 17, Application US/10257378
; Publication No. US20030190642A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Glenville
; APPLICANT: Petkovich, P. Martin
; APPLICANT: White, Jay
; APPLICANT: Ramehew, Heather A.
; APPLICANT: Stangle, Wayne A.
; TITLE OF INVENTION: A thymus Expressed Human Cytochrome P450 (P450TEC)
; FILE REFERENCE: 11812-65
; CURRENT APPLICATION NUMBER: US/10/257,378
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/208,785
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/198,617
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-378-17

Query Match 89.5%; Score 34; DB 12; Length 544;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSW 6
| | | | |
Db 46 LGWSWL 51

RESULT 15
US-10-067-668-8
; Sequence 8, Application US/10067668
; Publication No. US20030022334A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-136001

; CURRENT APPLICATION NUMBER: US/10/067,668
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-668-8

Query Match 89.5%; Score 34; DB 15; Length 544;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
| | | | |
Db 46 LGWSWL 51

Search completed: February 18, 2004, 15:41:56
Job time : 17.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-7

Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	6	23	Mutated IKKbeta NE
2	38	100.0	6	23	NBD mutant peptide
3	38	100.0	6	24	Human IKKbeta binding
4	38	100.0	756	23	Human IKKbeta muta
5	35	92.1	136	22	Propionibacterium
6	35	92.1	136	23	M. tuberculosis an
7	35	92.1	210	23	M. tuberculosis an
8	35	92.1	321	22	Drosophila melanog
9	35	92.1	329	22	Drosophila melanog

10	35	92.1	1055	21	AAV44787	Arabidopsis thalia
11	34	89.5	13	21	AAV78379	Human papillomavir
12	34	89.5	56	20	AAW88644	Secreted protein e
13	34	89.5	56	22	ABBS0411	Human secreted pro
14	34	89.5	64	22	ABG55123	Human liver peptid
15	34	89.5	64	22	ABB39983	Peptide #7489 enco
16	34	89.5	64	22	ABB24510	Protein #6509 enco
17	34	89.5	64	22	AAW60730	Human brain expres
18	34	89.5	64	22	AAW73401	Human bone marrow
19	34	89.5	64	22	AAW33604	Peptide #7641 enco
20	34	89.5	64	23	ABG43260	Human peptide enco
21	34	89.5	93	22	AAO03124	Human polypeptide
22	34	89.5	123	22	AAO08298	Human polypeptide
23	34	89.5	138	20	AAV42442	Novel amino acid s
24	34	89.5	140	20	AAV42443	Extended novel ami
25	34	89.5	164	22	ABG28076	Novel human diagno
26	34	89.5	170	21	AAV87324	Human signal pepti
27	34	89.5	199	22	ABG07731	Novel human diagno
28	34	89.5	320	21	AAV54132	Amino acid sequenc
29	34	89.5	331	21	AAV54127	Amino acid sequenc
30	34	89.5	369	21	AAV54129	Amino acid sequenc
31	34	89.5	432	22	AAU48985	Propionibacterium
32	34	89.5	468	21	AAV44496	Bacillus agaradher
33	34	89.5	468	21	AAV54125	Amino acid sequenc
34	34	89.5	468	23	ABB82020	Bacillus mannanase
35	34	89.5	476	21	AAV54123	A mannanase-linker
36	34	89.5	487	22	ABG60890	Drosophila melanog
37	34	89.5	490	21	AAV54122	Amino acid sequenc
38	34	89.5	493	21	AAV44495	Bacillus agaradher
39	34	89.5	493	21	AAV54124	Amino acid sequenc
40	34	89.5	493	23	ABG71218	Bacillus alkaline
41	34	89.5	493	23	ABB82019	B. agaradherens ma
42	34	89.5	544	23	AAE21061	Human drug metabol
43	34	89.5	544	23	AAU91320	Drosophila melanog
44	34	89.5	720	22	ABB66438	Human translocatio
45	34	89.5	2311	23	ABG95034	

ALIGNMENTS

RESULT 1

ABB08729

ID ABB08729 standard; peptide; 6 AA.

XX ABB08729;

AC ABB08729;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 7.

XX

IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; anti-allergic; dermatological; antibacterial; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antiulcer; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "wildtype Asp substituted by Ala"

XX

XX WO200183547-A2.

XX

XX

XX

XX

XX

PF 02-MAY-2001; 2001WO-US40654.
 XX
 KW 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S;
 XX
 KW WPI; 2002-179350/23.
 DR
 XX
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain
 XX
 PS Claim 23; Page 44; 82pp; English.
 XX
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
 CC (ABB77313). The compound has acts through selective inhibition of
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
 CC interaction results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also
 CC act (directly or indirectly) by blocking the recruitment of leukocytes
 CC into sites of acute and chronic inflammation, by down-regulating the
 CC expression of E-selectin on leukocytes or by blocking osteoclast
 CC differentiation. The compound is useful in treating NF-kB mediated
 CC conditions, where the condition is an inflammatory disorder, an
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
 CC telangiectasia. The inflammatory disorder is asthma, allergies,
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 38; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 1 LAWSWL 6
 |||||
 RESULT 2
 ID AAM48512
 XX AAM48512 standard; Peptide; 6 AA.
 AC AAM48512;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE NBD mutant peptide SEQ ID NO 7.

XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis
 PT
 XX Example 6; Page 47; 88pp; English.
 PS
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
 CC cytostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antithrombotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IkappaB kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 38; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 1 LAWSWL 6
 |||||
 RESULT 3
 ID ABU08422
 ABU08422 standard; peptide; 6 AA.

CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta
 CC mutant, useful in examples of the invention.
 CC Note: The present sequence is not given in the specification but is
 CC derived from GenBank Accession No. 014920 (ABB77294).

XX SQ Sequence 756 AA;

Query Match 100.0%; Score 38; DB 23; Length 756;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 Db 737 LAWSWL 742

RESULT 5
 AAU62777
 ID AAU62777 standard; Protein; 196 AA.

XX AC AAU62777;

DT 27-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #23673.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX OS Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX DR WPI; 2001-616774/71.

XX DR N-PSDB; AAS59629.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris -

XX PS Example 1; SEQ ID No 23972; 1069pp; English.

XX CC Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 196 AA;

Query Match 92.1%; Score 35; DB 22; Length 196;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 Db 102 VAWSWL 107

RESULT 6
 ABU05469
 ID ABU05469 standard; Protein; 196 AA.

XX AC ABU05469;

XX DT 08-APR-2003 (first entry)

XX DE M. tuberculosis and M. leprae marker protein #120.

XX KW Mycobacterioses; survival; virulence; protective antigen; vaccine;
 KW mycobacterial disease; tuberculosis; leprosy.

XX OS Mycobacterium tuberculosis.

XX OS Mycobacterium leprae.

XX PN WO200274903-A2.

XX PD 26-SEP-2002.

XX PF 22-FEB-2002; 2002WO-IB01973.

XX PR 22-FEB-2001; 2001US-270123P.

XX PA (INSP) INST PASTEUR.

XX PI Cole S;

XX DR WPI; 2002-759885/82.

XX PT Identifying and selecting genes for survival or virulence of
 PT mycobacteria by a comparative genomic analysis of the sequences of
 PT Mycobacterium tuberculosis and M. leprae -

XX PS Claim 17; Page 288-289; 874pp; English.

XX CC This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a
 CC polynucleotide sequence that is highly conserved in both genomes with no
 CC counterparts in other bacterial genomic sequences and that corresponds
 CC to an essential gene for the survival or virulence of mycobacterium
 CC species. The method of the invention is useful for detecting M.
 CC tuberculosis or M. leprae infection. The method reduces the number of
 CC potential new targets and protective antigens for new drugs and vaccine
 CC compositions to treat and prevent mycobacterial diseases, particularly
 CC tuberculosis and leprosy. The present sequence represents a marker
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
 CC identified using the method of the invention.

XX SQ Sequence 196 AA;

Query Match 92.1%; Score 35; DB 23; Length 196;
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 :|||||
 Db 109 VAWSWL 114

RESULT 7

ABU05897
 ID ABU05897 standard; Protein; 210 AA.

XX AC ABU05897;

XX DT 08-APR-2003 (first entry)

XX DE M. tuberculosis and M. leprae marker protein #548.

XX KW Mycobacterioses; survival; virulence; protective antigen; vaccine;
 mycobacterial disease; tuberculosis; leprosy.

XX OS Mycobacterium tuberculosis.

XX OS Mycobacterium leprae.

XX PN WO200274903-A2.

XX PD 26-SEP-2002.

XX PF 22-FEB-2002; 2002WO-1B01973.

XX PR 22-FEB-2001; 2001US-270123P.

XX PA (INSP) INST PASTEUR.

XX PI Cole S;

XX DR WPI; 2002-759885/82.

XX PT Identifying and selecting genes for survival or virulence of
 mycobacteria by a comparative genomic analysis of the sequences of
 PT Mycobacterium tuberculosis and M. leprae -

XX PS Claim 17; Page 763-764; 874pp; English.

XX CC This invention relates to a novel method for identifying essential genes
 for survival or virulence of mycobacteria species. The method comprises
 aligning the genomic sequence of a first mycobacterium species on a
 genomic sequence of a second mycobacterium species and selecting a
 polynucleotide sequence that is highly conserved in both genomes with no
 counterparts in other bacterial genomic sequences and that corresponds
 to an essential gene for the survival or virulence of mycobacterium
 species. The method of the invention is useful for detecting M.
 tuberculosis or M. leprae infection. The method reduces the number of
 potential new targets and protective antigens for new drugs and vaccine
 compositions to treat and prevent mycobacterial diseases, particularly
 tuberculosis and leprosy. The present sequence represents a marker
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
 CC identified using the method of the invention.

XX SQ Sequence 210 AA;

Query Match 92.1%; Score 35; DB 23; Length 210;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 :|||||
 Db 123 VAWSWL 128

RESULT 8

DE Drosophila melanogaster polypeptide SEQ ID NO 42342.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.

XX OS Drosophila melanogaster.

ABB64219

ID ABB64219 standard; Protein; 321 AA.

XX AC ABB64219;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 19449.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US09231.

XX PR 23-MAR-2000; 2000US-191637P.

XX PR 11-JUL-2000; 2000US-0614150.

XX PA (PEXE) PE CORP NY.

XX PI Venter JC, Adams M, Li PMD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL08322.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell
 interactions -

XX PS Disclosure; SEQ ID NO 19449; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins
 (ABBS7737-ABBY2072).

XX CC The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 321 AA;

Query Match 92.1%; Score 35; DB 22; Length 321;

Best Local Similarity 83.3%; Pred. No. 7.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6

Db 64 LWSWL 69

RESULT 9

ABB71850

ID ABB71850 standard; Protein; 329 AA.

XX AC ABB71850;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 42342.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.

XX OS Drosophila melanogaster.

XX WO200171042-A2.
 PN
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL15953.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 42342; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (AB857737-AB872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 329 AA;
 Query Match 92.1%; Score 35; DB 22; Length 329;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 17 LAWTWL 22
 RESULT 10
 AAY44787
 ID AAY44787 standard; Protein; 1055 AA.
 XX
 AC AAY44787;
 XX
 DT 04-MAY-2000 (first entry)
 XX
 DE Arabidopsis thaliana recombination repair protein, MIM.
 XX
 KW MIM; recombination; plant; DNA repair; hypersensitivity;
 KW SMC protein family; Structural Maintenance of Chromosomes; MIM;
 KW methyl methanesulphonate; irradiation; mitomycin C.
 XX
 OS Arabidopsis thaliana.
 PN
 XX
 FH Key Location/Qualifiers
 FT Binding-site 49..56
 FT /label= NTP_binding_domain
 FT Region 184..442
 FT /label= Coiled_coil_region-I
 FT Region 443..627
 FT /label= Hinge/spacer
 FT Region 628..909
 FT /label= Coiled_coil_region-II
 FT Domain 971..1007
 FT /label= DA-box
 FT

FT /note= "conserved motif which harbours a Walker B type
 FT NTP binding domain"
 PN WO200004174-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99WO-EP04984.
 XX
 PR 16-JUL-1998; 98GB-0015485.
 PR 14-JAN-1999; 99GB-0000760.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Mengiste T, Paszkowski J;
 XX
 DR WPI; 2000-182437/16.
 DR N-PSDB; AAZ50145, AAZ50146.
 XX
 PT New Arabidopsis polynucleotide encoding protein useful for assisting
 PT recombinant repair of DNA damage in plants -
 XX
 PS Claim 1; Pages 22-25; 30pp; English.
 XX
 CC The present sequence is a MIM protein from Arabidopsis thaliana, which
 CC contributes to recombination repair of DNA damage in plant cells.
 CC The protein was tracked down with the help of a T-DNA tagged Arabidopsis
 CC mutant showing hypersensitivity to methyl methanesulphonate (MMS). It
 CC shows homology to a member of SMC (Structural Maintenance of Chromosomes)
 CC protein family and confers hypersensitivity to treatment with MMS,
 CC X-rays, UV light or mitomycin C. The present sequence is useful for DNA
 CC repair in plant cells.
 XX
 SQ Sequence 1055 AA;
 Query Match 92.1%; Score 35; DB 21; Length 1055;
 Best Local Similarity 83.3%; Pred. No. 2.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 248 LAWSWV 253
 RESULT 11
 AAY78379
 ID AAY78379 standard; peptide; 13 AA.
 XX
 AC AAY78379;
 XX
 DT 08-MAY-2000 (first entry)
 XX
 DE Human papillomavirus E7 protein inhibiting peptide SEQ ID NO:5.
 XX
 KW HPV; E7 protein; inhibition; virucide; carcinoma.
 XX
 OS Human papillomavirus.
 OS Synthetic.
 XX
 PN EP969013-A1.
 XX
 PD 05-JAN-2000.
 XX
 PF 30-JUN-1998; 98EP-0112047.
 XX
 PR 30-JUN-1998; 98EP-0112047.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Jansen-Duerr P, Zwierschke W;
 XX
 DR WPI; 2000-149116/14.

XX New peptides used for the prevention and treatment of human papilloma
PT virus associated disease -
XX
XX
XX Claim 1; Page 22; 26pp; English.
XX
CC AAY78375 to AAY78415 represent peptides capable of inhibiting the human
CC papillomavirus (HPV) E7 protein. The peptides have virucide activity.
CC The peptides can be used in pharmaceutical compositions to inhibit
CC HPV E7 protein, which allows the prevention and/or treatment of HPV
CC associated diseases, which may comprise carcinomas.
XX
XX Sequence 13 AA;
XX
Query Match 89.5%; Score 34; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LAWSW 5
Db |||||
3 LAWSW 7

RESULT 12
AAW88644
ID AAW88644 standard; Protein; 56 AA.
XX
AC AAW88644;
XX
DT 01-MAR-1999 (first entry)
XX
DE Secreted protein encoded by gene 111 clone HTWB29.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
XX WO9854963-A2.
XX
XX 10-DEC-1998.
XX
XX 04-JUN-1998; 98WO-US11422.
XX
XX 18-DEC-1997; 97US-0070923.
XX 06-JUN-1997; 97US-0048877.
XX 06-JUN-1997; 97US-0048881.
XX 06-JUN-1997; 97US-0048884.
XX 06-JUN-1997; 97US-0048893.
XX 06-JUN-1997; 97US-0048896.
XX 06-JUN-1997; 97US-0048899.
XX 06-JUN-1997; 97US-0048915.
XX 06-JUN-1997; 97US-0048949.
XX 06-JUN-1997; 97US-0048964.
XX 06-JUN-1997; 97US-0048972.
XX 06-JUN-1997; 97US-0049020.
XX 06-JUN-1997; 97US-0049375.
XX 05-SEP-1997; 97US-0057628.
XX 05-SEP-1997; 97US-0057635.
XX 05-SEP-1997; 97US-0057644.
XX 05-SEP-1997; 97US-0057647.
XX 05-SEP-1997; 97US-0057650.
XX 05-SEP-1997; 97US-0057661.
XX 05-SEP-1997; 97US-0057667.
XX 05-SEP-1997; 97US-0057761.
XX 05-SEP-1997; 97US-0057764.
XX 05-SEP-1997; 97US-0057770.

05-SEP-1997; 97US-0057775.
05-SEP-1997; 97US-0057778.
06-JUN-1997; 97US-0048875.
06-JUN-1997; 97US-0048878.
06-JUN-1997; 97US-0048882.
06-JUN-1997; 97US-0048885.
06-JUN-1997; 97US-0048894.
06-JUN-1997; 97US-0048897.
06-JUN-1997; 97US-0048900.
06-JUN-1997; 97US-0048916.
06-JUN-1997; 97US-0048962.
06-JUN-1997; 97US-0048970.
06-JUN-1997; 97US-0048974.
06-JUN-1997; 97US-0049373.
05-SEP-1997; 97US-0057584.
05-SEP-1997; 97US-0057629.
05-SEP-1997; 97US-0057642.
05-SEP-1997; 97US-0057645.
05-SEP-1997; 97US-0057648.
05-SEP-1997; 97US-0057651.
05-SEP-1997; 97US-0057662.
05-SEP-1997; 97US-0057668.
05-SEP-1997; 97US-0057762.
05-SEP-1997; 97US-0057765.
05-SEP-1997; 97US-0057771.
06-JUN-1997; 97US-0057776.
06-JUN-1997; 97US-0048876.
06-JUN-1997; 97US-0048880.
06-JUN-1997; 97US-0048883.
06-JUN-1997; 97US-0048892.
06-JUN-1997; 97US-0048895.
06-JUN-1997; 97US-0048898.
06-JUN-1997; 97US-0048901.
06-JUN-1997; 97US-0048917.
06-JUN-1997; 97US-0048963.
06-JUN-1997; 97US-0049019.
06-JUN-1997; 97US-0049374.
05-SEP-1997; 97US-0057627.
05-SEP-1997; 97US-0057634.
05-SEP-1997; 97US-0057643.
05-SEP-1997; 97US-0057646.
05-SEP-1997; 97US-0057649.
05-SEP-1997; 97US-0057654.
05-SEP-1997; 97US-0057666.
05-SEP-1997; 97US-0057760.
05-SEP-1997; 97US-0057763.
05-SEP-1997; 97US-0057769.
05-SEP-1997; 97US-0057774.
05-SEP-1997; 97US-0057777.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
XX Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
XX Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW;
XX Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
XX Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX WPI; 1999-059865/05.
XX N-PSDB; AAV84521.
XX
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 11; Page 542; 772pp; English.
XX
XX The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
XX encoding human secreted proteins (AAW88534 to AAW88756). The secreted
XX protein gene sequences are deposited with the ATCC under deposit numbers
XX ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
XX 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host

CC cells comprising recombinant vectors containing the nucleic acid.
 CC sequences are used for the recombinant production of the secreted
 CC proteins. The polynucleotide and amino acid sequences are useful for are
 CC useful for preventing, treating or ameliorating medical conditions e.g.
 CC by protein or gene therapy. Pathological conditions can be also
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the polynucleotides, based on
 CC which tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, neurodegenerative
 CC disorders, developmental abnormalities and foetal deficiencies, blood
 CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
 CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
 CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
 CC such as osteoporosis, arthritis or malignancies, diseases of testes,
 CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The present sequence represents human secreted protein (see descriptor
 CC line for gene number and clone identification).

XX Sequence 56 AA;
 SQ Query Match 89.5%; Score 34; DB 20; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 DB 9 LAWSW 13
 |||||

RESULT 13
 ABB50411
 ID ABB50411 standard; Protein; 56 AA.

XX AC ABB50411;

XX DT 07-FEB-2002 (first entry)

XX DE Human secreted protein encoded by gene 111 SEQ ID NO:359.

XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KW dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 KW cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
 KW neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;
 KW Parkinson's disease; infectious disease; chromosome 10.

XX OS Homo sapiens.

XX PN WO200162891-A2.

XX PD 30-AUG-2001.

XX PF 21-FEB-2001; 2001WO-US05614.

XX PR 24-FEB-2000; 2000US-184836P.

XX PR 29-MAR-2000; 2000US-193170P.

XX PA (HUNA-) HUMAN GENOME SCI INC.

XX PI Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;

XX PI Ruben SM, Soppet DR, Young PB, Shi Y, Florence KA, Wei Y;

XX PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;

XX PI Feng P, Endress GA, Dillon FU, Carter KC, Brewer LA, Yu G;

XX PI Zeng Z, Greene JM;

XX WPI; 2001-625724/72.
 DR N-PSDB; ABA83304.
 XX
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 PS Claim 11; Page 1140; 1533pp; English.

XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy) neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention.

XX SQ Sequence 56 AA;

Query Match 89.5%; Score 34; DB 22; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 DB 9 LAWSW 13
 |||||

RESULT 14
 ABB55123

ID ABB55123 standard; Peptide; 64 AA.

XX AC ABB55123;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver peptide, SEQ ID NO 33771.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00664.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-48898/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human adult liver -
 XX Claim 27; SEQ ID NO 33771; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridizes at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (I) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 |||||
 Db 33 LAWSW 37

RESULT 15

ABB39983
 ID ABB39983 standard; Peptide; 64 AA.

AC ABB39983;

XX 04-FEB-2002 (first entry)

XX Peptide #7489 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX Claim 27; SEQ ID NO 32618; 639pp + sequence listing; English.

XX

CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5

|||||
 Db 33 LAWSW 37

Search completed: February 18, 2004, 14:26:20
 Job time : 23.7763 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	40	100.0	8	11	US-09-847-946A-78
6	40	100.0	9	11	US-09-847-946A-69
7	40	100.0	9	11	US-09-847-946A-72
8	40	100.0	9	11	US-09-847-946A-75
9	40	100.0	9	11	US-09-847-946A-76
10	40	100.0	10	11	US-09-847-946A-71
11	40	100.0	10	11	US-09-847-946A-74
12	40	100.0	11	11	US-09-847-946A-68
13	37	92.5	236	12	US-10-441-626-17
14	37	92.5	885	9	US-09-815-242-5090
15	36	90.0	6	10	US-09-847-940B-4

16	36	90.0	6	10	US-09-847-940B-5
17	36	90.0	6	11	US-09-847-946A-4
18	36	90.0	6	11	US-09-847-946A-5
19	36	90.0	6	11	US-09-847-946A-39
20	36	90.0	6	11	US-09-847-946A-40
21	36	90.0	6	11	US-09-847-946A-51
22	36	90.0	6	11	US-09-847-946A-62
23	36	90.0	7	11	US-09-847-946A-55
24	36	90.0	7	11	US-09-847-946A-66
25	36	90.0	8	11	US-09-847-946A-48
26	36	90.0	8	11	US-09-847-946A-56
27	36	90.0	8	11	US-09-847-946A-59
28	36	90.0	8	11	US-09-847-946A-67
29	36	90.0	9	11	US-09-847-946A-47
30	36	90.0	9	11	US-09-847-946A-50
31	36	90.0	9	11	US-09-847-946A-53
32	36	90.0	9	11	US-09-847-946A-54
33	36	90.0	9	11	US-09-847-946A-58
34	36	90.0	9	11	US-09-847-946A-61
35	36	90.0	9	11	US-09-847-946A-64
36	36	90.0	9	11	US-09-847-946A-65
37	36	90.0	10	11	US-09-847-946A-49
38	36	90.0	10	11	US-09-847-946A-52
39	36	90.0	10	11	US-09-847-946A-57
40	36	90.0	10	11	US-09-847-946A-60
41	36	90.0	10	11	US-09-847-946A-63
42	36	90.0	11	11	US-09-847-946A-46
43	36	90.0	173	15	US-10-156-761-15045
44	36	90.0	174	15	US-10-219-220-163
45	36	90.0	225	15	US-10-219-220-162

ALIGNMENTS

RESULT 1
US-09-847-946A-41
; Sequence 41, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

DB 1 ADMSWA 6

```
RESULT 2
US-09-847-946A-73
; Sequence 73, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-73

Query Match      100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      1 ADWSWA 6
        |||||

RESULT 3
US-09-847-946A-77
; Sequence 77, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 77
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-77

Query Match      100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      1 ADWSWA 6
        |||||

RESULT 4
US-09-847-946A-70
; Sequence 70, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-70

Query Match      100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      3 ADWSWA 8
        |||||

RESULT 5
US-09-847-946A-78
; Sequence 78, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 78
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-78

Query Match      100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      3 ADWSWA 8
        |||||
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```
QY      1 ADWSWA 6
      |||||
Db      1 ADWSWA 6

RESULT 6
US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-69

Query Match      100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      1 ADWSWA 6

RESULT 7
US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-72

Query Match      100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      1 ADWSWA 6

RESULT 8
US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-75

Query Match      100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      3 ADWSWA 8

RESULT 9
US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76
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; OTHER INFORMATION: sequence
US-09-847-946A-76

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 2 ADWSWA 7

RESULT 10

US-09-847-946A-71

; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: '09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-71

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 2 ADWSWA 7

RESULT 11

US-09-847-946A-74

; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: '09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-74

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 3 ADWSWA 8

RESULT 12

US-09-847-946A-68

; Sequence 68, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: '09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-68

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 3 ADWSWA 8

RESULT 13

US-10-441-626-17

; Sequence 17, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase
; FILE REFERENCE: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441.626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-626-17

Query Match 92.5%; Score 37; DB 12; Length 236;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 63 ADWSWS 68

RESULT 14

US-09-815-242-5090
; Sequence 5090, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5090
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5090

Query Match 92.5%; Score 37; DB 9; Length 885;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 563 ADWAWA 568

RESULT 15

US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 1 ADWSW 5

Search completed: February 18, 2004, 15:41:55
Job time : 16.7529 secs

No ant

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	40	100.0	6	23	AA48538
2	40	100.0	6	23	AA48570
3	40	100.0	7	23	AA48574
4	40	100.0	8	23	AA48567
5	40	100.0	8	23	AA48575
6	40	100.0	9	23	AA48566
7	40	100.0	9	23	AA48569
8	40	100.0	9	23	AA48572
9	40	100.0	9	23	AA48573

10	40	100.0	10	23	AA48568	Anti-inflammatory
11	40	100.0	10	23	AA48571	Anti-inflammatory
12	40	100.0	11	23	AA48565	Anti-inflammatory
13	37	92.5	33	22	AAU21305	Human novel foetal
14	37	92.5	103	20	AAU06332	Gliocladium roseum
15	37	92.5	236	20	AAU06363	Gliocladium roseum
16	37	92.5	236	21	AAU14876	Gliocladium roseum
17	37	92.5	236	21	AAU84341	Amino acid sequenc
18	37	92.5	236	23	AAU77428	Gliocladium roseum
19	37	92.5	236	23	AAU77584	G. roseum EGI11-li
20	37	92.5	274	23	ABP65718	Bifidobacterium lo
21	37	92.5	597	22	ABP62635	Drosophila melanog
22	37	92.5	885	22	AAU33594	Pseudomonas aerugi
23	36	90.0	6	23	ABB08727	Mutated IKKbeta NE
24	36	90.0	6	23	ABB08728	Mutated IKKbeta NE
25	36	90.0	6	23	AA48509	NBD mutant peptide
26	36	90.0	6	23	AA48510	NBD mutant peptide
27	36	90.0	6	23	AA48536	Anti-inflammatory
28	36	90.0	6	23	AA48537	Anti-inflammatory
29	36	90.0	6	23	AA48548	Anti-inflammatory
30	36	90.0	6	23	AA48559	Anti-inflammatory
31	36	90.0	6	24	ABU08420	Human NEMO binding
32	36	90.0	6	24	ABU08421	Human NEMO binding
33	36	90.0	7	23	AA48552	Anti-inflammatory
34	36	90.0	7	23	AA48563	Anti-inflammatory
35	36	90.0	8	23	AA48545	Anti-inflammatory
36	36	90.0	8	23	AA48553	Anti-inflammatory
37	36	90.0	8	23	AA48556	Anti-inflammatory
38	36	90.0	8	23	AA48564	Anti-inflammatory
39	36	90.0	9	23	AA48544	Anti-inflammatory
40	36	90.0	9	23	AA48547	Anti-inflammatory
41	36	90.0	9	23	AA48550	Anti-inflammatory
42	36	90.0	9	23	AA48551	Anti-inflammatory
43	36	90.0	9	23	AA48555	Anti-inflammatory
44	36	90.0	9	23	AA48558	Anti-inflammatory
45	36	90.0	9	23	AA48561	Anti-inflammatory

ALIGNMENTS

RESULT 1

AA48538

ID AA48538 standard; Peptide; 6 AA.

XX

AC AA48538;

XX

DT 20-MAR-2002 (first entry)

XX

DE Anti-inflammatory peptide SEQ ID NO 41.

XX

KW Antinflammatory; antiasthmatic; cytostatic; antiporiatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW cytotoxic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX

PN WO200183554-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14346.

XX

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX

PA (PRAB-) PRAECIS PHARM INC.

OS Synthetic.
 XX WO200183554-A2.
 PN
 XX
 XX
 PD 08-NOV-2001.
 XX
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWA 6
 Db 1 ADWSWA 6
 |||||
 RESULT 4
 AAM48567
 ID AAM48567 standard; Peptide; 8 AA.
 XX
 XX AAM48567;
 AC
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 70.
 DE
 XX
 XX Antinflammatory; antiasthmatic; cytostatic; antiporiatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
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 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
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 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWA 6
 Db 3 ADWSWA 8
 |||||
 RESULT 5
 AAM48575
 ID AAM48575 standard; Peptide; 8 AA.
 XX
 XX AAM48575;
 AC
 XX 20-MAR-2002 (first entry)
 DT
 XX

DE Anti-inflammatory peptide SEQ ID NO 78.
 XX
 XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV VALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWA 6
 Db 1 ADWSWA 6
 |||||
 RESULT 6
 AAM48566

ID AAM48566 standard; Peptide; 9 AA.
 XX
 AC AAM48566;
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 69.
 DE
 XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14346.
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV VALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
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 CC amino acid residues, fused to a NEMO binding sequence
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWA 6

|||||
1 ADWSA 6

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

RESULT 7

AAW48569

ID AAW48569 standard; Peptide; 9 AA.

XX AC

XX AAW48569;

XX DT

XX 20-MAR-2002 (first entry)

XX DE

XX Anti-inflammatory peptide SEQ ID NO 72.

XX KW

XX Antiinflammatory; antiaesthatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS

XX Synthetic.

XX PN

XX WO200183554-A2.

XX PD

XX 08-NOV-2001.

XX XX

XX 02-MAY-2001; 2001WO-US14346.

XX XX

XX 02-MAY-2000; 2000US-201261P.

XX PR

XX 22-AUG-2000; 2000US-0643260.

XX XX

XX (PRAE-) PRAECIS PHARM INC.

XX PA

XX (UYVA) UNIV YALE.

XX XX

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR

XX WPI; 2002-121889/16.

XX XX

XX Novel antiinflammatory compound comprising membrane translocation
XX PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX PT factor kappaB activation, and for treating asthma, lung inflammation,
XX PT psoriasis -

XX XX

XX Claim 6; Page 62; 88pp; English.

XX PS

XX The invention relates to an antiinflammatory compound (especially
XX CC AAW48628-AAW48645), comprising a membrane translocation domain
XX CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
XX CC amino acid residues, fused to a NEMO binding sequence
XX CC (AAW48525-AAW48619). The antiinflammatory compounds have antiaesthatic,
XX CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
XX CC antibacterial, immunosuppressive, dermatological, neuroprotective,
XX CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
XX CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
XX CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
XX CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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XX CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
XX CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
XX CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
XX CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
XX CC telangiectasia. The compounds are also useful for treating
XX CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
XX CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
XX CC arthritis.

XX SQ

XX Sequence 9 AA;

RESULT 8

AAW48572

ID AAW48572 standard; Peptide; 9 AA.

XX AC

XX AAW48572;

XX XX

XX 20-MAR-2002 (first entry)

XX DE

XX Anti-inflammatory peptide SEQ ID NO 75.

XX KW

XX Antiinflammatory; antiaesthatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS

XX Synthetic.

XX PN

XX WO200183554-A2.

XX XX

XX 08-NOV-2001.

XX XX

XX 02-MAY-2001; 2001WO-US14346.

XX PF

XX 02-MAY-2000; 2000US-201261P.

XX PR

XX 22-AUG-2000; 2000US-0643260.

XX XX

XX (PRAE-) PRAECIS PHARM INC.

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XX (UYVA) UNIV YALE.

XX XX

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX PI

XX WPI; 2002-121889/16.

XX DR

XX XX

XX Novel antiinflammatory compound comprising membrane translocation
XX PT domain fused to NEMO binding sequence, useful for blocking nuclear
XX PT factor kappaB activation, and for treating asthma, lung inflammation,
XX PT psoriasis -

XX XX

XX Claim 6; Page 62; 88pp; English.

XX PS

XX The invention relates to an antiinflammatory compound (especially
XX CC AAW48628-AAW48645), comprising a membrane translocation domain
XX CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
XX CC amino acid residues, fused to a NEMO binding sequence
XX CC (AAW48525-AAW48619). The antiinflammatory compounds have antiaesthatic,
XX CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
XX CC antibacterial, immunosuppressive, dermatological, neuroprotective,
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XX CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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XX CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
XX CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
XX CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADWSWA 6
 Db 3 ADWSWA 8
 |||||

RESULT 9
 AAM48573
 ID AAM48573 standard; Peptide; 9 AA.
 XX
 AC AAM48573;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 76.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 PS Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
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 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADWSWA 6
 Db 2 ADWSWA 7
 |||||

RESULT 10
 AAM48568
 ID AAM48568 standard; Peptide; 10 AA.
 XX
 AC AAM48568;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 71.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 XX
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
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 PT psoriasis -
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The

CC antibacterial, immunosuppressive, dermatological, neuroprotective, CC
 CC nontropic, antiatherosclerotic, virucide and anti-allergic activity. The CC
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at CC
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase CC
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, CC
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; CC
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC
 CC telangiectasia. The compounds are also useful for treating CC
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis, CC
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC
 CC arthritis. XX
 XX Sequence 10 AA; 0; Gaps 0; Indels 0; Mismatches 0; DB 23; Length 10;
 Query Match 100.0%; Score 40; Pred. No. 1.8;
 Best Local Similarity 100.0%;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 Db 2 ADMSWA 7
 |||||

RESULT 11
 AAM48571 ID AAM48571 standard; Peptide; 10 AA.
 XX AC AAM48571;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 74.
 XX KW Anti-inflammatory; antiaesthetic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX OS Synthetic.
 XX PN WO200183554-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US14346.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYUA) UNIV YALE.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WP; 2002-121889/16.
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis. XX
 XX Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
 Db 3 ADMSWA 8
 |||||

RESULT 12
 AAM48565 ID AAM48565 standard; Peptide; 11 AA.
 XX AC AAM48565;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 68.
 XX KW Anti-inflammatory; antiaesthetic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX OS Synthetic.
 XX PN WO200183554-A2.
 XX PD 08-NOV-2001.
 XX PF 02-MAY-2001; 2001WO-US14346.
 XX PR 02-MAY-2000; 2000US-201261P.
 XX PR 22-AUG-2000; 2000US-0643260.
 XX PA (PRAE-) PRAECIS PHARM INC.
 XX PA (UYUA) UNIV YALE.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WP; 2002-121889/16.
 XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis

PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytotostatic, antiproliferative, antirheumatic, antiarthritic, osteoprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma;
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 11 AA;

Query Match 100.0%; Score 40; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADWSA 6
 |||||
 Db 3 ADWSA 8

RESULT 13

AAU21305

ID AAU21305 standard; Protein; 33 AA.

XX AC AAU21305;

XX DT 18-DEC-2001 (first entry)

XX Human novel foetal antigen, SEQ ID NO 1549.

XX Human; foetal tissue antigen; antiinflammatory; neuroprotective;
 KW immunomodulator; cardiovascular; cytostatic; nephroprotective;
 KW cardiovascular; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; breast neoplasm; cancer;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; food additive.

XX Homo sapiens.

XX WO200155312-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01321.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225269.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.

PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
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 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
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 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249267.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0251989.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-488782/53.

XX N-PSDB; AAS34125.

XX New polynucleotides and polypeptides for diagnosing, treating,
 PT preventing or prognosing e.g. diseases or disorders of the nervous,
 PT musculoskeletal, excretory, gastrointestinal, reproductive, and
 PT respiratory systems

XX Claim 11; SEQ ID No 1549; 642pp; English.

XX The invention relates to novel nucleic acids encoding novel human foetal

CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g.
 CC by gene therapy) or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
 CC are also used in diagnosing a pathological condition or susceptibility
 CC to a pathological condition. The antibodies to the antigens can also
 CC be used in alleviating symptoms associated with the disorders and in
 CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
 CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated
 CC include autoimmune diseases e.g. rheumatoid arthritis
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
 CC and ocular disorders e.g. corneal infection. The polypeptides can also
 CC be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors and other nutritional components. Numerous
 CC examples of diseases and disorders treated by the nucleic acids and
 CC proteins are given in the specification. The present sequence

Query Match 92.5%; Score 37; DB 22; Length 33;

Best Local Similarity 83.3%; Pred. No. 19;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 9 ADWTWA 14

RESULT 14

AA06332

ID AAY06332 standard; Protein; 103 AA.

XX AC AAY06332;

DT 06-SEP-1999 (first entry)

XX Gliocladium roseum EGIII-like cellulase (partial sequence).

XX Cellulase; endoglucanase; EGIII; textile; feed additive; baking;
 KW food processing; grain wet milling; pulp; paper.

XX Gliocladium roseum.

XX WO931255-A2.

PD 24-JUN-1999

PF 14-DEC-1998; 98WO-US26552.

PR 16-DEC-1997; 97US-0991720.

XX (GEMV) GENENCOR INT INC.

PI Bower BS, Fowler T, Phillips JI;

XX WPI; 1999-395187/33.

XX EGIII like cellulase

XX Example; Fig 3; 47pp; English.

CC The present polypeptide represents a partial sequence of a novel
 CC EGIII-like cellulase of Gliocladium roseum. It was deduced from
 CC a partial gene sequence isolated from genomic DNA using PCR
 CC primers (see AAX59180-91) based on conserved motifs (see AAY06325-29)
 CC of Trichoderma reesei EGIII cellulase and related enzymes. PCR
 CC has been used to identify novel EGIII-like enzymes, including the
 CC present polypeptide, from bacterial and fungal sources (see

CC AAY06331-70). Also provided by the invention are vectors, host
CC cells and methods for the recombinant production of such enzymes,
CC which can be used in the treatment of cellulose-containing textiles,
CC as feed additives, in the treatment of wood pulp, in the reduction
CC of biomass to glucose, in the stone washing of indigo dyed denim,
CC or as laundry detergent components (all claimed).
XX
SQ Sequence 103 AA;

Query Match 92.5%; Score 37; DB 20; Length 103;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
DB 29 ADWSWS 34
|||||:

RESULT 15
AAY06363
ID AAY06363 standard; Protein; 236 AA.
XX
AC AAY06363;
XX
DT 06-SEP-1999 (first entry)
XX
DE Gliocladium roseum EGIII-like cellulase.
XX
KW Cellulase; endoglucanase; EGIII; textile; feed additive; baking;
KW food processing; grain wet milling; pulp; paper.
XX
OS Gliocaldium roseum.
XX
PN WO9931255-A2.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US26552.
XX
PR 16-DEC-1997; 97US-0991720.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Bower BS, Fowler T, Phillips JI;
XX
DR WPI; 1999-395187/33.
XX
PT EGIII like cellulase
XX
PS Example; Fig 6; 47pp; English.

CC The present polypeptide represents a full-length sequence of a
CC novel EGIII-like cellulase of Gliocladium roseum. It was deduced
CC from a gene sequence isolated from genomic DNA using PCR
CC primers (see AAX59180-91) based on conserved motifs (see AAY06325-29)
CC of Trichoderma reesei EGIII cellulase and related enzymes. PCR
CC has been used to identify novel EGIII-like enzymes, including the
CC present protein, from bacterial and fungal sources (see AAY06331-70).
CC The sequence shows homology to T. reesei EGIII (see AAY06330). Also
CC provided by the invention are vectors, host cells and methods
CC for the recombinant production of such enzymes, which can be used
CC in the treatment of cellulose-containing textiles, as feed
CC additives, in the treatment of wood pulp, in the reduction of
CC biomass to glucose, in the stone washing of indigo dyed denim, or
CC as laundry detergent components (all claimed).
XX
SQ Sequence 236 AA;

Query Match 92.5%; Score 37; DB 20; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 63 ADWSWS 68
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Job time : 22.7763 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-643-260-5
Perfect score: 40
Sequence: 1 LDWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PCRU COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	242	US-09-345-236B-3	Sequence 3, Appli
2	38	95.0	445	US-09-252-991A-22368	Sequence 22368, A
3	37	92.5	316	US-09-252-991A-17312	Sequence 17312, A
4	36	90.0	68	US-09-252-991A-18367	Sequence 18367, A
5	36	90.0	100	US-08-241-853-28	Sequence 28, Appl
6	36	90.0	100	US-08-241-853-29	Sequence 29, Appl
7	36	90.0	100	US-08-850-917-28	Sequence 28, Appl
8	36	90.0	100	US-08-850-917-29	Sequence 29, Appl
9	36	90.0	462	US-09-252-991A-21704	Sequence 21704, A
10	36	90.0	745	US-08-887-518-3	Sequence 3, Appli
11	36	90.0	745	US-09-023-321-3	Sequence 3, Appli
12	36	90.0	745	US-08-890-853-4	Sequence 4, Appli
13	36	90.0	745	US-09-032-475-3	Sequence 3, Appli
14	36	90.0	745	US-09-099-125A-4	Sequence 4, Appli
15	36	90.0	745	US-09-099-124A-4	Sequence 4, Appli
16	36	90.0	745	US-09-032-476-4	Sequence 4, Appli
17	36	90.0	745	US-08-890-854-4	Sequence 4, Appli
18	36	90.0	745	US-09-023-324-4	Sequence 4, Appli
19	36	90.0	745	US-09-168-629-2	Sequence 2, Appli
20	36	90.0	745	US-08-910-820-10	Sequence 10, Appl
21	36	90.0	745	US-08-810-131A-2	Sequence 2, Appli
22	36	90.0	745	US-09-109-986-4	Sequence 4, Appli
23	36	90.0	745	US-09-844-908-10	Sequence 10, Appl
24	36	90.0	745	US-09-868-758-3	Sequence 3, Appli
25	36	90.0	756	US-08-887-518-4	Sequence 4, Appli
26	36	90.0	756	US-09-023-321-4	Sequence 4, Appli
27	36	90.0	756	US-08-890-853-2	Sequence 2, Appli

28	36	90.0	756	2	US-09-032-475-4	Sequence 4, Appli
29	36	90.0	756	2	US-09-099-125A-2	Sequence 2, Appli
30	36	90.0	756	2	US-09-099-124A-2	Sequence 2, Appli
31	36	90.0	756	3	US-09-032-476-2	Sequence 2, Appli
32	36	90.0	756	3	US-08-890-854-2	Sequence 2, Appli
33	36	90.0	756	3	US-09-023-324-2	Sequence 2, Appli
34	36	90.0	756	3	US-09-168-629-15	Sequence 15, Appl
35	36	90.0	756	3	US-08-910-820-9	Sequence 9, Appli
36	36	90.0	756	4	US-09-109-986-2	Sequence 9, Appli
37	36	90.0	756	4	US-09-844-908-9	Sequence 9, Appli
38	36	90.0	756	4	US-09-868-758-4	Sequence 4, Appli
39	36	90.0	982	2	US-08-673-789-4	Sequence 4, Appli
40	36	90.0	983	1	US-08-162-809-16	Sequence 16, Appl
41	36	90.0	983	1	US-08-167-919A-10	Sequence 10, Appl
42	36	90.0	983	2	US-08-449-645A-21	Sequence 21, Appl
43	36	90.0	983	2	US-08-702-367A-21	Sequence 21, Appl
44	36	90.0	983	3	US-08-715-106-10	Sequence 10, Appl
45	36	90.0	983	5	PCT-US95-04681-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-09-345-236B-3
; Sequence 3, Application US/09345236B
; Patent No. 6521454
; GENERAL INFORMATION:
; APPLICANT: Becnel, James J.
; APPLICANT: Tokuo, Fukuda
; APPLICANT: Moser, Bettina
; APPLICANT: Cockburn, Andrew
; APPLICANT: White, Susan E.
; APPLICANT: Undeen, Albert H.
; TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
; TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
; FILE REFERENCE: 21042.0004
; CURRENT APPLICATION NUMBER: US/09/345,236B
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 242
; TYPE: PRT
; ORGANISM: mosquito baculovirus
US-09-345-236B-3

Query Match 100.0% ; Score 40 ; DB 4 ; Length 242 ;
Best Local Similarity 100.0% ; Pred. No. 31 ;
Matches 6 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY 1 LDWSWA 6
Db |||||
79 LDWSWA 84

RESULT 2

US-09-252-991A-22368
; Sequence 22368, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22368

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; LENGTH: 445
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

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Query Match 95.0%; Score 38; DB 4; Length 445;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels

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Qy      1 LDWSWA 6
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Db      303 MDWSWA 308
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RESULT 3
US-09-252-991A-17312
; Sequence 17312, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17312
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17312

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Query Match 92.5%; Score 37; DB 4; Length 316;
Best Local Similarity 83.3%; Pred. NO. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWA 6
|||:|
Dp 271 LDWSWA 276

```

RESULT 4
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

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```
Query Match          90.0%; Score 36; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 DWSWA 6

Db 2 DWSWA 6

RESULT 5
US-08-241-853-28
; Sequence 28, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,853
; FILING DATE: 12-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-241-853-28

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Query Match          90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LDWSW 5
Db 19 LDWSW 23

RESULT 6
US-08-241-853-29
; Sequence 29, Application US/08241853
; Patent No. 5693488
; GENERAL INFORMATION:
; APPLICANT: Fang, Kathy S.
; APPLICANT: Hanafusa, Hidesaburo
; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-241-853-29

Query Match 90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 19 LDWSW 23

RESULT 7
US-08-850-917-28
Sequence 28, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-29

Query Match 90.0%; Score 36; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 19 LDWSW 23

TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-28

Query Match 90.0%; Score 36; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 19 LDWSW 23

RESULT 8
US-08-850-917-29
Sequence 29, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-29

Query Match 90.0%; Score 36; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 19 LDWSW 23

QY 1 LDWSW 5
Db 19 LDWSW 23

RESULT 9
US-09-252-991A-21704
; Sequence 21704, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21704
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 169 DWSWA 173

RESULT 10
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 11
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 12
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.

APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 13
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
Db 738 LDWSW 742

RESULT 14
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goettel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5

Db 738 LDWSW 742

RESULT 15
US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5

Db 738 LDWSW 742

Search completed: February 18, 2004, 14:41:46
Job time : 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDWSWA 6

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	40	100.0	6	AA48510	NBD mutant peptide
3	40	100.0	6	AA48537	Anti-inflammatory
4	40	100.0	6	AA48559	Anti-inflammatory
5	40	100.0	6	ABU08421	Human NEMO binding
6	40	100.0	7	AA48563	Anti-inflammatory
7	40	100.0	8	AA48556	Anti-inflammatory
8	40	100.0	8	AA48564	Anti-inflammatory
9	40	100.0	9	AA48555	Anti-inflammatory

10	40	100.0	9	23	AA48558	Anti-inflammatory
11	40	100.0	9	23	AA48561	Anti-inflammatory
12	40	100.0	9	23	AA48562	Anti-inflammatory
13	40	100.0	10	23	AA48554	Anti-inflammatory
14	40	100.0	10	23	AA48557	Anti-inflammatory
15	40	100.0	10	23	AA48560	Anti-inflammatory
16	40	100.0	745	23	ABB77292	Human IKKalpha mut
17	40	100.0	756	23	ABB77309	Human IKKbeta mut
18	36	90.0	6	23	ABB08725	IKKbeta NEMO bindi
19	36	90.0	6	23	AA48530	Anti-inflammatory
20	36	90.0	6	23	AA48538	Anti-inflammatory
21	36	90.0	6	23	AA48570	Anti-inflammatory
22	36	90.0	6	23	AA48565	NBD mutant peptide
23	36	90.0	6	24	ABU08418	Human NEMO binding
24	36	90.0	7	23	AA48534	Anti-inflammatory
25	36	90.0	7	23	AA48574	Anti-inflammatory
26	36	90.0	8	23	AA48527	Anti-inflammatory
27	36	90.0	8	23	AA48535	Anti-inflammatory
28	36	90.0	8	23	AA48567	Anti-inflammatory
29	36	90.0	8	23	AA48575	Anti-inflammatory
30	36	90.0	9	20	AA96182	IKK-alpha polypept
31	36	90.0	9	23	AA48526	Anti-inflammatory
32	36	90.0	9	23	AA48529	Anti-inflammatory
33	36	90.0	9	23	AA48532	Anti-inflammatory
34	36	90.0	9	23	AA48533	Anti-inflammatory
35	36	90.0	9	23	AA48566	Anti-inflammatory
36	36	90.0	9	23	AA48569	Anti-inflammatory
37	36	90.0	9	23	AA48572	Anti-inflammatory
38	36	90.0	9	23	AA48573	Anti-inflammatory
39	36	90.0	10	23	ABB77313	IKKbeta NEMO bindi
40	36	90.0	10	23	AA48528	Anti-inflammatory
41	36	90.0	10	23	AA48531	Anti-inflammatory
42	36	90.0	10	23	AA48568	Anti-inflammatory
43	36	90.0	10	23	AA48571	Anti-inflammatory
44	36	90.0	11	23	ABB77311	Human NBD peptide
45	36	90.0	11	23	AA48506	Human IKKbeta pept

ALIGNMENTS

RESULT 1

ABB08728

ID ABB08728 standard; peptide; 6 AA.

XX ABB08728;

XX 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiaesthetic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antitumor; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX FT Misc-difference 6

XX FT /note= "Wildtype Leu substituted by Ala"

XX WO200183547-A2.

XX PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US40654.
XX
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S;
XX
XX WPI; 2002-179350/23.
XX
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain -
XX
XX
XX Claim 23; Page 44; 82pp; English.
XX
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of Ikbapab. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammation
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
XX binding domain of IKKbeta.
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 40; DB 23; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LDWSWA 6
XX |||||
XX 1 LDWSWA 6
XX
XX RESULT 2
XX AAM48510
XX ID AAM48510 standard; Peptide; 6 AA.
XX
XX AC AAM48510;
XX
XX DT 20-MAR-2002 (first entry)
XX
XX DE NBD mutant peptide SEQ ID NO 5.

XX
KW Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
OS
XX WO200183554-A2.
PN
XX 08-NOV-2001.
PD
XX
XX 02-MAY-2001; 2001WO-US14346.
PF
XX
XX 02-MAY-2000; 2000US-201261P.
PR
XX 22-AUG-2000; 2000US-0643260.
PR
XX (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
PA
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
PI
XX WPI; 2002-121889/16.
DR
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
PT
XX Example 6; Page 47; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective, The
CC nootropic, antiatherosclerotic, virucide and anti allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IkappaB kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 40; DB 23; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LDWSWA 6
XX |||||
XX 1 LDWSWA 6
XX
XX RESULT 3
XX AAM48537
XX ID AAM48537 standard; Peptide; 6 AA.

XX AAM48537;
 XX
 XX
 XX 20-MAR-2002 (first entry)
 XX
 XX Anti-inflammatory peptide SEQ ID NO 40.
 DE
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 XX Synthetic.
 OS
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX
 XX Claim 6; Page 61; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWA 6
 |||||

Db 1 LDWSWA 6
 RESULT 4
 AAM48559
 ID AAM48559 standard; Peptide; 6 AA.
 XX
 XX AAM48559;
 AC
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 62.
 DE
 XX
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 XX Synthetic.
 OS
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PT
 XX
 XX Claim 6; Page 62; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 40; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 DB 1 LDWSWA 6
 |||||

RESULT 5
 ABU08421
 ID ABU08421 standard; peptide; 6 AA.
 XX
 AC ABU08421;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human NEMO binding site (NBD) mutant peptide #4.
 XX
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
 KW nuclear factor-kappaB induction; inflammatory disorder;
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
 KW atherosclerosis; viral infection; Ataxia telangiectasia;
 KW transplantation detection; immunosuppressive; osteopathic;
 KW cytotatic; neutropic; neuroprotective; antiatherosclerotic; virucide;
 KW vasotropic; antiirheumatic; antiarthritic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2002156000-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 02-MAY-2001; 2001US-0847940.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 XX
 PI May MJ, Ghosh S;
 XX
 DR WPI; 2003-209142/20.
 XX
 PT Novel antiinflammatory peptide compounds comprising NEMO binding
 PT domain, useful for modulating NF-kappaB induction in a cell and for
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
 PT psoriasis, vasculitis -
 XX
 PS Claim 22; Page 17; 47pp; English.
 XX
 CC The present invention relates to antiinflammatory compounds comprising
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
 CC in a cell, where the compounds are capable of blocking the interaction
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
 CC antiinflammatory compound further comprises at least one membrane
 CC translocation domain. The compounds are useful for treating
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
 CC telangiectasia, and for transplantation detection. The compounds of
 CC the invention block NF-kappaB induction by IKK but do not inhibit
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
 CC NBD mutant peptides.

QY Sequence 6 AA;
 SQ

Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 DB 1 LDWSWA 6
 |||||

RESULT 6
 AAM48563
 ID AAM48563 standard; Peptide; 7 AA.
 XX
 AC AAM48563;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 66.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 OS
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA; Length 7; DB 23; Indels 0; Gaps 0;
 Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWA 6
 Db 1 LDWSWA 6
 |||||
 RESULT 7
 AAM48556
 ID AAM48556 standard; Peptide; 8 AA.
 XX
 AC AAM48556;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 59.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 XX
 PS Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, neuroprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWA 6
 Db 3 LDWSWA 8
 |||||
 RESULT 8
 AAM48564
 ID AAM48564 standard; Peptide; 8 AA.
 XX
 AC AAM48564;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 67.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PA
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI
 XX WPI; 2002-121889/16.
 DR
 XX
 XX
 PS Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, neuroprotective,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 8 AA;

Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 DB 1 LDWSWA 6
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RESULT 9
 AAM48555
 ID AAM48555 standard; Peptide; 9 AA.

XX AC AAM48555;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 58.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX XX (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA) UNIV YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -

XX PS Claim 6; Page 62; 89pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neutropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 DB 1 LDWSWA 6
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RESULT 10

AAM48558
 ID AAM48558 standard; Peptide; 9 AA.

XX AC AAM48558;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 61.

XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

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 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -
 XX
 PS
 XX
 Claim 6; Page 62; 88pp; English.
 CC
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 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
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 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic,
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWA 6
 Db | | | | |
 1 LDWSWA 6
 RESULT 11
 AAM48561
 ID AAM48561 standard; Peptide; 9 AA.
 XX
 AC AAM48561;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 64.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 PR
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYIA) UNIV YALE.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX
 DR WPI; 2002-121889/16.
 XX
 PT Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
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 PT psoriasis -
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 XX Claim 6; Page 62; 88pp; English.
 PS
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 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
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 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWA 6
 Db | | | | |
 3 LDWSWA 8
 RESULT 12
 AAM48562
 ID AAM48562 standard; Peptide; 9 AA.
 XX
 AC AAM48562;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 65.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 OS Synthetic.
 XX
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 PR
 PR 02-MAY-2000; 2000US-201261P.
 XX

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PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYA ) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSWA 6
Db 2 LDWSWA 7
RESULT 13
AAM48554
ID AAM48554 standard; Peptide; 10 AA.
XX AAM48554;
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 57.
DE
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
OS
XX WO200183554-A2.
PN
22-AUG-2000; 2001WO-US14346.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYA ) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
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CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX Sequence 10 AA;
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Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSWA 6
Db 2 LDWSWA 7
RESULT 14
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ID AAM48557 standard; Peptide; 10 AA.
XX AAM48557;
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 60.
DE
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;

```

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14346.
 XX
 PR 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PA (UYA) UNIV YALE.
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 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWA 6
 Db |||||
 2 LDWSWA 7
 RESULT 15
 ID AAM48560
 AC AAM48560 standard; Peptide; 10 AA.
 XX
 AC AAM48560;
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX Anti-inflammatory peptide SEQ ID NO 63.
 DE
 XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nontropic;
 KW

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
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 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
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 XX
 OS Synthetic.
 XX
 PN WO200183554-A2.
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 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db |||||
 3 LDWSWA 8
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 Job time : 23.7763 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	Mutated IKKbeta NE
2	40	100.0	6	23	NBD mutant peptide
3	40	100.0	6	23	Anti-inflammatory
4	40	100.0	6	23	Anti-inflammatory
5	40	100.0	6	24	Human NEMO binding
6	40	100.0	7	23	Anti-inflammatory
7	40	100.0	8	23	Anti-inflammatory
8	40	100.0	8	23	Anti-inflammatory
9	40	100.0	9	23	Anti-inflammatory

10	40	100.0	9	23	AAW48547	Anti-inflammatory
11	40	100.0	9	23	AAW48550	Anti-inflammatory
12	40	100.0	9	23	AAW48551	Anti-inflammatory
13	40	100.0	10	23	AAW48546	Anti-inflammatory
14	40	100.0	10	23	AAW48549	Anti-inflammatory
15	40	100.0	11	23	AAW48543	Anti-inflammatory
16	40	100.0	276	22	AAW39444	Human ORFX ORF1817
17	40	100.0	277	21	AAW42053	Human polypeptide
18	40	100.0	371	22	AAW41230	Human polypeptide
19	40	100.0	452	22	AAW93545	Human IKKalpha mut
20	40	100.0	745	23	ABB77291	Human IKKbeta muta
21	40	100.0	756	23	ABB77308	Insulin/insulin-li
22	37	92.5	31	23	AAU07085	Human IKKbeta muta
23	37	92.5	756	23	ABB77310	IKKbeta NEMO bindi
24	36	90.0	6	23	ABB08725	Anti-inflammatory
25	36	90.0	6	23	AAW48530	Anti-inflammatory
26	36	90.0	6	23	AAW48538	Anti-inflammatory
27	36	90.0	6	23	AAW48570	Anti-inflammatory
28	36	90.0	6	23	AAW48655	NBD mutant peptide
29	36	90.0	6	24	ABU08418	Human NEMO binding
30	36	90.0	7	23	AAW48534	Anti-inflammatory
31	36	90.0	7	23	AAW48574	Anti-inflammatory
32	36	90.0	8	23	AAW48527	Anti-inflammatory
33	36	90.0	8	23	AAW48535	Anti-inflammatory
34	36	90.0	8	23	AAW48567	Anti-inflammatory
35	36	90.0	8	23	AAW48575	Anti-inflammatory
36	36	90.0	9	20	AAW96182	IKK-alpha polypept
37	36	90.0	9	23	AAW48526	Anti-inflammatory
38	36	90.0	9	23	AAW48529	Anti-inflammatory
39	36	90.0	9	23	AAW48532	Anti-inflammatory
40	36	90.0	9	23	AAW48533	Anti-inflammatory
41	36	90.0	9	23	AAW48566	Anti-inflammatory
42	36	90.0	9	23	AAW48569	Anti-inflammatory
43	36	90.0	9	23	AAW48572	Anti-inflammatory
44	36	90.0	9	23	AAW48573	Anti-inflammatory
45	36	90.0	10	23	ABB77313	IKKbeta NEMO bindi

ALIGNMENTS

RESULT 1

ABB08727

ID ABB08727 standard; peptide; 6 AA.

XX ABB08727;

AC ABB08727;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 4.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

XX autoimmune disease; transplant rejection; osteoporosis; cancer;

XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;

XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;

XX corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;

XX osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;

XX antiarteriosclerotic; virucide; antiaesthetic; antiallergic;

XX dermatological; antibacterial; antipsoriatic; antirheumatic;

XX antiarthritic; osteopathic; antiulcer; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

XX Misc-difference 1

XX /note= "wildtype Leu substituted by Ala"

XX WO200183547-A2.

XX 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US40654.
XX
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S;
XX
XX WPI; 2002-179350/23.
DR
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain -
XX
PS Claim 23; Page 44; 82pp; English.
XX
CC The invention relates to modulating NF-kappaB (NF-KB) induction in a cell
CC comprising contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of Ikbapab. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking NF-kB mediated
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWL 6
Db 1 ADWSWL 6
|||||
RESULT 2
ID AAM48509
XX AAM48509 standard; Peptide; 6 AA.
XX
AC AAM48509;
XX
XX
DT 20-MAR-2002 (first entry)
XX
XX NBD mutant peptide SEQ ID NO 4.
DE

XX
KW Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; neurotropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NfKappaB; Ikbapab kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
XX 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYVA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
XX WPI; 2002-121889/16.
DR
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
XX Example 6; Page 47; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NfKappaB
CC activation by blocking interaction of Ikbapab kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of Ikbapab kinase
CC activation and subsequent decreased phosphorylation of Ikbapab. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWL 6
Db 1 ADWSWL 6
|||||
RESULT 3
ID AAM48536
XX AAM48536 standard; Peptide; 6 AA.

XX AAM48536;
 XX
 XX
 XX 20-MAR-2002 (first entry)
 XX
 XX DE Anti-inflammatory peptide SEQ ID NO 39.
 XX
 XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 XX Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 61; 88pp; English.
 XX
 XX The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 CC antibacterial, immunosuppressive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 100.0%; Score 40; DB 23; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 ADWSWL 6
 XX |||||

Db 1 ADWSWL 6
 RESULT 4
 AAM48548
 ID AAM48548 standard; Peptide; 6 AA.
 XX
 XX AAM48548;
 XX
 XX 20-MAR-2002 (first entry)
 XX
 XX DE Anti-inflammatory peptide SEQ ID NO 51.
 XX
 XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 XX Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel anti-inflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX
 XX The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, dermatological, neuroprotective,
 CC antibacterial, immunosuppressive, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 XX Sequence 6 AA;

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 40; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 |||||
 Db 1 ADMSWL 6
 RESULT 7
 AAM48545
 ID AAM48545 standard; Peptide; 8 AA.
 XX
 AC AAM48545;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 48.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 |||||
 Db 3 ADMSWL 8
 RESULT 8
 AAM48553
 ID AAM48553 standard; Peptide; 8 AA.
 XX
 AC AAM48553;
 XX
 DT 20-MAR-2002 (first entry)
 DE Anti-inflammatory peptide SEQ ID NO 56.
 XX
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX
 OS Synthetic.
 XX
 XX WO200183554-A2.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX (UYA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation
 XX domain fused to NEMO binding sequence, useful for blocking nuclear
 XX factor kappaB activation, and for treating asthma, lung inflammation,
 XX psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 XX
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 40; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
 DB 1 ADWSWL 6

RESULT 9
 AAM48544
 ID AAM48544 standard; Peptide; 9 AA.
 AC AAM48544;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 47.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECTIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 XX
 XX Claim 6; Page 62; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.

XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
 DB 1 ADWSWL 6

RESULT 10
 AAM48547
 ID AAM48547 standard; Peptide; 9 AA.
 AC AAM48547;
 XX
 DT 20-MAR-2002 (first entry)
 XX
 DE Anti-inflammatory peptide SEQ ID NO 50.
 XX
 KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR
 XX 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECTIS PHARM INC.
 PA (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 PI WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -
 PS Claim 6; Page 62; 88pp; English.
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 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
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 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 Db | | | | |
 1 ADMSWL 6

RESULT 11
 AAM48550
 ID AAM48550 standard; Peptide; 9 AA.
 XX AAM48550;
 AC
 DT 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 53.
 DE
 XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-AUG-2000; 2000US-0643260.
 PR
 XX (PRAE-) PRACIS PHARM INC.
 PA (UYA) UNIV YALE.
 XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.
 DR
 XX Novel antiinflammatory compound comprising membrane translocation
 PT domain fused to NEMO binding sequence, useful for blocking nuclear
 PT factor kappaB activation, and for treating asthma, lung inflammation,
 PT psoriasis -
 PS Claim 6; Page 62; 88pp; English.
 CC The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
 CC amino acid residues, fused to a NEMO binding sequence
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,
 CC neurotropic, antiatherosclerotic, virucide and anti-allergic activity. The
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase
 CC activation and subsequent decreased phosphorylation of IkappaB. The
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 Db | | | | |
 3 ADMSWL 8

RESULT 12
 AAM48551
 ID AAM48551 standard; Peptide; 9 AA.
 XX AAM48551;
 AC
 DT 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 54.
 DE
 XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US14346.
 PF
 XX 02-MAY-2000; 2000US-201261P.
 PR

```

PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYA ) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
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CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nontropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX Sequence 9 AA;
SQ
Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 2 ADWSWL 7

RESULT 13
AAM48546
ID AAM48546 standard; Peptide; 10 AA.
XX AC AAM48546;
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 49.
DE
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.
PN

XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US14346.
XX 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX (PRAE-) PRAECIS PHARM INC.
PA (UYA ) UNIV YALE.
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 40; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 2 ADWSWL 7

RESULT 14
AAM48549
ID AAM48549 standard; Peptide; 10 AA.
XX AC AAM48549;
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 52.
DE
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nontropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.
PN

```

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 PN 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA (UYVA) UNIV YALE.
 PA
 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWL 6
 Db 3 ADWSWL 8
 RESULT 15
 AAM48543
 ID AAM48543 standard; Peptide; 11 AA.
 XX
 XX AAM48543;
 AC
 XX
 XX 20-MAR-2002 (first entry)
 DT
 XX
 XX Anti-inflammatory peptide SEQ ID NO 46.
 DE
 XX
 KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nontropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 XX WO200183554-A2.
 PN 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US14346.
 XX
 XX 02-MAY-2000; 2000US-201261P.
 PR 22-AUG-2000; 2000US-0643260.
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 XX (PRAE-) PRAECIS PHARM INC.
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;
 XX WPI; 2002-121889/16.
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 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
 CC telangiectasia. The compounds are also useful for treating
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
 CC arthritis.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 40; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSWL 6
 Db 3 ADWSWL 8
 Search completed: February 18, 2004, 14:26:18
 Job time : 22.7763 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 16.5789 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWQNRKMKKTKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	69.6	224	1 HXB6_HUMAN	P17509 homo sapien
2	103	69.6	224	1 HXB6_MOUSE	P09023 mus musculu
3	100	67.6	105	1 HXA7_RAT	P09634 rattus norv
4	100	67.6	229	1 HXA7_MOUSE	P02830 mus musculu
5	99	66.9	75	1 HXSA_SALSA	P09636 salmo salar
6	98	66.2	84	1 HXB6_CHICK	P14839 gallus gall
7	96.5	65.2	96	1 HXC6_BRARE	P15862 brachydanio
8	96	64.9	208	1 HXA7_HETFR	P09125 heterodontu
9	96	64.9	234	1 HXC6_XENLA	P02832 xenopus lae
10	95	64.2	153	1 HXC6_SHEEP	P49925 ovis aries
11	95	64.2	230	1 HXA7_HUMAN	P31268 homo sapien
12	95	64.2	230	1 HXB5_XENLA	P09019 xenopus lae
13	95	64.2	234	1 HXC6_NOTVI	P14858 notophthalm
14	95	64.2	235	1 HXC6_HUMAN	P09630 homo sapien
15	95	64.2	235	1 HXC6_MOUSE	P10629 mus musculu
16	95	64.2	242	1 HXA7_COTJA	P24061 coturnix co
17	94.5	63.9	81	1 HXSL_BRARE	P09013 brachydanio
18	94.5	63.9	269	1 HXB5_HUMAN	P09067 homo sapien
19	94.5	63.9	269	1 HXB5_MOUSE	P09079 mus musculu
20	94.5	63.9	275	1 HXB5_BRARE	P09014 brachydanio
21	94	63.5	48	1 HXB6_XENLA	P31256 xenopus lae
22	94	63.5	49	1 HXA5_SHEEP	P02859 ovis aries
23	94	63.5	71	1 HXA7_SHEEP	P02860 ovis aries
24	94	63.5	71	1 HXC5_NOTVI	P31262 notophthalm
25	94	63.5	74	1 HM90_APIME	P15860 apis mellif
26	94	63.5	76	1 HXC4_RAT	P18865 rattus norv
27	94	63.5	78	1 HXA5_SALSA	P09637 salmo salar
28	94	63.5	80	1 HXA4_LINSA	P81192 lineus sang
29	94	63.5	82	1 HXB5_CHICK	P14838 gallus gall
30	94	63.5	86	1 SCR_APIME	P15859 apis mellif
31	94	63.5	87	1 HXC5_XENLA	P09020 xenopus lae
32	94	63.5	93	1 HXB8_PIG	P09078 sus scrofa
33	94	63.5	105	1 HXB4_BRARE	P22574 brachydanio

RESULT 1

ID	Accession	Standard	PRT	AA
AC	P17509	P09068; Q9HB11; Q9UGH2;		224 AA.
DT	01-NOV-1988	(Rel. 09, Created)		
DT	18-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Homeobox protein Hox-B6 (Hox-2B) (Hox-2) (HU-2).			
GN	HOXB6 OR HOXB2B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.; AND ALTERNATIVE SPLICING.			
RC	TISSUE=Placenta;			
RX	MEDLINE=91187672; PubMed=1672751;			
RA	Shen W.-F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,			
RA	Largman C.;			
RT	"Alternative splicing of the HOX 2.2 homeobox gene in human			
RT	hematopoietic cells and murine embryonic and adult tissues.";			
RL	Nucleic Acids Res. 19:539-545(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.;			
RT	"Expression of HOX genes in T lymphocytes and hairy leukemia cell			
RT	lines.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Kidd K.K., Busygina V., Demille M.M.C., Speed W.C., Ruggeri V.,			
RA	Kidd J.R., Pakstis A.J.;			
RT	"Overall linkage disequilibrium in 33 populations for highly			
RT	informative multisite haplotypes spanning the HOXB gene cluster.";			
RL	Am. J. Hum. Genet. 67:233-235(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Srausberg R.L., Paingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			

ALIGNMENTS

34	94	63.5	112	1	HXB7_RAT	P18864 rattus norv
35	94	63.5	148	1	HXA5_AMBME	P50208 ambystoma m
36	94	63.5	209	1	HXA7_XENLA	P09071 xenopus lae
37	94	63.5	217	1	HXB7_BOVIN	O9tt89 bos taurus
38	94	63.5	217	1	HXB7_HUMAN	P09629 homo sapien
39	94	63.5	217	1	HXB7_MOUSE	P09024 mus musculu
40	94	63.5	220	1	HB7A_XENLA	O91771 xenopus lae
41	94	63.5	220	1	HB7B_XENLA	P04476 xenopus lae
42	94	63.5	222	1	HXC5_HUMAN	O00444 homo sapien
43	94	63.5	222	1	HXC5_MOUSE	P32043 mus musculu
44	94	63.5	225	1	HXA7_MORSA	Q9pww4 morone saxa
45	94	63.5	228	1	HXB6_BRARE	P15861 brachydanio

RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RN SEQUENCE OF 135-224 FROM N.A.
 RX MEDLINE=90046832; PubMed=2573064;
 RA Shen W.-P., Largman C., Lowney P., Corral J.C., Detmer K.,
 RA Hausser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
 RT "Lineage-restricted expression of homeobox-containing genes in human
 RT hematopoietic cell lines";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
 [6]
 RN PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
 RX MEDLINE=95024858; PubMed=6091895;
 RA Levine M., Rubin G.M., Tjian R.;
 RT "Human DNA sequences homologous to a protein coding region conserved
 RT between homeotic genes of Drosophila";
 RL Cell 38:667-673(1984).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=p17509-1; Sequence=displayed;
 CC Name=2; Synonyms=Homeobox-less;
 CC IsoId=p17509-2; Sequence=VSP_002388, VSP_002389;
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; X58431; CAA41335.1; -;
 CC ENBL; X58431; CAA41336.1; -;
 CC ENBL; AJ270993; CAB65909.1; -;
 CC ENBL; AF287967; AAG31552.1; -;
 CC ENBL; BC014651; AAH14651.1; -;
 CC ENBL; M30597; AAA36004.1; -;
 CC ENBL; K02571; -; NOT_ANNOTATED_CDS.
 CC PIR; S26400; S26400.
 CC HSP; P02833; IHOM.
 CC TRANSFAC; T01732; -;
 CC Genew; HGNC:5117; HOXB6.
 CC MIM; 142961; -; C.nucleus; NAS.
 CC GO; GO:0005634; C.nucleus; NAS.
 CC GO; GO:0003700; F:transcription factor activity; NAS.
 CC GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEOBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00027; HOMEOBOX_1; 1.
 CC PROSITE; PS00071; HOMEOBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 RT Transcription regulation; Alternative splicing.
 SITE 127 132 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 146 205 HOMEOBOX.
 FT DOMAIN 216 220 POLY-GLU.
 FT VARSPPLIC 140 140
 FT Missing (in isoform 2).
 FT Missing (in isoform 2).
 FT VARSPPLIC 141 224
 FT Missing (in isoform 2).
 FT Missing (in isoform 2).
 FT

FT CONFLICT 24 25 HV -> QL (IN REF. 3 AND 4).
 FT CONFLICT 33 33 A -> R (IN REF. 1).
 FT CONFLICT 60 60 P -> R (IN REF. 1).
 FT CONFLICT 73 73 D -> A (IN REF. 1).
 FT CONFLICT 149 150 GR -> A (IN REF. 5).
 SQ SEQUENCE 224 AA; 25427 MW; D8F96AFAC93D878 CRC64;
 Query Match 69.6%; Score 103; DB 1; Length 224;
 Best Local Similarity 70.0%; Pred. No. 1.2e-08;
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;
 QY 1 DRQIKWIFQNRKMKWKTA--LDASALQTE 28
 DB 187 ERQIKWIFQNRKMKWKSKULLSASQLSAE 216
 RESULT 2
 HXB6 MOUSE
 ID HXB6 MOUSE STANDARD; PRT; 224 AA.
 AC P09023;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
 GN HOXB6 OR HOXB-6 OR HOX-2.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88289762; PubMed=2899893;
 RA Schughart K., Utset M.F., Awgulewitsch A., Ruddle F.H.;
 RT "Structure and expression of Hox-2.2, a murine homeobox-containing
 RT gene";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91187672; PubMed=1672751;
 RA Shen W.F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
 RA Largman C.;
 RT "Alternative splicing of the HOX 2.2 homeobox gene in human
 RT hematopoietic cells and murine embryonic and adult tissues";
 RL Nucleic Acids Res. 19:539-545(1991).
 RN [3]
 RP SEQUENCE OF 144-224 FROM N.A.
 RX MEDLINE=88054465; PubMed=2890503;
 RA Lonai P., Arman E., Czosnek H., Ruddle F.H., Blatt C.;
 RT "New murine homeoboxes: structure, chromosomal assignment, and
 RT differential expression in adult erythropoiesis";
 RL DNA 6:409-418(1987).
 RN [4]
 RP SEQUENCE OF 140-224 FROM N.A.
 RX MEDLINE=8805193; PubMed=2891608;
 RA Hart C.P., Fainsod A., Ruddle F.H.;
 RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes:
 RT evolutionary and structural comparisons";
 RL Genomics 1:182-195(1987).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 CC ENBL; M18166; AAA37844.1; -;

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CC -----
 CC EMBL; M17192; AAA37833.1; --
 CC EMBL; U15972; AAC52160.1; --
 CC PIR; A03314; A03314.
 CC PIR; A28329; A28329.
 CC HSSP; P02833; 9ANT.
 CC TRANSFAC; T01278; --
 CC MGD; MGI:96179; Hoxa7.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; Hox; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00027; HOMEBOX; 1.
 CC PROSITE; PS50071; HOMEBOX 2; 1.
 CC Transcription regulation.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC SITE 118 123 ANTP-TYPE HEXAPEPTIDE.
 CC DNA_BIND 129 188 HOMEBOX.
 CC DOMAIN 156 159 POLY-ARG.
 CC DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).
 CC DOMAIN 215 229 POLY-GLU.
 CC CONFLICT 43 45 GAG -> APA (IN REF. 1).
 CC SEQUENCE 229 AA; 25682 MW; D36G6D61D8D5C6F CRC64;

Query Match 67.6%; Score 100; DB 1; Length 229;
 Best Local Similarity 70.4%; Pred. No. 3.5e-08;
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMRMKWKKTALDASALQT 27
 :|||||
 DB 170 ERQIKIFQNRMRMKWKKEHKSQAPT 196

RESULT 5

HMSA_SALSA STANDARD; PRT; 75 AA.
 ID HMSA_SALSA
 AC P09636;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Sl2-A (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88226009; PubMed=2897318;
 RA Fjose A., Molven A., Eiken H.G.;
 RT "Molecular cloning and characterization of homeo-box-containing genes
 RT from Atlantic salmon";
 RL Gene 62:141-152(1988).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC -----
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CC -----
 CC EMBL; M18903; AAA49559.1; --
 CC PIR; I51341; I51341.
 CC HSSP; P02833; 9ANT.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; Hox; 1.
 CC PROSITE; PS00027; HOMEBOX; 1.
 CC PROSITE; PS50071; HOMEBOX 2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 CC FT NON_TER 1 1
 CC FT DNA_BIND 1 60 HOMEBOX.
 CC FT NON_TER 75 75
 CC FT SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;
 SQ
 Query Match 66.9%; Score 99; DB 1; Length 75;
 Best Local Similarity 75.0%; Pred. No. 1.5e-08;
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMRMKWKKTALDASA 24
 :|||||
 DB 42 ERQIKIFQNRMRMKWKKHDESS 65

RESULT 6

HXB6_CHICK STANDARD; PRT; 84 AA.
 ID HXB6_CHICK
 AC P14839;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B6 (GHOX-2.2) (Fragment).
 GN HOXB6 OR GHOX-2.2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=90126373; PubMed=2575515;
 RA Wedden S.E., Pang K., Eichele G.;
 RT "Expression pattern of homeobox-containing genes during chick
 RT embryogenesis";
 RL Development 105:639-650(1989).
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC -----
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CC EMBL; X16847; CAA34744.1; --
 CC HSSP; P02833; 1HOW.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC InterPro; IPR000047; HTH lamb-repressr.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00031; HTHREPRESSR.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; Hox; 1.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 CC PROSITE; PS50071; HOMEBOX 2; 1.

KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX.
SQ SEQUENCE 84 AA; 10279 MW; BC06B10165B19E71 CRC64;

Query Match 66.2%; Score 98; DB 1; Length 84;
Best Local Similarity 66.7%; Pred. No. 2.4e-08;
Matches 20; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DRQIKWFOQRNRKWK--TALDASALQTE 28
:|||||
DB 48 ERQIKWFOQRNRKWK--TALDASALQTE 77
:|||||

RESULT 7

HXC6_BRARE STANDARD; PRT; 96 AA.
AC P15862;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (ZF-61) (Fragment).
GN HXC6 OR HXC6A OR HXC6 OR ZF-61.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90151628; PubMed=1968004;
RA Njolstad P.R., Mølven A., Apold J., Fjose A.;
RT "The zebrafish homeobox gene hox-2.2: transcription unit, potential
regulatory regions and in situ localization of transcripts.";
RL EMBO J. 9:515-524(1990).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.

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EMBL; X17266; CAA3170.1; --
PIR; S08639; S08639.
HSP; P02833; 9ANT.

ZFIN; ZDB-GENE-990415-113; hoxc6a.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; Hox; 1.
PROSITE; PS00027; HOMEBOX 1; 1.
PROSITE; PS00032; ANTENNAPEDIA.
PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX.
SQ SEQUENCE 96 AA; 11638 MW; F1ED7AFAA3B640C0 CRC64;

Query Match 65.2%; Score 96.5; DB 1; Length 96;
Best Local Similarity 69.0%; Pred. No. 4.7e-08;
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQIKWFOQRNRKWK--TALDASALQTE 28
:|||||
DB 48 ERQIKWFOQRNRKWK--TALDASALQTE 76
:|||||

RESULT 8

HXA7_HETFR STANDARD; PRT; 208 AA.
AC Q91A25;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7.
GN HXA7.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontoides; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144096; PubMed=10677514;
RA Kim C.B., Amemiya C., Bailey W., Kawasaki K., Mezey J., Miller W.,
RA Minoshima S., Shimizu N., Wagner G., Ruddle F.;
RT "Hox cluster genomics in the horn shark, Heterodontus francisci.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1655-1660(2000).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.

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EMBL; AF224262; AAF44645.1; --
HSP; P02833; 9ANT.
TRANSFAC; T04478; --

InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; Hox; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEBOX 1; 1.
PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT SITE 129 129 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 135 194 HOMEBOX.
SQ SEQUENCE 208 AA; 23786 MW; 71B661AB78E064D0 CRC64;

Query Match 64.9%; Score 96; DB 1; Length 208;
Best Local Similarity 66.7%; Pred. No. 1.3e-07;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRNRKWK--TALDASALQTE 27
:|||||
DB 176 ERQIKWFOQRNRKWK--TALDASALQTE 202
:|||||

RESULT 9

HXC6_XENLA STANDARD; PRT; 234 AA.
ID_HXC6_XENLA

```
AC P02832;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (Xlhb6x-1) (AC1).
GN HOXC6 OR XLHBX1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329002; PubMed=2901347;
RA Cho K.W.Y., Goetz J., Wright C.V.E., Fritz A., Hardwicke J.,
de Robertis E.M.;
RT "Differential utilization of the same reading frame in a Xenopus
homeobox gene encodes two related proteins sharing the same
DNA-binding specificity.";
RL EMBO J. 7:2139-2149(1988).
RN [2]
RP SEQUENCE OF 121-234 FROM N.A.
RX MEDLINE=88157707; PubMed=2894634;
RA Fritz A., de Robertis E.M.;
RT "Xenopus homeobox-containing cDNAs expressed in early development.";
RL Nucleic Acids Res. 16:1453-1469(1988).
RN [3]
RP SEQUENCE OF 134-200 FROM N.A.
RX MEDLINE=84205675; PubMed=6327066;
RA Carrasco A.E., McGinnis W., Gehring W.J., de Robertis E.M.;
RT "Cloning of an X. laevis gene expressed during early embryogenesis
coding for a peptide region homologous to Drosophila homeotic
genes.";
RL Cell 37:409-414(1984).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY XENOPUS
EMBRYOS.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
DR EMBL; X12499; CAA31020.1; ALT_INIT.
DR EMBL; X12500; CAA31021.1; -.
DR EMBL; X01943; AAA49743.1; -.
DR EMBL; X07101; CAA30122.1; -.
DR PIR; S00992; S00992.
DR HSP; P02833; 9ANT.
DR TRANSFAC; T01745; -.
DR TRANSFAC; T01746; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEIDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEIDIA; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
FT CHAIN 1 234 HOMEBOX PROTEIN HOX-C6 PRII.
FT CHAIN 83 234 HOMEBOX PROTEIN HOX-C6 PRI.
FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
```

```
FT DNA_BIND 141 200 HOMEBOX.
FT VARIANT 139 139 T -> S.
SQ SEQUENCE 234 AA; 26689 MW; 4C371CC5252D2C58 CRC64;

Query Match 64.9%; Score 96; DB 1; Length 234;
Best Local Similarity 72.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKKYALDASAL 25
DB 182 ERQIKWQNRRMKWKKESNLTSL 206

RESULT 10
ID HXC6 SHEEP STANDARD; PRT; 153 AA.
AC P49925;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6.
GN HOXC6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Cosby N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
DR EMBL; U33049; AAA75473.1; -.
DR HSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEIDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEIDIA; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
FT SITE 40 45 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 59 118 HOMEBOX.
FT DOMAIN 86 89 POLY-ARG.
FT DOMAIN 126 130 POLY-GLY.
FT DOMAIN 139 153 GLU/LYS-RICH.
SQ SEQUENCE 153 AA; 17804 MW; 291E24399159621E CRC64;

Query Match 64.2%; Score 95; DB 1; Length 153;
Best Local Similarity 72.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKKYALDASAL 25
DB 100 ERQIKWQNRRMKWKKESNLTSL 124
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RESULT 11
ID HXA7_HUMAN STANDARD; PRT; 230 AA.
AC P31268; O43368; O43486; O95655; O9NSC8; Q9UDM1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).
GN HXA7 OR HXA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Polakowska R., LaCelle P.T.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9023755; PubMed=9804983;
RA McIlhatton M.A., Bremner F.S., McMullin M.F., Maxwell A.P.,
RA Winter P.C., Lappin T.R.;
RT "Sequence characterisation and expression of homeobox Hox A7 in the
RT multi-potential erythroleukaemic cell line TF-1.";
RL Biochim. Biophys. Acta 1442:329-333(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Bradshaw H., Hinds K., Keppler D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=20369265; PubMed=10911612;
RA Kim M.H., Jin H., Seol E.Y., Yoo M., Park H.W.;
RT "Sequence analysis and tissue specific expression of human HOXA7.";
RL Mol. Biotechnol. 14:19-24(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE=Placenta;
RA Albrechtsen R., Wewer U.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-91 FROM N.A.
RA Cho M., Kim M.H., Hwang C.Y., Min W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 130-195 FROM N.A.
RA MEDLINE=90215256; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
RT "Organization of human class I homeobox genes.";
RL Genome 31:745-756(1989).
CC CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF026397; AAB94604.1; -
DR EMBL; AJ005814; CAAG0713.1; -
DR EMBL; AC004080; -; NOT ANNOTATED_CDS.
DR EMBL; AF032095; AAD01939.2; -
DR EMBL; U92543; AAD00727.1; -
DR EMBL; X84803; CAA59270.1; -

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EMBL; X84804; CAA59270.1; JOINED.

PIR; S15536; S15536.

HSSP; P02833; 9ANT.

TRANSFAC; T01705; -.

Genew; HGNC:5108; HOXA7.

MIM; 142950; -.

GO; GO:0003700; F:transcription factor activity; TAS.

InterPro; IPR001827; Antennapedia.

InterPro; IPR001356; Homeobox.

Pfam; PF00046; homeobox; 1.

PRINTS; PR00025; ANTENNAPEDIA.

PRINTS; PR00024; HOMEBOX.

ProDom; PD000010; Homeobox; 1.

SMART; SM00389; HOK; 1.

PROSITE; PS00032; ANTENNAPEDIA; 1.

PROSITE; PS00027; HOMEBOX_1; 1.

PROSITE; PS00071; HOMEBOX_2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;

Transcription regulation.

SITE 119 124 ANTP-TYPE HEXAPEPTIDE.

DNA_BIND 130 189 HOMEBOX.

DOMAIN 157 160 POLY-ARG.

DOMAIN 196 199 POLY-ALA.

DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).

DOMAIN 223 230 POLY-GLU.

CONFLICT 18 18 T -> A (IN REF. 3).

CONFLICT 75 76 DA -> RR (IN REF. 6).

CONFLICT 78 78 MISSING (IN REF. 5).

CONFLICT 174 174 I -> V (IN REF. 4).

CONFLICT 194 195 PT -> RL (IN REF. 5).

CONFLICT 195 195 T -> I (IN REF. 7).

CONFLICT 222 222 D -> Y (IN REF. 5).

SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 230;

Best Local Similarity 81.0%; Pred. No. 2.1e-07;

Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRNRMKWKKTALD 21

DB 171 ERQIKWFOQRNRMKWKKEHKD 191

RESULT 12

HXB5_XENLA

ID HXB5_XENLA STANDARD; PRT; 230 AA.

AC P09019;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein Hox-B5 (XlHbox-4) (Hox-1B) (Fragment).

GN HOXB5 OR XLHBOX4.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88157707; PubMed=2894634;

RA Fritz A., de Robertis E.M.;

RT "Xenopus homeobox-containing cDNAs expressed in early development.";

RL Nucleic Acids Res. 16:1453-1469(1988).

RN [2]

RP SEQUENCE OF 155-214 FROM N.A.

RX MEDLINE=86274626; PubMed=3015593;

RA Harvey R.P., Tabin C.J., Melton D.A.;

RT "Embryonic expression and nuclear localization of Xenopus homeobox

(Xhox) gene products.";

RL EMBO J. 5:1237-1244(1986).

CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF

A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH

SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EMBRYO.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC
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 CC
 CC EMBL; X07104; CAA30125.1; -;
 CC EMBL; M26883; AAA49755.1; -;
 CC PIR; S00592; S00592.
 CC HSP; P02833; ISAN.
 CC
 CC TRANSFAC; T03764; -;
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEOBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEOBOX 1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00071; HOMEOBOX 2; 1.
 CC KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC NON TER 1 1
 CC SITE 137 142 ANTP-TYPE HEXAPEPTIDE.
 CC DNA BIND 155 214 HOMEOBOX.
 CC SEQUENCE 230 AA; 25276 MW; AD040C030F95532B CRC64;
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 CC Query Match 64.2%; Score 95; DB 1; Length 230;
 CC Best Local Similarity 58.8%; Pred. No. 2.1e-07;
 CC Matches 20; Conservative 2; Mismatches 4; Indels 8; Gaps 1;
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 CC QY 1 DROIKIWFQNRMRKWKK-----TALDASALQ 26
 CC DB 196 ERQIKIWFQNRMRKWKKNLKSMSLATGSSAFQ 229
 CC
 CC RESULT 13
 CC HXC6 NOTVI STANDARD; PRT; 234 AA.
 CC AC P14858; P14857;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-APR-1990 (Rel. 14, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Homeobox protein Hox-C6 (NvHox-1) (FH-2).
 CC GN HXC6 OR NVHox1.
 CC OS Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 CC OC Notoththalmus.
 CC OX NCBI_TaxID=8316;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=89210814; PubMed=2907476;
 CC RA Savard P., Gates P.B., Brookes J.P.;
 CC RT "Position dependent expression of a homeobox gene transcript in
 CC relation to amphibian limb regeneration.";
 CC RL ENBO J. 7:4275-4282(1988).
 CC RN [2]
 CC RP SEQUENCE OF 131-234 FROM N.A.
 CC RX MEDLINE=90091821; PubMed=2574663;
 CC RA Tabin C.J.;
 CC RT "Isolation of potential vertebrate limb-identity genes.";
 CC RL Development 105:813-820(1989).
 CC CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC
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 CC
 CC EMBL; X13957; CAA32139.1; -;
 CC EMBL; X16848; CAA34745.1; -;
 CC PIR; S02014; S02014.
 CC HSP; P02833; 9ANT.
 CC TRANSFAC; T01747; -;
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEOBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEOBOX 1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00071; HOMEOBOX 2; 1.
 CC KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
 CC DNA BIND 141 200 HOMEOBOX.
 CC SEQUENCE 234 AA; 26901 MW; EA15EDD91ED294B0 CRC64;
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 CC Query Match 64.2%; Score 95; DB 1; Length 234;
 CC Best Local Similarity 72.0%; Pred. No. 2.1e-07;
 CC Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 CC
 CC QY 1 DROIKIWFQNRMRKWKKTALDASAL 25
 CC DB 182 ERQIKIWFQNRMRKWKESNLSTL 206
 CC
 CC RESULT 14
 CC HXC6 HUMAN STANDARD; PRT; 235 AA.
 CC AC P09630;
 CC DT 01-MAR-1989 (Rel. 10, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25).
 CC GN HXC6 OR HOX3C.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A. (ISOFORM 1).
 CC RX MEDLINE=87260899; PubMed=2885844;
 CC RA Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,
 CC RA Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,
 CC RA Peschle C.;
 CC RT "Two human homeobox genes, c1 and c8: structure analysis and
 CC expression in embryonic development.";
 CC RL Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
 CC RN [2]
 CC RP SEQUENCE FROM N.A. (ISOFORM 1).
 CC RX MEDLINE=88262550; PubMed=2898768;
 CC RA Simeone A., Pannese M., Acampora D., D'Esposito M., Boncinelli E.;
 CC RT "At least three human homeoboxes on chromosome 12 belong to the same
 CC transcription unit.";
 CC RL Nucleic Acids Res. 16:5379-5390(1988).
 CC RN [3]
 CC RP SEQUENCE FROM N.A. (ISOFORM 2).
 CC RX MEDLINE=97024425; PubMed=8870653;

RA Chariot A., Castronovo V., Le P., Gillet C., Sobel M.E., Gielen J.;
 RT "Cloning and expression of a new HOXC6 transcript encoding a
 RL repressing protein.";
 RN Biochem. J. 319:91-97(1996).
 RN [4]
 RP SEQUENCE OF 141-206 FROM N.A.
 RX MEDLINE=90215256; PubMed=2576652;
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simone A.;
 RT "Organization of human class I homeobox genes.";
 RL Genome 31:745-756(1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P09630-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P09630-2; Sequence=VSP_002392;
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 CC EMBL; S82986; AAB46892.1; --
 CC EMBL; M16938; AAA36007.1; --
 CC EMBL; B28030; WJHU3C.
 CC HSP; P02833; 9ANT.
 CC TRANSFAC; T01742; --
 CC Genew; HGNC:5128; HOXC6.
 CC MIM; 142972; --
 CC GO; GO:0003714; F:transcription co-repressor activity; TAS.
 CC GO; GO:0007275; P:development; TAS.
 CC GO; GO:0006357; P:regulation of transcription from Pol II pro. . . ; TAS.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00071; HOMEBOX 2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW transcription regulation; Alternative splicing.
 FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 141 200 HOMEBOX.
 FT DOMAIN 168 171 POLY-ARG.
 FT DOMAIN 208 212 POLY-GLY.
 FT DOMAIN 221 235 GLU/LYS-RICH.
 FT VARSPPLIC 1 82 Missing (in isoform 2).
 FT CONFLICT 218 218 M -> L (IN REF. 3).
 FT SEQUENCE 235 AA; 26933 MW; BD68870347CB71C0 CRC64;
 Query Match 64.2%; Score 95; DB 1; Length 235;
 Best Local Similarity 72.0%; Pred. No. 2.1e-07;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DRQIKWIFQNRMRKWKKTALDASAL 25
 DB 182 ERQIKWIFQNRMRKWKKSNTSTL 206
 RESULT 15

HOXC6 MOUSE
 ID -HXC6_MOUSE STANDARD; PRT; 235 AA.
 AC P10629; Q61683;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C6 (Hox-3.3) (Hox-6.1).
 GN HOXC6 OR HOXC-6 OR HOXC-3.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94131843; PubMed=7905473;
 RA Shimeld S.M., Gaunt S.J., Coletta P.L., Geada A.M., Sharpe P.T.;
 RT "Spatial localisation of transcripts of the Hox-C6 gene.";
 RL J. Anat. 183:515-523(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92102952; PubMed=1684715;
 RA Coletta P.L., Shimeld S.M., Chaudhuri C., Mueller U., Clarke J.P.,
 RA Sharpe P.T.;
 RT "Characterisation of the murine Hox-3.3 gene and its promoter.";
 RL Mech. Dev. 35:129-142(1991).
 RN [3]
 RP SEQUENCE OF 15-235 FROM N.A.
 RC TISSUE=Bone marrow, and Spleen;
 RX MEDLINE=88329001; PubMed=2901346;
 RA Kongsewan K., Webb E., Housiaux P., Adams J.M.;
 RT "Expression of multiple homeobox genes within diverse mammalian
 RL haemopoietic lineages.";
 RL EMBO J. 7:2131-2138(1988).
 RN [4]
 RP SEQUENCE OF 131-235 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=88328811; PubMed=2458223;
 RA Sharpe P.T., Miller J.R., Evans E.P., Burtenshaw M.D., Gaunt S.J.;
 RT "Isolation and expression of a new mouse homeobox gene.";
 RL Development 102:397-407(1988).
 RN [5]
 RP SEQUENCE OF 133-235 FROM N.A.
 RX MEDLINE=89357988; PubMed=2570032;
 RA Schughart K., Pravtcheva D., Newman M.S., Hunihan L.W., Jiang Z.,
 RA Ruddle F.H.;
 RT "Isolation and regional localization of the murine
 RL homeobox-containing gene Hox-3.3 to mouse chromosome region 15E.";
 RL Genomics 5:76-83(1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=PRII;
 CC IsoId=P10629-1; Sequence=Displayed;
 CC Name=PRI;
 CC IsoId=P10629-2; Sequence=VSP_002393;
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
 CC -----
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 CC -----
 CC EMBL; J03074; AAA37832.1; --
 CC EMBL; M35986; AAA37854.1; --
 CC EMBL; X16511; CAA34518.1; --
 CC EMBL; X16510; CAA34517.1; --
 CC EMBL; S74185; AAB20717.1; --

DR EMBL; X12504; CAA31022.1; -
 DR EMBL; X12504; CAA31023.1; -
 DR EMBL; X15838; CAA34737.1; -
 DR PIR; A32167; A32167.
 DR PIR; A56568; A56568.
 DR PIR; S00987; WJMSX6.
 DR HSP; P02833; 9ANT.
 DR TRANSFAC; T01743; -
 DR TRANSFAC; T01744; -
 DR MGD; MGI:96197; Hoxc6.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00025; ANTENNAPEDIA.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation; Alternative splicing.
 FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 141 200 HOMEBOX.
 FT DOMAIN 221 235 GLU/LYS-RICH.
 FT VARSPLIC 1 82 Missing (in isoform PRI).
 FT FTID=VSP_002393.
 FT CONFLICT 15 18 AGGQ -> QGRP (IN REF. 3).
 FT CONFLICT 131 131 S -> N (IN REF. 4).
 FT CONFLICT 192 192 R -> A (IN REF. 4).
 FT CONFLICT 228 229 TE -> QK (IN REF. 1 AND 2).
 SQ SEQUENCE 235 AA; 26915 MW; BD695C7347CB71C0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 235;
 Best Local Similarity 72.0%; Pred. No. 2.le-07;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRQIKWFOQRNRMKWKKTALDASAL 25
 Db 182 ERQIKWFOQRNRMKWKESNLTSTL 206

Search completed: February 18, 2004, 14:28:15
 Job time : 17.5789 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 81.0526 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFQNRKWKTKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_nhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.5	74.7	274	5 Q9XYT7	Q9XYT7 cassiopea x
2	101.5	68.6	627	5 Q95YH8	Q95YH8 daphnia mag
3	100	67.6	108	11 Q8JZW2	Q8JZW2 mus musculus
4	98	66.2	93	5 Q9U9Z5	Q9U9Z5 lingua ung
5	97	65.5	60	5 Q26375	Q26375 styela clav
6	97	65.5	90	5 Q8I7C9	Q8I7C9 ciona intes
7	97	65.5	181	5 Q26611	Q26611 styela plic
8	97	65.5	194	5 Q26478	Q26478 styela clav
9	97	65.5	435	5 Q8I7C8	Q8I7C8 ciona intes
10	96.5	65.2	231	13 Q9PVM4	Q9PVM4 brachydanio
11	96	64.9	101	13 Q9PSD5	Q9PSD5 gallus gall
12	95.5	64.5	82	13 Q9PVS0	Q9PVS0 oryzias lat
13	95	64.2	219	13 Q9OVZ9	Q9OVZ9 gallus gall
14	94.5	63.9	43	13 Q57359	Q57359 brachydanio
15	94.5	63.9	80	5 Q05008	Q05008 artemia san
16	94.5	63.9	230	11 Q9CZV0	Q9CZV0 mus musculus

17	94.5	63.9	275	13 Q8AWY7	Q8AWY7 brachydanio
18	94.5	63.9	276	13 Q8JH53	Q8JH53 brachydanio
19	94.5	63.9	276	13 Q9PVM0	Q9PVM0 brachydanio
20	94.5	63.9	348	5 Q8WRG6	Q8WRG6 artemia san
21	94	63.5	39	13 Q57368	Q57368 brachydanio
22	94	63.5	46	13 Q9PVR9	Q9PVR9 oryzias lat
23	94	63.5	51	5 Q27413	Q27413 ctenodrilus
24	94	63.5	51	5 Q23743	Q23743 ctenodrilus
25	94	63.5	51	5 Q26407	Q26407 ctenodrilus
26	94	63.5	57	13 Q9PVR8	Q9PVR8 oryzias lat
27	94	63.5	58	5 Q9I188	Q9I188 priapulus c
28	94	63.5	58	5 Q25208	Q25208 junonia coe
29	94	63.5	58	13 Q57362	Q57362 brachydanio
30	94	63.5	59	5 Q8WRM9	Q8WRM9 lithobius a
31	94	63.5	59	5 Q9NB42	Q9NB42 anopheles g
32	94	63.5	59	13 Q9PVR5	Q9PVR5 oryzias lat
33	94	63.5	60	5 Q77143	Q77143 archegozete
34	94	63.5	60	5 Q77139	Q77139 archegozete
35	94	63.5	60	13 Q8QGL5	Q8QGL5 petromyzon
36	94	63.5	60	13 Q8QGL6	Q8QGL6 petromyzon
37	94	63.5	60	13 Q8QGL2	Q8QGL2 petromyzon
38	94	63.5	60	13 Q8QGL8	Q8QGL8 petromyzon
39	94	63.5	60	13 Q8QGL7	Q8QGL7 petromyzon
40	94	63.5	61	5 Q27910	Q27910 polyandroca
41	94	63.5	63	5 Q77138	Q77138 archegozete
42	94	63.5	63	5 Q8MXB2	Q8MXB2 holopneuste
43	94	63.5	66	13 Q57356	Q57356 brachydanio
44	94	63.5	69	5 Q9U9T4	Q9U9T4 nereis vire

ALIGNMENTS

RESULT 1

Q9XYT7 PRELIMINARY; PRT; 274 AA.
ID Q9XYT7
AC Q9XYT7; (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Scx-3 homeodomain protein (Fragment).
GN SCOX-3.
OS Cassiopea xamachana.
OC Eukaryota; Metazoa; Cnidaria; Scyphozoa; Rhizostomaeae; Cassiopeidae;
OC Cassiopea.
OX NCBI_TaxID=12993;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuhn K., Streit B., Schierwater B.;
RT "Isolation of Hox genes from the scyphozoan Cassiopeia xamachana:
RT Implications for the early evolution of Hox genes.";
RL J. Exp. Zool. 0:0-0(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF124593; AAD32577.1; -;
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 274 AA; 31041 MW; 58BE91F6E540C3A9 CRC64;

Query Match 74.7%; Score 110.5; DB 5; Length 274;
Best Local Similarity 67.7%; Pred. No. 1.7e-08;
Matches 21; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

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QY 1 DROIKIWFQNRMMKWK--TALDASALQTE 28
:|||||
Db 182 ERQIKIWFQNRMMKWKKGTTSDANLEERE 212

RESULT 2
Q95YH8 PRELIMINARY; PRT; 627 AA.
AC Q95YH8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Homeotic protein.
OS Daphnia magna.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Diplostraca;
OC Cladocera; Anomopoda; Daphniidae; Daphnia.
OX NCBI_TaxID=35525;
RN [1]
RP SEQUENCE FROM N.A.
RA Shiga Y., Yasumoto R., Havaashi S., Yamagata H.;
RT "Functional diversification of homeotic protein Antennapedia in
  arthropod evolution.";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB069680; BAB64346.1; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 627 AA; 69425 MW; A5A7962761CB5D10 CRC64;

Query Match 68.6%; Score 101.5; DB 5; Length 627;
Best Local Similarity 69.0%; Pred. No. 9.2e-07;
Matches 20; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 DROIKIWFQNRMMKWK---KTALDASALQ 26
:|||||
Db 587 ERQIKIWFQNRMMKWKKNKAKLDAGCLE 615

RESULT 3
Q8JZW2 PRELIMINARY; PRT; 108 AA.
AC Q8JZW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Tissue-Colon;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036986; AAH36986.1; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambrepres.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.

QY 1 DROIKIWFQNRMMKWKKTALDASALQ 27
:|||||
Db 49 ERQIKIWFQNRMMKWKKEHQSAPT 75

RESULT 4
Q9U9Z5 PRELIMINARY; PRT; 93 AA.
AC Q9U9Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sex combs reduced homeodomain protein (Fragment).
OS Lingula unguis.
OC Eukaryota; Metazoa; Brachiopoda; Linguliformea; Lingulata; Lingulida;
OC Linguloides; Lingulidae; Lingula.
OX NCBI_TaxID=7574;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99318125; PubMed=10391241;
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution.";
RL Nature 399:772-776(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF144674; AAD45589.1; -.
DR HSP; P02833; 1SAN.
DR TRANSFAC; T03872; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambrepres.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

Query Match 66.2%; Score 98; DB 5; Length 93;
Best Local Similarity 67.9%; Pred. No. 4.3e-07;
Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKWKKTALDASALQTE 28
:|||||
Db 48 ERQIKIWFQNRMMKWKKEQKLAHLTKTE 75

RESULT 5
Q26375 PRELIMINARY; PRT; 60 AA.
AC Q26375;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DNA binding protein AHOX2 (Fragment).
GN AHOX2.
OS Styela clava (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
```

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RX MEDLINE=95011617; PubMed=7926803;
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like homeobox gene in the ascidians
RT Styela clava and S. plicata.";
RL Gene 147:219-222(1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; S73920; AAB33061.2; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 7630 MW; F506301E9679BA25 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 60;
Best Local Similarity 94.1%; Pred. No. 3.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRKWK 17
Db 42 DROVKIWFQNRMRKWK 58

RESULT 6
Q817C9 PRELIMINARY; PRT; 90 AA.
AC Q817C9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative homeobox protein Hox6/7 (Fragment).
GN Hox6/7.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OC NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristatore F., Di Gregorio A., Aniello F., Branno M.,
RA Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
RT Ciona intestinalis.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ35674; CAU59670.1; -.
KW Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 90 AA; 11352 MW; CAAAD6B261FE908E CRC64;

Query Match 65.5%; Score 97; DB 5; Length 90;
Best Local Similarity 94.3%; Pred. No. 5.9e-07;
Matches 18; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRKWKTDASALQTE 28
Db 57 ERQIKIWFQNRMRKWKENKDIAESNNE 84

RESULT 7
Q26611 PRELIMINARY; PRT; 181 AA.
AC Q26611;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Homeobox protein (Fragment).
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OS Styela plicata (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OC NCBI_TaxID=7726;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
RT Styela clava and plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05600; AAL16288.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepreser.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 181 181
SQ SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 181;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRKWK 17
Db 80 DROVKIWFQNRMRKWK 96

RESULT 8
Q26478 PRELIMINARY; PRT; 194 AA.
ID Q26478;
AC Q26478;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Homeobox protein (Fragment).
OS Styela clava (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Styela.
OC NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
RT Styela clava and plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05571; AAL16226.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepreser.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 1
FT NON_TER 194 AA; 21886 MW; 8AD1B15B3E4800BC CRC64;

Query Match 65.5%; Score 97; DB 5; Length 194;
```

Best Local Similarity 94.1%; Pred. No. 1.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMKWK 17
|||:|||||
Db 52 DRQIKWFQNRMKWK 68

RESULT 9
Q817C8 PRELIMINARY; PRT; 435 AA.
AC Q817C8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative homeobox protein Hox10.
GN HOX10.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
[1]
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristatore F., Di Gregorio A., Aniello F., Branno M.,
RA Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
RT Ciona intestinalis.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535675; CAD59671.1; -;
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 435 AA; 48739 MW; D8D0F579C02BC9E2 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 435;
Best Local Similarity 94.1%; Pred. No. 3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMKWK 17
|||:|||||
Db 295 DRQIKWFQNRMKWK 311

RESULT 10
Q9PWM4 PRELIMINARY; PRT; 231 AA.
AC Q9PWM4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Homeobox protein.
GN HOXC6A.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99051425; PubMed=9831563;
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,
RA Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,
RA Postlethwait J.;
RT "Zebrafish hox clusters and vertebrate genome evolution.";
RL Science 282:1711-1714(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF071265; AAD15958.1; -;
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T03667; -;
DR ZFIN; ZDB-GENE-990415-113; hoxc6a.
DR InterPro; IPR001827; Antennapedia.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.

DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 231 AA; 26733 MW; 65164A13541D7E8A CRC64;

Query Match 65.2%; Score 96.5; DB 13; Length 231;
Best Local Similarity 69.0%; Pred. No. 1.8e-06;
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQIKWFQNRMKWK-TALDASALOTE 28
:|||||:|||||:|:|
Db 183 ERQIKWFQNRMKWKETNLSTVPGTE 211

RESULT 11
Q9PSD5 PRELIMINARY; PRT; 101 AA.
AC Q9PSD5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE HOXC-6 product (HOXC-6 protein).
GN HOXC-6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RC MEDLINE=95151548; PubMed=7848839;
RA Gaunt S.J.;
RT "Conservation in the Hox code during morphological evolution.";
RL Int. J. Dev. Biol. 38:549-552(1994).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; X80114; CAB94151.1; -;
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 101 AA; 11592 MW; 9837DE0AAB85546D CRC64;

Query Match 64.9%; Score 96; DB 13; Length 101;
Best Local Similarity 72.0%; Pred. No. 9.4e-07;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWFQNRMKWK-TALDASAL 25
:|||||:|||||:|:|
Db 49 ERQIKWFQNRMKWKESNLSTL 73

RESULT 12
Q9PVS0 PRELIMINARY; PRT; 82 AA.
AC Q9PVS0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE HOXB5A (Fragment).
GN HOXB5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medakafish *Oryzias latipes*.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB026959; BAA86242.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
SQ SEQUENCE 82 AA; 9939 MW; 6B6828D280511888 CRC64;
Query Match 64.5%; Score 95.5; DB 13; Length 82;
Best Local Similarity 60.0%; Pred. No. 9e-07; Indels 9; Gaps 1;
Matches 21; Conservative 1; Mismatches 4;
QY 1 DRQIKWQNRMRKWKK-----TALDASALQ 26
:|||||
DB 47 ERQIKWQNRMRKWKKNKVKMSLTAPGASHFQ 81
:|||||
RESULT 13
Q90VZ9 PRELIMINARY; PRT; 219 AA.
AC Q90VZ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hoxa-7 protein (Homeodomain transcription factor HoxA-7).
GN HoxA-7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21255551; Pubmed=11357191;
RA Gaunt S.J.;
RT "Gradients and forward spreading of vertebrate Hox gene expression
detected using a Hox/lacZ transgene.";
RL Dev. Dyn. 221:26-36(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Oberg K.C., Eichele G.;
RT "Hox gene expression and regulation in the presumptive wing region of
the chick lateral plate mesoderm (Abstract # 286).";
RL Dev. Biol. 210:228-228(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Oberg K.C., Pira C.U., Creamer D.H., Revelli J.-P., Eichele G.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AJ291729; CAC37629.1; -.
DR EMBL; AF408695; AAL01899.1; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.

KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 219 AA; 24952 MW; 4BAE9046D52C0705 CRC64;
Query Match 64.2%; Score 95; DB 13; Length 219;
Best Local Similarity 70.8%; Pred. No. 2.9e-06;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DRQIKWQNRMRKWKKTALDASA 24
:|||||
DB 170 ERQIKWQNRMRKWKKEHKESS 193
:|||||
RESULT 14
O57359 PRELIMINARY; PRT; 43 AA.
AC O57359;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hoxa5 protein (Fragment).
GN HOXB5 OR HOXA5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
expression patterns in the trunk.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14526; CAA74861.1; -.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;
Query Match 63.9%; Score 94.5; DB 13; Length 43;
Best Local Similarity 67.9%; Pred. No. 6.5e-07;
Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
QY 1 DRQIKWQNRMRKWKKTALDASALQ 27
:|||||
DB 9 ERQIKWQNRMRKWKKNKLSMSLT 36
:|||||
RESULT 15
Q05008 PRELIMINARY; PRT; 80 AA.
AC Q05008;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Antp protein (Fragment).
GN ANTP.
OS Artemia salinifera (Brine shrimp) (Artemia franciscana).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=6661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=North arm of Great Salt Lake;
RA Averoof M., Akam M.;
RT "HOM/HOX genes in a crustacean: implication for the origin of insect
and crustacean body plans.";

RL Curr. Biol. 3:73-78(1993).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; X70077; CAA49682.1; -;
 DR HSSP; P02833; 9ANT.

DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON TER 1
 SQ SEQUENCE 80 AA; 9878 MW; 48472705C0EDFCB7 CRC64;

Query Match 63.9%; Score 94.5; DB 5; Length 80;
 Best Local Similarity 64.3%; Pred. No. 1.2e-06;
 Matches 18; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 DROIKIWFQNRMMKWK--KTALDASAL 25
 :|||||:|||||:|:|:
 Db 42 ERQIKIWFQNRMMKWKENKSKVDGCL 69

Search completed: February 18, 2004, 14:36:01
 Job time : 81.0526 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 30.7632 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKIWFQNRMRMKWKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	69.6	81	2 B29585	homeotic protein H
2	103	69.6	96	2 A05266	homeotic protein H
3	103	69.6	97	2 C27176	homeotic protein H
4	103	69.6	224	2 S26400	homeotic protein H
5	103	69.6	224	2 A31324	homeotic protein H
6	100	67.6	105	2 A27471	homeotic protein H
7	100	67.6	119	2 A03314	homeotic protein H
8	100	67.6	229	2 A28329	homeotic protein H
9	99	66.9	75	2 I51341	homeo box protein
10	98	66.2	86	2 S08303	homeotic protein H
11	97	65.5	60	2 PC2399	antennapedia-like
12	97	65.5	60	2 PC2400	antennapedia-like
13	96.5	65.2	96	2 S08639	homeotic protein z
14	96	64.9	234	2 S00992	homeotic protein H
15	95	64.2	66	2 S15536	homeotic protein H
16	95	64.2	103	2 A32167	homeotic protein H
17	95	64.2	153	1 WJHU3C	homeotic protein H
18	95	64.2	153	1 WJMSX6	homeotic protein H
19	95	64.2	230	2 S00592	homeotic protein H
20	95	64.2	234	1 S02014	homeotic protein H
21	95	64.2	235	2 S56568	homeotic protein H
22	95	64.2	235	2 S72429	homeotic protein H
23	95	64.2	242	1 A39164	homeotic protein H
24	94.5	63.9	118	2 A24777	homeotic protein H
25	94.5	63.9	118	2 JT0273	homeotic protein H
26	94.5	63.9	118	2 B24777	homeotic protein M
27	94.5	63.9	269	1 A43551	homeotic protein H
28	94.5	63.9	269	2 A45578	homeotic protein H
29	94.5	63.9	275	1 WJZPX2	homeotic protein H

30	94	63.5	33	2 S57235	antennapedia prote
31	94	63.5	42	2 I65241	homeotic protein H
32	94	63.5	45	2 PC1216	homeotic protein D
33	94	63.5	48	2 I51439	homeobox protein -
34	94	63.5	66	2 S15538	homeotic protein H
35	94	63.5	71	2 JC1161	homeotic protein H
36	94	63.5	71	2 A60084	homeotic protein H
37	94	63.5	74	2 D34510	homeotic protein H
38	94	63.5	75	2 S58852	homeotic protein S
39	94	63.5	76	2 C43559	homeotic protein R
40	94	63.5	78	2 I51342	homeo box protein
41	94	63.5	81	2 S47605	homeotic protein H
42	94	63.5	82	2 S08302	homeotic protein H
43	94	63.5	83	2 S47603	homeotic protein H
44	94	63.5	83	2 S50066	homeotic protein H
45	94	63.5	86	2 A34510	homeotic protein H

ALIGNMENTS

RESULT 1

B29585

homeotic protein Hox 2.2 precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997

C;Accession: B29585

R;Lonal, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.

DNA 6, 409-418, 1987

A;Title: New murine homeoboxes: structure, chromosomal assignment, and differential exp

A;Reference number: A29585; MUID:88054465; PMID:2890503

A;Accession: B29585

A;Molecule type: DNA

A;Residues: 1-81 <LON>

A;Cross-references: GB:M18167

A;Note: the authors translated the codon CAG for residue 69 as Glu

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;4-60/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 81;
Best Local Similarity 70.0%; Pred. No. 4.5e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DRQIKIWFQNRMRMKWKKTALDASALQTE 28
Db 44 EROIKIWFQNRMRMKWKKSLSASQLSAE 73

RESULT 2

A05266

homeotic protein Hox B6 - human (fragment)

N;Alternate names: homeotic protein Hox 2B; homeotic protein Hu2

C;Species: Homo sapiens (man)

C;Date: 05-Jun-1987 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997

C;Accession: A05266; S15537

R;Levine, M.; Rubin, G.M.; Tjian, R.

Cell 38, 667-673, 1984

A;Title: Human DNA sequences homologous to a protein coding region conserved between ho

A;Reference number: A05265; MUID:85024858; PMID:6091895

A;Accession: A05266

A;Molecule type: DNA

A;Residues: 1-96 <LEV>

A;Cross-references: EMBL:K02571

A;Note: this reading frame extends between two stop codons and does not begin with a st

R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; St

Genome 31, 745-756, 1989

A;Title: Organization of human class I homeobox genes.

A;Reference number: S15036; MUID:90215256; PMID:2576652

A;Accession: S15537

A;Molecule type: DNA

A;Residues: 18-19,'R',21-83 <BON>

C;Genetics:

```
A;Gene: GDB:HOXB6
A;Cross-references: GDB:120659; OMIM:142961
A;Map position: 17q21.3-17q21.3
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;19-75/Domain: homeobox homology <HOX>

Query Match          69.6%; Score 103; DB 2; Length 96;
Best Local Similarity 70.0%; Pred. No. 5.3e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWQNRRMKWKKTA--LDASALQTE 28
   :|||||:|||||:|||||:
Db 59 ERQIKWQNRRMKWKKESKLSASQLSAE 88

RESULT 3
homeotic protein Hox 2.2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C;Accession: C27176
R;Schughart, K.; Utset, M.F.; Awgulewitsch, A.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
A;Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary
A;Reference number: A27176; MUID:88085193; PMID:2891608
A;Accession: C27176
A;Molecule type: DNA
A;Residues: 1-97 <HAR>
A;Cross-references: GB:M18401; NID:g193936; PIDN:AAC27130.1; PID:g3335322
C;Genetics:
A;Gene: Hox-2.2
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;20-76/Domain: homeobox homology <HOX>

Query Match          69.6%; Score 103; DB 2; Length 97;
Best Local Similarity 70.0%; Pred. No. 5.4e-08;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWQNRRMKWKKTA--LDASALQTE 28
   :|||||:|||||:|||||:
Db 60 ERQIKWQNRRMKWKKESKLSASQLSAE 89

RESULT 4
homeotic protein Hox 2.2 (variant 1) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
C;Accession: S26400; S26401
R;Shen, W.; Detmer, K.; Simonitch-Eason, T.A.; Lawrence, H.J.; Largman, C.
Nucleic Acids Res. 19, 539-545, 1991
A;Title: Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells
A;Reference number: S26400; MUID:91187672; PMID:1672751
A;Accession: S26400
A;Molecule type: DNA
A;Residues: 1-224 <SHE>
A;Cross-references: EMBL:X58431; NID:g32369; PIDN:CAA41335.1; PID:g32370
A;Experimental source: tissue-type placenta
A;Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60
A;Accession: S26401
A;Molecule type: DNA
A;Residues: 1-139, 'E' <SH2>
A;Cross-references: EMBL:X58431; NID:g32369; PIDN:CAA41336.1; PID:g32371
A;Experimental source: tissue-type placenta
A;Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60
C;Genetics: 139/1
A;Introns: 139/1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation
F;147-203/Domain: homeobox homology <HOX>

Query Match          69.6%; Score 103; DB 2; Length 224;
Best Local Similarity 70.0%; Pred. No. 1.3e-07;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWQNRRMKWKKTA--LDASALQTE 28
   :|||||:|||||:|||||:
Db 187 ERQIKWQNRRMKWKKESKLSASQLSAE 216

RESULT 5
homeotic protein Hox 2.2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C;Accession: A31324
R;Schughart, K.; Utset, M.F.; Awgulewitsch, A.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988
A;Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
A;Reference number: A31324; MUID:88289762; PMID:2899893
A;Accession: A31324
A;Molecule type: mRNA
A;Residues: 1-224 <SCH>
A;Cross-references: GB:J03782; NID:g193929; PIDN:AAA37843.1; PID:g387203
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;147-203/Domain: homeobox homology <HOX>

Query Match          69.6%; Score 103; DB 2; Length 224;
Best Local Similarity 70.0%; Pred. No. 1.3e-07;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWQNRRMKWKKTA--LDASALQTE 28
   :|||||:|||||:|||||:
Db 187 ERQIKWQNRRMKWKKESKLSASQLSAE 216

RESULT 6
homeotic protein R5 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
C;Accession: A27471
R;Palzon, M.; Sanderson, N.; Chung, S.Y.
Gene 54, 23-32, 1987
A;Title: Cloning and expression of rat homeo-box-containing sequences.
A;Reference number: A91576; MUID:87277429; PMID:2886401
A;Accession: A27471
A;Molecule type: DNA
A;Residues: 1-105 <PAL>
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;6-62/Domain: homeobox homology <HOX>

Query Match          67.6%; Score 100; DB 2; Length 105;
Best Local Similarity 70.4%; Pred. No. 1.6e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWQNRRMKWKKTA--LDASALQTE 27
   :|||||:|||||:|||||:
Db 46 ERQIKWQNRRMKWKKESKLSASQLSAE 72

RESULT 7
homeotic protein m6 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997
C;Accession: A03314; S14043
R;Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
Nature 314, 713-718, 1985
A;Title: Structural analysis of murine genes containing homeo box sequences and their
A;Reference number: A03314; MUID:85188311; PMID:2986010
```


A;Accession: A03314
A;Molecule type: DNA
A;Residues: 1-119 <COL>
R;Breier, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.
EMBO J. 5, 2209-2215, 1986
A;Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation
A;Reference number: S13785; MUID:87053860; PMID:2877873
A;Accession: S14043
A;Molecule type: DNA
A;Residues: 19-48, 'RI', 51-87 <BRE>
C;Genetics:
A;Gene: m6
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;20-76/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 119;
Best Local Similarity 70.4%; Pred. No. 1.8e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKKKTALDASALQT 27
:|||||
Db 60 ERQIKIWFQNRMRMKKKEHDESOAPT 86

RESULT 8
A28329
homeotic protein Hox A7 - mouse
N;Alternate names: homeotic protein Hox 1.1; m6 homeotic protein
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C;Accession: A28329; I49131
R;Kessel, M.; Schulze, F.; Fibi, M.; Gruss, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987
A;Title: Primary structure and nuclear localization of a murine homeodomain protein.
A;Reference number: A28329; MUID:87260976; PMID:2885847
A;Accession: A28329
A;Molecule type: mRNA
A;Residues: 1-229 <RES>
A;Cross-references: GB:M17192; NID:g193906; PIDN:AAA37833.1; PID:g309313
R;Parikh, H.; Shah, S.; Hilt, D.; Peterkofsky, A.
Gene 154, 237-242, 1995
A;Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.
A;Reference number: I49131; MUID:95197009; PMID:7890170
A;Accession: I49131
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-42, 'GAG', 46-229 <RES>
A;Cross-references: EMBL:U15972; NID:g664757; PIDN:AAC52160.1; PID:g664758
C;Genetics:
A;Gene: Hoxa7
A;Introns: 126/1
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;130-186/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 229;
Best Local Similarity 70.4%; Pred. No. 3.6e-07;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKKKTALDASALQT 27
:|||||
Db 170 ERQIKIWFQNRMRMKKKEHDESOAPT 196

RESULT 9
I51341
homeo box protein - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C;Accession: I51341
R;Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988

A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlan
A;Reference number: I51341; MUID:88226009; PMID:2897318
A;Accession: I51341
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-75 <FOO>
A;Cross-references: GB:M19903; NID:g213797; PIDN:AAA49559.1; PID:g213798
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>

Query Match 66.9%; Score 99; DB 2; Length 75;
Best Local Similarity 75.0%; Pred. No. 1.6e-07;
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKKKTALDASA 24
:|||||
Db 42 ERQIKIWFQNRMRMKKKHDESS 65

RESULT 10
S08303
homeotic protein Hox 2.2 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C;Accession: S08303
R;Wedden, S.E.; Pang, K.; Eichele, G.
Development 105, 639-650, 1989
A;Title: Expression pattern of homeobox-containing genes during chick embryogenesis.
A;Reference number: S08302; MUID:90126373; PMID:2575515
A;Accession: S08303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WED>
A;Cross-references: EMBL:X16847
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;10-66/Domain: homeobox homology <HOX>

Query Match 66.2%; Score 98; DB 2; Length 86;
Best Local Similarity 66.7%; Pred. No. 2.6e-07;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DROIKIWFQNRMRMKK--TALDASALQTE 28
:|||||
Db 50 ERQIKIWFQNRMRMKKENKLSSSQISAE 79

RESULT 11
PC2399
antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)
C;Species: Styela clava
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
C;Accession: PC2399
R;Ge, T.; Lee, H.; Tomlinson, C.R.
Gene 147, 219-222, 1994
A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c
A;Reference number: PC2399; MUID:95011617; PMID:7926803
A;Accession: PC2399
A;Molecule type: DNA
A;Residues: 1-60 <GET>
A;Cross-references: GB:S73920; NID:g693714; PIDN:AAB33061.2; PID:g7387472
A;Note: The authors translated the codon ATT for residue 47 as Glu
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>

Query Match 65.5%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. No. 2.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKK 17
|||||

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Db          42 DRQKIFQNRMRMKWK 58

RESULT 12
PC2400
Antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)
C:Species: Styela plicata
C>Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997
C:Accession: PC2400
R:Ge, T.; Lee, H.; Tomlinson, C.R.
Gene 147, 219-222, 1994
A:Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela cl
A:Reference number: PC2399; MUID:95011617; PMID:7926803
A:Accession: PC2400
A:Molecule type: DNA
A:Residues: 1-60 <GET>
A:Note: The authors translated the codon ATA for residue 47 as Glu
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>

Query Match      65.5%; Score 97; DB 2; Length 60;
Best Local Similarity 94.1%; Pred. No. 2.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQKIFQNRMRMKWK 17
|||:|||||
Db 42 DRQKIFQNRMRMKWK 58

RESULT 13
S08639
homeotic protein zf-61 - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: S08639
R:Niolland, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A:Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory i
A:Reference number: S08639; MUID:90151628; PMID:1968004
A:Accession: S08639
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <NTO>
A:Cross-references: EMBL:X17266; NID:g62538; PIDN:CAA35170.1; PID:e16657; PID:gl334622
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;8-64/Domain: homeobox homology <HOX>

Query Match      65.2%; Score 96.5; DB 2; Length 96;
Best Local Similarity 69.0%; Pred. No. 4.8e-07;
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQKIFQNRMRMKWK-TALDASALQTE 28
|||:|||||
Db 48 ERQKIFQNRMRMKWKETNLSTVPGTE 76

RESULT 14
S00992
homeotic protein Hox 1 - African clawed frog
N:Alternate names: development-controlling protein; homeotic protein AC1; homeotic prote
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 11-Jan-2002
C:Accession: S00992; A03316; S00590; T01066
R:Cho, K.W.Y.; Goetz, J.; Wright, C.V.E.; Fritze, A.; Hardwicke, J.; de Robertis, E.M.
EMBO J. 7, 2139-2149, 1988
A:Title: Differential utilization of the same reading frame in a Xenopus homeobox gene e
A:Reference number: S00991; MUID:88329002; PMID:29011347
A:Accession: S00992
A:Molecule type: DNA
A:Residues: 1-234 <CHO>
A:Cross-references: EMBL:X12500; NID:g64743; PIDN:CAA31021.1; PID:g64744

A:Note: 216-Ser and 225-Gln were also found and are interpreted as minor allelic differ
A:Accession: S00993
A:Molecule type: DNA
A:Residues: 83-215,'S',217-224,'Q',226-234 <CHW>
A:Cross-references: EMBL:X12499; NID:g64740; PIDN:CAA31020.1; PID:g64742
R:Carasco, A.E.; McGinnis, W.; Gehring, W.J.; De Robertis, E.M.
Cell 37, 409-414, 1984
A:Title: Cloning of an Xenopus laevis gene expressed during early embryogenesis coding i
A:Reference number: A03316; MUID:84205675; PMID:6327066
A:Accession: A03316
A:Molecule type: DNA
A:Residues: 134-138,'S',140-200 <CAR>
A:Cross-references: GB:K01943; NID:g214242; PIDN:AAA49743.1; PID:g214243
A:Note: the authors translated the codon AGC for residue 200 as Arg
R:Fritz, A.; de Robertis, E.M.
Nucleic Acids Res. 16, 1453-1469, 1988
A:Title: Xenopus homeobox-containing cDNAs expressed in early development.
A:Reference number: S00589; MUID:88157707; PMID:2894634
A:Accession: S00590
A:Molecule type: mRNA
A:Residues: 121-215,'S',217-224,'Q',226-234 <PRI>
A:Cross-references: EMBL:X07101; NID:g64738; PIDN:CAA30122.1; PID:gl334649
C:Genetics:
A:Gene: AC1
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-234/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT1>
F;83-215/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT>
F;142-198/Domain: homeobox homology <HOX>

Query Match      64.9%; Score 96; DB 2; Length 234;
Best Local Similarity 72.0%; Pred. No. 1.4e-06;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQKIFQNRMRMKWK-TALDASAL 25
|||:|||||
Db 182 ERQKIFQNRMRMKKESNLSSTL 206

RESULT 15
S15536
homeotic protein Hox A7 - human (fragment)
N:Alternate names: homeotic protein Hox 1A
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
C:Accession: S15536
R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; St
Genome 31, 745-756, 1989
A:Title: Organization of human class I homeobox genes.
A:Reference number: S15036; MUID:90215256; PMID:2576652
A:Accession: S15536
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-66 <BON>
C:Genetics:
A:Gene: GDB:HOXA7
A:Cross-references: GDB:120647; OMIM:142950
A:Map position: 7p15.3-7p15.3
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>

Query Match      64.2%; Score 95; DB 2; Length 66;
Best Local Similarity 81.0%; Pred. No. 5.4e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQKIFQNRMRMKWK-TALD 21
|||:|||||
Db 42 ERQKIFQNRMRMKKHKD 62

Search completed: February 18, 2004, 14:38:53
Job time : 30.7632 secs
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 32.9737 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWQNRMMKKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	64.2	24	4	US-09-419-826-34
2	95	64.2	27	4	US-09-040-725A-2
3	94	63.5	34	4	US-09-347-504-79
4	94	63.5	61	2	US-08-202-044-3
5	94	63.5	61	3	US-08-751-344B-3
6	94	63.5	61	3	US-08-751-344B-6
7	94	63.5	61	3	US-08-751-344B-9
8	93	62.8	22	4	US-09-057-363C-50
9	93	62.8	27	3	US-09-051-934-51
10	93	62.8	27	3	US-09-051-934-52
11	93	62.8	61	3	US-08-751-344B-7
12	92	62.2	16	2	US-08-928-958-7
13	92	62.2	16	2	US-08-810-540-3
14	92	62.2	16	2	US-08-810-540-6
15	92	62.2	16	2	US-09-072-429-7
16	92	62.2	16	3	US-08-964-302A-6
17	92	62.2	16	3	US-09-116-294-4
18	92	62.2	16	3	US-08-964-614A-4
19	92	62.2	16	3	US-08-849-486-1
20	92	62.2	16	3	US-08-849-486-4
21	92	62.2	16	3	US-09-208-966-54
22	92	62.2	16	3	US-09-308-935-8
23	92	62.2	16	3	US-09-441-416A-6
24	92	62.2	16	4	US-09-236-089-33
25	92	62.2	16	4	US-09-419-826-35
26	92	62.2	16	4	US-09-302-305C-10
27	92	62.2	16	4	US-09-346-847-1

28	92	62.2	16	4	US-09-346-847-25	Sequence 25, Appl
29	92	62.2	16	4	US-09-057-363C-47	Sequence 47, Appl
30	92	62.2	16	4	US-09-043-560B-3	Sequence 3, Appl
31	92	62.2	17	4	US-09-346-847-17	Sequence 17, Appl
32	92	62.2	17	4	US-09-346-847-20	Sequence 20, Appl
33	92	62.2	17	4	US-09-346-847-22	Sequence 22, Appl
34	92	62.2	17	4	US-09-346-847-27	Sequence 27, Appl
35	92	62.2	18	3	US-08-838-545-20	Sequence 20, Appl
36	92	62.2	18	3	US-09-349-532-20	Sequence 20, Appl
37	92	62.2	19	4	US-09-346-847-23	Sequence 23, Appl
38	92	62.2	19	4	US-09-658-517C-7	Sequence 7, Appl
39	92	62.2	20	4	US-09-466-772-3	Sequence 3, Appl
40	92	62.2	20	4	US-09-346-847-16	Sequence 16, Appl
41	92	62.2	20	4	US-09-346-847-18	Sequence 18, Appl
42	92	62.2	20	4	US-09-346-847-30	Sequence 30, Appl
43	92	62.2	20	4	US-09-658-517C-8	Sequence 8, Appl
44	92	62.2	22	4	US-09-346-847-28	Sequence 28, Appl
45	89	60.1	42	3	US-08-751-344B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-419-826-34
; Sequence 34, Application US/09419826
; Patent No. 6306832
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDE ANTIESTROGEN COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 39
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/419,826
; FILING DATE: 14-OCT-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/07711
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/043,545
; FILING DATE: 14-APR-1997
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: /note= "X = Phosphotyrosine"
US-09-419-826-34

Query Match 64.2%; Score 95; DB 4; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWQNRMMKKKTALD 21
Db 1 RQIKWQNRMMKKKPLXD 20

RESULT 2
US-09-040-725A-2
; Sequence 2, Application US/09040725A
; Patent No. 6399584
; GENERAL INFORMATION:
; APPLICANT: Institut Curie
; APPLICANT: CNRS

```
; APPLICANT: Arpin, Monique
; APPLICANT: Crepaldi, Tiziana
; APPLICANT: Gautreau, Alexis
; APPLICANT: Louvard, Daniel
; TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated
; FILE REFERENCE: 391082000100
; CURRENT APPLICATION NUMBER: US/09/040,725A
; CURRENT FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (22)
; OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2

Query Match 64.2%; Score 95; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRMKWKTALDASALQTE 28
Db 1 RQIKWIFQNRMRMKWKLRLQDXEEKYK 27

RESULT 3
US-09-347-504-79
; Sequence 79, Application US/09347504
; Patent No. 6399075
; GENERAL INFORMATION:
; APPLICANT: Howley, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-504-79

Query Match 63.5%; Score 94; DB 4; Length 34;
Best Local Similarity 94.1%; Pred. No. 2.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKWK 17
Db 1 EROIKIWFQNRMRMKWK 17

RESULT 4
US-08-202-044-3
; Sequence 3, Application US/08202044
; Patent No. 5858973
; GENERAL INFORMATION:
; APPLICANT: Habener M.D., Joel P.
; APPLICANT: Miller Ph.D., Christopher P.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
```

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; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,044
; FILING DATE: 23-FEB-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen A.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: MGH-124XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-202-044-3

Query Match 63.5%; Score 94; DB 2; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMRMKWK 17
Db 43 EROIKIWFQNRMRMKWK 59

RESULT 5
US-08-751-344B-3
; Sequence 3, Application US/08751344B
; Patent No. 6210960
; GENERAL INFORMATION:
; APPLICANT: Habener M.D., Joel P.
; APPLICANT: Miller Ph.D., Christopher P.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,344B
; FILING DATE: 19-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,044
; FILING DATE: 23-Feb-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-3

Query Match 63.5%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOFRRMKWK 17
:|||||
Db 43 ERQIKWFOFRRMKWK 59

RESULT 6
US-08-751-344B-6
; Sequence 6, Application US/08751344B
; Patent No. 6210960

GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-6

Query Match 63.5%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOFRRMKWK 17

Db 43 ERQIKWFOFRRMKWK 59
:|||||

RESULT 7
US-08-751-344B-9
; Sequence 9, Application US/08751344B
; Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel P.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-9

Query Match 63.5%; Score 94; DB 3; Length 61;
Best Local Similarity 94.1%; Pred. No. 4.3e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFOFRRMKWK 17
:|||||
Db 43 ERQIKWFOFRRMKWK 59

RESULT 8
US-09-057-363C-50
; Sequence 50, Application US/09057363C
; Patent No. 6551994
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle

STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-057-363C-50

Query Match 62.8%; Score 93; DB 4; Length 22;
Best Local Similarity 94.1%; Pred. NO. 2e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQKIWFQNRMRKWKX 17
DB 6 NRQKIWFQNRMRKWKX 22

RESULT 9
US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match 62.8%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. NO. 2.5e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKWKKTALD 21
DB 1 ROIKIWFQNRMRKWKKHIE 20

RESULT 10
US-09-051-934-52

Sequence 52, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
FEATURE:
NAME/KEY: MOD RES
LOCATION: {24}
OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match 62.8%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. NO. 2.5e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRKWKKTALD 21
DB 1 ROIKIWFQNRMRKWKKHIE 20

RESULT 11
US-08-751-344B-7
Sequence 7, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-751-344B-7

Query Match 62.8%; Score 93; DB 3; Length 61;
Best Local Similarity 88.2%; Pred. No. 6e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQIKWIFQNRMRMKWK 17
Db 43 ERQVKWIFQNRMRMKWK 59

RESULT 12
US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282
GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEAVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFAR, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-958-7

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQIKWIFQNRMRMKWK 17
Db 1 RQIKWIFQNRMRMKWK 16

RESULT 13
US-08-810-540-3
Sequence 3, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-810-540-3

Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQIKWIFQNRMRMKWK 17
Db 1 RQIKWIFQNRMRMKWK 16

RESULT 14
US-08-810-540-6
Sequence 6, Application US/08810540
Patent No. 5929042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

US-09-072-429-7

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 81.0526 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWFQNRMRKWKKTALDWSWLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101.5	62.7	274	5 Q9XYT7	Q9xyt7 cassiopea x
2	97	59.9	60	5 Q26375	Q26375 atyela clav
3	97	59.9	108	11 Q8J2W2	Q8j2w2 mus musculus
4	97	59.9	181	5 Q26611	Q26611 styela plic
5	97	59.9	194	5 Q26478	Q26478 atyela clav
6	97	59.9	435	5 Q817C8	Q817c8 ciona intes
7	95.5	59.0	90	5 Q817C9	Q817c9 ciona intes
8	94	58.0	39	13 Q57368	Q57368 brachydanio
9	94	58.0	43	13 Q57359	Q57359 brachydanio
10	94	58.0	46	13 Q9PVR9	Q9pvr9 oryzias lat
11	94	58.0	51	5 Q27413	Q27413 cttenodrilus
12	94	58.0	51	5 Q23743	Q23743 cttenodrilus
13	94	58.0	51	5 Q26407	Q26407 cttenodrilus
14	94	58.0	57	13 Q9PVR8	Q9pvr8 oryzias lat
15	94	58.0	58	5 Q9Y188	Q9y188 priapulus c
16	94	58.0	58	5 Q25208	Q25208 junonia coe

17	94	58.0	58	13	O57362	O57362 brachydanio
18	94	58.0	59	5	Q8WRM9	Q8wrm9 lithobius a
19	94	58.0	59	5	Q9NB42	Q9nb42 anopheles g
20	94	58.0	59	13	Q9PVR5	Q9pvr5 oryzias lat
21	94	58.0	60	5	O77143	O77143 archeogozete
22	94	58.0	60	5	O77139	O77139 archeogozete
23	94	58.0	60	13	Q8QGL5	Q8qgl5 petromyzon
24	94	58.0	60	13	Q8QGL3	Q8qgl3 petromyzon
25	94	58.0	60	13	Q8QGL6	Q8qgl6 petromyzon
26	94	58.0	60	13	Q8QGL2	Q8qgl2 petromyzon
27	94	58.0	60	13	Q8QGL8	Q8qgl8 petromyzon
28	94	58.0	60	13	Q8QGL7	Q8qgl7 petromyzon
29	94	58.0	61	5	Q27910	Q27910 polyandroca
30	94	58.0	63	5	O77138	O77138 archeogozete
31	94	58.0	63	5	Q8MXB2	Q8mbx2 holopneuste
32	94	58.0	66	13	O57356	O57356 brachydanio
33	94	58.0	69	5	Q9U9T4	Q9u9t4 nerdis vire
34	94	58.0	69	5	Q9BMF7	Q9bmf7 halloctis as
35	94	58.0	70	5	Q967W5	Q967w5 folsomia ca
36	94	58.0	71	13	Q9PVS3	Q9pvs3 oryzias lat
37	94	58.0	71	13	Q9PVS1	Q9pvs1 oryzias lat
38	94	58.0	73	5	Q9Y186	Q9y186 priapulus c
39	94	58.0	74	13	O57367	O57367 brachydanio
40	94	58.0	75	5	Q25209	Q25209 junonia coe
41	94	58.0	75	13	Q9PVR6	Q9pvr6 oryzias lat
42	94	58.0	76	5	O44257	O44257 ethmostigmu
43	94	58.0	77	5	O44260	O44260 ethmostigmu
44	94	58.0	77	5	Q9Y187	Q9y187 priapulus c
45	94	58.0	77	5	Q9U924	Q9u924 lingula ung

ALIGNMENTS

RESULT 1

Q9XYT7 PRELIMINARY; PRT; 274 AA.
ID Q9XYT7
AC Q9XYT7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Scx-3 homeodomain protein (Fragment)
GN SCOX-3.
OS Cassiopea xamachana.
OC Eukaryota; Metazoa; Cnidaria; Scyphozoa; Rhizostomeae; Cassiopeidae;
OC Cassiopea.
OC NCBI_TaxID=12993;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuhn K., Streit B., Schierwater B.;
RT "Isolation of Hox genes from the scyphozoan Cassiopeia xamachana:
RT Implications for the early evolution of Hox genes."
RL J. Exp. Zool. 0:0-0(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF124593; AAD32577.1; -;
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF000046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
FT DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
SQ SEQUENCE 274 AA; 31041 MW; 58EE91F6E540C3A9 CRC64;

Query Match 62.7%; Score 101.5; DB 5; Length 274;
Best Local Similarity 64.5%; Pred. No. 7e-06;
Matches 20; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

Qy	1	DROIKWQNRRMKWK--TALDWSWLQTE	28
	:		: :
Db	182	ERQIKWIFONRRMKWKRGTTSIDANELERE	212

RESULT 2

Q26375	PRELIMINARY;	PRT;	60 AA.
ID	Q26375		
AC	Q26375;		
DT	01-NOV-1996	(TrEMBLrel. 01, Created)	
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)	
DE	DNA binding protein Ahox2 (Fragment).		
GN	AHOX2.		
OS	Styela clava (Sea squirt).		
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;		
OC	Stolidobranchia; Styelidae; Styela.		
OX	NCBI TaxID=7725;		

RP SEQUENCE FROM N.A.

RX	MEDLINE=95011617; PubMed=7926803;
RA	Ge T., Lee H., Tomlinson C.N.;
RT	"Identification of an antennapedia-like homeobox gene in the ascidians
RI	Styela clava and S. plicata.";
RL	Gene 147:219-222(1994).
CC	CC - EMBL SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR	EMBL; S73920; AAB33061.2; -;
DR	HSSP; P02833; 9ANT.
DR	InterPro; IPR001356; Homeobox.
DR	InterPro; IPR000047; HTH_lambdarepressor.
DR	Pfam; PF000046; homeobox; 1.
DR	PRINTS; PR00024; HOMEBOX.
DR	PRINTS; PR00031; HTHREPRESSR.
DR	ProDom; PD000010; Homeobox; 1.
DR	SMART; SM00389; HOX; 1.
DR	PROSITE; PS00027; HOMEBOX 1; 1.
DR	PROSITE; PS50071; HOMEBOX_2; 1.
KW	DNA-binding; Homeobox; Nuclear protein.
FT	NON_TER 1 1
FT	NON_TER 60 60
FT	SEQUENCE 60 AA; 7630 MW; F506301B9679BA25 ARC64;
SQ	

Query Match 59.9%; Score 97; DB 5; Length 60;
Best Local Similarity 94.1%; Pred. No. 6.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels

Qy 1 DRQIKIWFQRRRMKWK 17
|||:|||||||
Db 42 DRQKIWFQRRRMKWK 58

RESULT. T 3

Q8JZW2	Q8JZW2	PRELIMINARY;	PRT; 108 AA.
ID	Q8JZW2		
AC	Q8JZW2;		
CC	Q8JZW2;		
DT	01-OCT-2002 (TReMBLrel. 22, Created)		
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)		
DT	01-WAR-2003 (TReMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
DE	Hypothetical protein.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Colon;		
RL	Strausberg R.;		
RA	Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.		
DR	EMBL; BC036986; AAH36986.1; -;		
DR	InterPro; IPR001356; Homeobox.		
DR	InterPro; IPR000047; HTH lambdarepressr.		
DR	Pfam; PF000046; homeobox; 1.		
DR	PRINTS; PR00024; HOMEBOX.		

DR PRINTS; PRO0031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; PS00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; P55071; HOMEBOX_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 108 AA; 13070 MW; 1

Query Match 59.9%; Score 97; DB 11; Length 108;
Best Local Similarity 70.4%; Pred. No. 1.1e-05;
Matches 19; Conservative 1; Mismatches 7; Indels

Qy	1	D	R	O	I	K	I	W	F	Q	N	R	R	M	K	W	K	T	A	L	D	W	S	L	Q	T	27	
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Db	49	E	R	O	I	K	I	W	F	Q	N	R	R	M	K	W	K	E	H	K	D	E	S	O	A	P	T	75

RESULT 4

Q26611	PRELIMINARY;	PRT;	181 AA.
ID	Q26611		
AC	Q26611;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	Homeobox protein (Fragment);		
DE	Styela plicata (Sea squirt);		
OS	Styela plicata	(Sea squirt);	
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;		
OC	Stolidobranchia; Styelidae; Styela.		
OX	NCBI_TaxID=7726;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Ascidian;		
RA	Ge T., Lee H., Tomlinson C.R.;		
RT	"Identification of an Antennapedia-like Homeobox Gene in the Ascidians		
RT	Styela clavis and plicata."		
RL	Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.		
CC	-/- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		

DR HSSP; P02833; 9ANT.
DR InterPro; IPR000047; HTH lambrepressor.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR000047; HTH lambrepressor.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR000047; HTH lambrepressor.

DR FRAM; FR00048; HOMEBOX; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESS.
DR ProDom; PD000010; Homebox; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.

FI	NON_IER	I81	I81
SO	SEQUENCE	181 AA:	20873 MW: AF39911408F06672 CRC64:

Query Match 59.9%; Score 97; DB 5; Length 181;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16: Conservative 1; Mismatches 0; Indels

Qy 1 DRQIKIWFQNRRMKWKK 17
|||:|||||||
Db 80 DROVKIWFQNRRMKWKK 96

RESIT.T 5

AC	Q26478	PRELIMINARY;	PRT;	194 AA.
AC	Q26478;			
DT	01-NOV-1996	(T-EMBLrel. 01, Created)		
DT	01-NOV-1996	(T-EMBLrel. 01, Last sequence update)		
DT	01-MAR-2003	(T-EMBLrel. 23, Last annotation update)		
DE	Homeobox protein (fragment).			
OS	Styela clava (Sea squirt).			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;			
OC	Stolidobranchia; Stvelidae; Stvela.			

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OX NCBI_TaxID=7725;
RN [1]
RP SEQUENCE FROM N.A.
RA Ge T., Lee H., Tomlinson C.R.;
RC STRAIN=Acidian;
RA "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
RT Styela clava and plicata.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05571; AAA16226.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 194 AA; 21886 MW; 8AD1B15B3E48008C CRC64;

Query Match 59.9%; Score 97; DB 5; Length 194;
Best Local Similarity 94.1%; Pred. No. 2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFWNRMKWK 17
DB 52 DRQVKIWFQNRMRKWK 68

RESULT 6
Q817C8 ID Q817C8 PRELIMINARY; PRT; 435 AA.
AC Q817C8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative homeobox protein Hox10.
GN HOX10.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoratore F., Di Gregorio A., Aniello F., Branno M.,
RA Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535675; CAD59671.1; -.
DR Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 435 AA; 48739 MW; D8D0F579C02BC9E2 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 435;
Best Local Similarity 94.1%; Pred. No. 4.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFWNRMKWK 17
DB 295 DRQVKIWFQNRMRKWK 311

RESULT 7
Q817C9 ID Q817C9 PRELIMINARY; PRT; 90 AA.
AC Q817C9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
```

```
DE Putative homeobox protein Hox6/7 (Fragment).
GN HOX6/7.
OS Ciona intestinalis. Chordata; Urochordata; Ascidiacea; Enterogona;
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoratore F., Di Gregorio A., Aniello F., Branno M.,
RA Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535674; CAD59670.1; -.
DR Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 90 AA; 11352 MW; CAAAD6B261FE908E CRC64;

Query Match 59.0%; Score 95.5; DB 5; Length 90;
Best Local Similarity 57.6%; Pred. No. 1.5e-05;
Matches 19; Conservative 3; Mismatches 6; Indels 5; Gaps 1;

QY 1 DRQIKWFWNRMKWK 28
DB 57 ERQIKIWFQNRMRKWK 89

RESULT 8
O57368 ID O57368 PRELIMINARY; PRT; 39 AA.
AC O57368;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hoxc5 protein (Fragment).
GN HOXC5A OR HOXC5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14539; CAA74874.1; -.
DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12E58860 CRC64;

Query Match 58.0%; Score 94; DB 13; Length 39;
Best Local Similarity 94.1%; Pred. No. 1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFWNRMKWK 17
DB 13 ERQIKIWFQNRMRKWK 29

RESULT 9
```

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O57359
ID O57359 PRELIMINARY; PRT; 43 AA.
AC O57359;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hoxa5 protein (Fragment).
GN HOB5B OR HOB5
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14526; CAAY4861.1; -.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match 58.0%; Score 94; DB 13; Length 43;
Best Local Similarity 94.1%; Pred. No. 1.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMMKWK 17
Db :|||||

RESULT 10
Q9PVR9 PRELIMINARY; PRT; 46 AA.
AC Q9PVR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE HOXC5A (Fragment).
GN HOXC5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medakafish Oryzias latipes."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AS026960; BAA86243.1; -.
DR HSSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT SEQUENCE 46 AA; 5955 MW; 6039999ED4294DD3 CRC64;
```

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Query Match 58.0%; Score 94; DB 13; Length 46;
Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMMKWK 17
Db :|||||

RESULT 11
Q27413 PRELIMINARY; PRT; 51 AA.
AC Q27413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LOX5 ORTHOLOG homeobox (Fragment).
GN CTS-LOX5.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OC NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RX MEDLINE=94356262; PubMed=7915607;
RA Dick M.H., Buss L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT (Annelida: Polychaeta).";
RL Mol. Phylogenet. Evol. 3:146-158(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U26629; AAC46851.1; -.
DR EMBL; S76226; AAB31777.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepreser.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 51
FT SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMMKWK 17
Db :|||||

RESULT 12
Q23743 PRELIMINARY; PRT; 51 AA.
AC Q23743;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Deformed ortholog homeobox (Fragment).
GN CTS-DFD.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
```

OX NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607;
RA Dick M.H., Buss L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RL (Annelida: Polychaeta).";
RN Mol. Phylogenet. Evol. 3:146-158(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dick M.H., Buss L.W.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U26627; AAC46849.1; -;
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWQNRMRMKWK 17
DB 22 ERQIKWQNRMRMKWK 38

RESULT 13

Q26407 ID Q26407 PRELIMINARY; PRT; 51 AA.
AC Q26407;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CTS-Dfd protein (Fragment).
GN CTS-DFD
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OX NCBI_TaxID=40316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94356262; PubMed=7915607;
RA Dick M.H., Buss L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RL (Annelida: Polychaeta).";
RN Mol. Phylogenet. Evol. 3:146-158(1994).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; S76416; AAB31775.1; -;
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWQNRMRMKWK 17
DB 22 ERQIKWQNRMRMKWK 38

RESULT 14

Q9PVR8 ID Q9PVR8 PRELIMINARY; PRT; 57 AA.
AC Q9PVR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE HOXA5A (Fragment).
GN HOXA5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medakafish Oryzias latipes.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB026961; BAA86244.1; -;
DR HSSP; P02833; 1HOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;

Query Match 58.0%; Score 94; DB 13; Length 57;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRQIKWQNRMRMKWK 17
DB 22 ERQIKWQNRMRMKWK 38

RESULT 15

Q9Y188 ID Q9Y188 PRELIMINARY; PRT; 58 AA.
AC Q9Y188;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE HBI homeodomain protein (fragment).
RN HBI.
OS Priapulid caudatus.
OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulidus.
OX NCBI_TaxID=37621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99318125; PubMed=10391241;
RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
RA Carroll S.B., Balavoine G.;
RT "Hox genes in brachiopods and priapulids and protostome evolution.";
RL Nature 399:772-776(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF144888; AAD40644.1; -;
DR HSSP; P02833; 9ANT.

DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressr.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A613 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 58;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRMRMKKK 17
:|||||
Db 23 ERQIKIWFQNRMRMKKK 39

Search completed: February 18, 2004, 14:36:01
Job time : 83.0526 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 16.5789 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKWFQNRMRKWKTKALDWSLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	59.9	105	1 HXA7_RAT	P09634 rattus norv
2	97	59.9	229	1 HXA7_MOUSE	P02830 mus musculu
3	96	59.3	75	1 HMSA_SALSA	P09636 salmo salar
4	95	58.6	224	1 HXB6_HUMAN	P17509 homo sapien
5	95	58.6	224	1 HXB6_MOUSE	P09023 mus musculu
6	95	58.6	230	1 HXA7_HUMAN	P31288 homo sapien
7	94	58.0	48	1 HXB6_XENLA	P31256 xenopus lae
8	94	58.0	49	1 HXA5_SHEEP	Q28599 ovis aries
9	94	58.0	71	1 HXA7_SHEEP	Q28600 ovis aries
10	94	58.0	71	1 HXC5_NOTVI	P31262 notophthalm
11	94	58.0	74	1 HM90_APTME	P15860 apis mellif
12	94	58.0	76	1 HXC4_RAT	P18865 rattus norv
13	94	58.0	78	1 HXA5_SALSA	P09637 salmo salar
14	94	58.0	80	1 HXA4_LINSA	P81192 lineus sang
15	94	58.0	81	1 HX5L_BRARE	P09013 brachydanio
16	94	58.0	82	1 HXB5_CHICK	P14838 gallus gall
17	94	58.0	84	1 HXB6_CHICK	P14839 gallus gall
18	94	58.0	86	1 SCR_APTME	P15859 apis mellif
19	94	58.0	87	1 HXC5_XENLA	P09020 xenopus lae
20	94	58.0	93	1 HXB8_PIG	P09078 sus scrofa
21	94	58.0	96	1 HXC6_BRARE	P15862 brachydanio
22	94	58.0	105	1 HXB4_BRARE	P22574 brachydanio
23	94	58.0	112	1 HXB7_RAT	P18864 rattus norv
24	94	58.0	148	1 HXA5_AMEME	P50208 ambystoma m
25	94	58.0	153	1 HXC6_SHEEP	P49925 ovis aries
26	94	58.0	208	1 HXA7_HETFR	Q91a25 heterodontu
27	94	58.0	209	1 HXA7_XENLA	P09071 xenopus lae
28	94	58.0	217	1 HXB7_BOVIN	Q9t89 bos taurus
29	94	58.0	217	1 HXB7_HUMAN	P09629 homo sapien
30	94	58.0	217	1 HXB7_MOUSE	P09024 mus musculu
31	94	58.0	220	1 HB7A_XENLA	Q91771 xenopus lae
32	94	58.0	220	1 HB7B_XENLA	P04476 xenopus lae
33	94	58.0	222	1 HXC5_HUMAN	Q00444 homo sapien

34	94	58.0	222	1 HXC5_MOUSE	P32043 mus musculu
35	94	58.0	225	1 HXA7_MORSA	Q9pvd4 morone saxa
36	94	58.0	228	1 HXB6_BRARE	P15861 brachydanio
37	94	58.0	229	1 HXA6_HETFR	Q91a24 heterodontu
38	94	58.0	230	1 HXB5_XENLA	P09019 xenopus lae
39	94	58.0	232	1 HXA6_MOUSE	P09092 mus musculu
40	94	58.0	232	1 HXB4_XENLA	P09070 xenopus lae
41	94	58.0	232	1 HXC5_BRARE	P09074 brachydanio
42	94	58.0	233	1 HXA5_RAT	P52949 rattus norv
43	94	58.0	233	1 HXA6_HUMAN	P31267 homo sapien
44	94	58.0	234	1 HXC6_NOTVI	P14858 notophthalm
45	94	58.0	234	1 HXC6_XENLA	P02832 xenopus lae

ALIGNMENTS

RESULT 1

HXA7_RAT

ID HXA7_RAT STANDARD; PRT; 105 AA.

AC P09634;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).

GN HOXA7 OR HOXA-7.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=87277429; PubMed=2886401;

RA Falzon M., Sanderson N., Chung S.Y.;

RT "Cloning and expression of rat homeo-box-containing sequences.";

RL Gene 54:23-32(1987).

CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF

CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH

CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.

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CC EMBL; M16807; -, NOT_ANNOTATED_CDS.

DR PIR; A27471; A27471.

DR HSSP; P02833; 9ANT.

DR TRANSFAC; T01707; -.

DR InterPro; IPR001827; Antennapedia.

DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00024; HOMEBOX.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS00071; HOMEBOX_2; 1.

KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;

FT NON_TER 1 1

FT DNA_BIND 5 64 HOMEBOX.

FT DOMAIN 91 105 GLU-RICH (ACIDIC).

SEQUENCE 105 AA; 12552 MW; 106C1DF938F2864B CRC64;

Query Match 59.9%; Score 97; DB 1; Length 105;
Best Local Similarity 70.4%; Pred. No. 1.1e-06;

Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKWKKTALDWSWLOT 27
Db 46 ERQIKWIFQNRMRKWKKEHKSQAPT 72

RESULT 2
HX7 MOUSE
ID HX7_MOUSE STANDARD; PRT; 229 AA.
AC P02830;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).
GN HOXA7 OR HOXA-7 OR HOX-1.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260976; PubMed=2885847;
RA Kessel M., Schulze F., Fibi M., Gruss P.;
RT "Primary structure and nuclear localization of a murine homeodomain
protein";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95197009; PubMed=7890170;
RA Parikh H., Shah S., Hilt D., Peterkofsky A.;
RT "Organization, sequence and regulation of expression of the murine
Hoxa-7 gene";
RL Gene 154:237-242(1995).
RN [3]
RP SEQUENCE OF 126-229 FROM N.A.
RX MEDLINE=85188311; PubMed=2986010;
RA Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;
RT "Structural analysis of murine genes containing homeo box sequences
and their expression in embryonal carcinoma cells";
RL Nature 314:713-718(1985).
RN [4]
RP SEQUENCE OF 129-197 FROM N.A.
RX MEDLINE=87053860; PubMed=2877873;
RA Breier G., Bucan M., Franke U., Colberg-Poley A.M., Gruss P.;
RT "Sequential expression of murine homeo box genes during F9 EC cell
differentiation";
RL EMBO J. 5:2209-2215(1986).
RN [5]
RP FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC
CC EMBL; M17192; AAA37833.1; -.
CC EMBL; U15972; AAC52160.1; -.
CC PIR; A03314; A03314.
CC PIR; A28329; A28329.
CC HSSP; P02833; 9ANT.
CC TRANSFAC; T01278; -.
CC MGD; MGI:96179; Hoxa7.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.

DR PRINTS; P00025; ANTENNAPEDIA.
DR PRINTS; P00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT SITE 118 123 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 129 188 HOMEBOX.
FT DOMAIN 156 159 POLY-ARG.
FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 215 229 POLY-GLU.
FT CONFLICT 43 45 GAG->APA (IN REF. 1).
SQ SEQUENCE 229 AA; 25682 MW; D36E6BD61D8D5C6F CRC64;

Query Match 59.9%; Score 97; DB 1; Length 229;
Best Local Similarity 70.4%; Pred. No. 2.4e-06;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWIFQNRMRKWKKTALDWSWLOT 27
Db 170 ERQIKWIFQNRMRKWKKEHKSQAPT 196

RESULT 3
HMSA_SALSA
ID HMSA_SALSA STANDARD; PRT; 75 AA.
AC P09636;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Sl2-A (fragment).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes
from Atlantic salmon";
RL Gene 62:141-152(1988).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC
CC EMBL; M18903; AAA49559.1; -.
CC PIR; I51341; I51341.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1 HOMEBOX.
FT DNA_BIND 1 60
FT NON_TER 75 75
SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match 59.3%; Score 96; DB 1; Length 75;

Best Local Similarity 78.3%; Pred. No. 1e-06;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DROIKWFOQRNRKKKTKALDWS 23
Db 42 ERQIKWFOQRNRKKKTKDHDES 64

RESULT 4

HXB6 HUMAN
ID HXB6_HUMAN STANDARD; PRT; 224 AA.
AC P17509; P09068; Q9H811; Q9UGH2;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2B) (Hox-2.2) (HU-2).
GN HXB6 OR Hox2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Placenta;
RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.-F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
RA Largman C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human
RT hematopoietic cells and murine embryonic and adult tissues.";
RL Nucleic Acids Res. 19:539-545(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Frezza D., D'Eposito M., Migliaccio E., Santini S.M., Fruscalzo A.;
RT "Expression of HOX genes in T lymphocytes and hairy leukemia cell
RT lines.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kidd K.K., Bueyguina V., DeMille M.M.C., Speed W.C., Ruggeri V.,
RA Kidd J.R., Paketis A.J.;
RT "Overall linkage disequilibrium in 33 populations for highly
RT informative multistate haplotypes spanning the HOXB gene cluster.";
RL Am. J. Hum. Genet. 67:235-235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 135-224 FROM N.A.
RX MEDLINE=90046832; PubMed=2573064;
RA Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,
RA Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
RT "Lineage-restricted expression of homeobox-containing genes in human

RT hematopoietic cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
RN [6]
RP PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
RX MEDLINE=85024858; PubMed=6091895;
RA Levine M., Rubin G.M., Tjian R.;
RT "Human DNA sequences homologous to a protein coding region conserved
RT between homeotic genes of Drosophila.";
RL Cell 38:667-673(1984).
CC
CC !- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC !- SUBCELLULAR LOCATION: Nuclear.
CC !- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P17509-1; Sequence=Displayed;
CC Name=2; Synonyms=Homeobox-less;
CC IsoId=P17509-2; Sequence=VSP 002388, VSP 002389;
CC !- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC
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CC
CC EMBL; X58431; CAA41335.1; -
CC EMBL; X58431; CAA41336.1; -
CC EMBL; AJ270993; CAB65909.1; -
CC EMBL; AF287967; AAG31552.1; -
CC EMBL; BC014651; AAH14651.1; -
CC EMBL; M30597; AAA36004.1; -
CC EMBL; K02571; -; NOT_ANNOTATED_CDS.
CC PIR; S26400; S26400.
CC HSSP; P02833; IHOM.
CC TRANSFAC; T01732; -
CC Genew; HGNC:5117; HOXB6.
CC MIM; 142961; -
CC GO; GO:0005634; C:nucleus; NAS.
CC GO; GO:0003700; F:transcription factor activity; NAS.
CC GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation; Alternative splicing.
FT SITE 127 132 ANTP-TYPE HEXAPEPTIDE.
FT DNA BIND 146 205 HOMEBOX.
FT DOMAIN 216 220 POLY-GLU.
FT VARSPLIC 140 140 S -> E (in isoform 2).
FT VARSPLIC 141 224 /FTId=VSP 002388.
FT Missing (in isoform 2).
FT /FTId=VSP_002389.
FT HV -> QL (IN REF. 3 AND 4).
FT CONFLICT 24 25 A -> R (IN REF. 1).
FT CONFLICT 33 33 P -> R (IN REF. 1).
FT CONFLICT 60 60 D -> A (IN REF. 1).
FT CONFLICT 73 73 GR -> A (IN REF. 5).
FT CONFLICT 149 150 MW; D8F96AFAC893D878 CRC64;
FT SEQUENCE 224 AA; 25427 MW; 58.6%; Score 95; DB 1; Length 224;
SQ
Query Match 58.6%; Score 95; DB 1; Length 224;
Best Local Similarity 66.7%; Pred. No. 4.5e-06;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DROIKIWFQNRKWKKTAA--LDWSWLOTE 28
DB 187 EROIKIWFQNRKWKKSLLSASLSAE 216

RESULT 5
HXB6 MOUSE
ID HXB6_MOUSE STANDARD; PRT; 224 AA.
AC P09023;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
GN HXB6 OR HXB6-6 OR HXB6-2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88289762; PubMed=2899893;
RA Schughart K., Utset M.F., Awgulewitsch A., Ruddle F.H.;
RT "Structure and expression of Hox-2.2, a murine homeobox-containing
RT gene."
RT Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187672; PubMed=1672751;
RA Shen W.F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
RA Largman C.;
RT "Alternative splicing of the Hox 2.2 homeobox gene in human
RT hematopoietic cells and murine embryonic and adult tissues."
RL Nucleic Acids Res. 19:539-545(1991).
RN [3]
RP SEQUENCE OF 144-224 FROM N.A.
RX MEDLINE=88054465; PubMed=2890503;
RA Lonai P., Aman E., Czosnek H., Ruddle F.H., Blatt C.;
RT "New murine homeoboxes: structure, chromosomal assignment, and
RT differential expression in adult erythropoiesis."
RL DNA 6:409-418(1987).
RN [4]
RP SEQUENCE OF 140-224 FROM N.A.
RX MEDLINE=88085193; PubMed=2891608;
RA Hart C.P., Fainsod A., Ruddle F.H.;
RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes:
RT evolutionary and structural comparisons."
RL Genomics 1:182-195(1987).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC -----
DR ENBL; M18166; AAA37844.1; -;
DR ENBL; X56459; CAA39834.1; -;
DR ENBL; M18401; AAC27130.1; ALT_SEQ.
DR ENBL; J03782; AAA37843.1; -;
DR PIR; A31324; A31324.
DR HSSP; P02833; IHOM.
DR TRANSFAC; T01733; -;
DR MGD; MGI:96187; Hoxb6.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT SITE 127 132 ANTP-TYPE HEXAPEPTIDE.
FT DNA BIND 146 205 HOMEBOX.
FT DOMAIN 216 220 POLY-GLU.
FT CONFLICT 186 186 T -> P (IN REF. 3).
SQ SEQUENCE 224 AA; 25310 MW; E8FC0BDEB57F5C3D CRC64;
Query Match 58.6%; Score 95; DB 1; Length 224;
Best Local Similarity 66.7%; Pred. No. 4.5e-06;
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DROIKIWFQNRKWKKTAA--LDWSWLOTE 28
DB 187 EROIKIWFQNRKWKKSLLSASLSAE 216

RESULT 6
HXA7_HUMAN
ID HXA7_HUMAN STANDARD; PRT; 230 AA.
AC P31268; O43368; O43486; O95655; Q9UDM1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).
GN HOXA7 OR HOXA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Polakowska R., LaCelle P.T.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99023755; PubMed=9804983;
RA McIlhathon M.A., Bremner P.S., McMullin M.F., Maxwell A.P.,
RA Winter P.C., Lappin T.R.;
RT "Sequence characterisation and expression of homeobox HOX A7 in the
RT multi-potential erythroleukaemic cell line TF-1."
RL Biochim. Biophys. Acta 1442:329-333(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Bradshaw H., Hinds K., Keppeler D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20369265; PubMed=10911612;
RA Kim M.H., Jin H., Seol E.Y., Yoo M., Park H.W.;
RT "Sequence analysis and tissue specific expression of human HOXA7."
RL Mol. Biotechnol. 14:19-24(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUEPlacenta;
RA Albrechtsen R., Wewer U.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-91 FROM N.A.
RA Cho M., Kim M.H., Hwang C.Y., Min W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 130-195 FROM N.A.
RX MEDLINE=90215256; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,

RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
 RT "Organization of human class I homeobox genes.";
 RL Genome 31:745-756(1989).
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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 CC -----
 CC EMBL; AF026397; AAB94604.1; -;
 CC EMBL; AJ005814; CRA06713.1; -;
 CC EMBL; AC004080; -; NOT ANNOTATED_CDS.
 CC EMBL; AF032095; AAD01939.2; -;
 CC EMBL; U92543; RAD00727.1; -;
 CC EMBL; X84803; CAA59270.1; -;
 CC EMBL; X84804; CAA59270.1; JOINED.
 CC PIR; S15536; S15536.
 CC HSSP; P02833; 9ANT.
 CC TRANSFAC; T01705; -;
 CC Genew; HGNC:5108; HOXA7.
 CC MIM; 142950; -;
 CC GO; GO:0003700; F:transcription factor activity; TAS.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00025; ANTENNAPEIDIA.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00032; HOMEBOX_1; 1.
 CC PROSITE; PS00027; HOMEBOX_2; 1.
 CC PROSITE; PS00071; HOMEBOX_2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 KW SITE 119 124 ANTP-TYPE HEXAPEPTIDE.
 FT SITE 119 124 HOMEBOX.
 FT DNA_BIND 130 189 POLY-ARG.
 FT DOMAIN 157 160 POLY-ALA.
 FT DOMAIN 196 199 POLY-ALA.
 FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 223 230 POLY-GLU.
 FT DOMAIN 18 18 T -> A (IN REF. 3).
 FT CONFLICT 18 18 DA -> RR (IN REF. 6).
 FT CONFLICT 75 76 MISSING (IN REF. 5).
 FT CONFLICT 78 78 I -> V (IN REF. 4).
 FT CONFLICT 174 174 FT -> RL (IN REF. 5).
 FT CONFLICT 194 195 T -> I (IN REF. 7).
 FT CONFLICT 195 195 D -> Y (IN REF. 5).
 FT CONFLICT 222 222
 SQ SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;
 Query Match 58.6%; Score 95; DB 1; Length 230;
 Best Local Similarity 81.0%; Pred. No. 4.6e-06;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DRQIKWFOQRNRKMKKTD 21
 Db :|||||
 171 ERQIKWFOQRNRKMKKEHKD 191
 RESULT 7
 HXB6 XENLA
 ID HXB6 XENLA STANDARD; PRT; 48 AA.
 AC P31256;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).
 GS HXB6 OR XLHox-2.2.
 ON Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93043517; PubMed=1384809;
 RA Leroy P., de Robertis E.M.;
 RT "Effects of lithium chloride and retinoic acid on the expression of
 RT genes from the Xenopus laevis Hox 2 complex.";
 RL Dev. Dyn. 194:21-32(1992).
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
 CC -----
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 CC -----
 CC EMBL; M91587; AAA49750.1; -;
 CC PIR; I51439; I51439.
 CC InterPro; IPR001827; Antennapedia.
 CC InterPro; IPR001356; Homeobox.
 CC Pfam; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEBOX_1; 1.
 CC PROSITE; PS00032; ANTENNAPEIDIA; PARTIAL.
 CC PROSITE; PS00071; HOMEBOX_2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 FT NON_TER 1 1
 FT DNA_BIND <1 29 HOMEBOX.
 SQ SEQUENCE 48 AA; 5716 MW; BC39E36822EDD2A CRC64;
 Query Match 58.0%; Score 94; DB 1; Length 48;
 Best Local Similarity 94.1%; Pred. No. 1.2e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRQIKWFOQRNRKMKKK 17
 Db :|||||
 11 ERQIKWFOQRNRKMKKK 27
 RESULT 8
 HXB5 SHEEP
 ID HXB5 SHEEP STANDARD; PRT; 49 AA.
 AC Q28599;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-A5 (Fragment).
 GN HXB5 OR HOXA-5.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Roche P.J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF

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CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC 5'-CYNATTA[GTG]-3'.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
CC -----
CC EMBL; U61978; AAB04754.1; -.
CC HSSP; P02833; 1HOM.
CC
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEOBOX_1; 1.
CC PROSITE; PS50071; HOMEOBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC FT NON_TER 1 1
CC FT DNA_BIND <1 49 HOMEBOX.
CC FT NON_TER 49 49
CC SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;
CC
CC Query Match 58.0%; Score 94; DB 1; Length 49;
CC Best Local Similarity 94.1%; Pred. No. 1.2e-06;
CC Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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CC QY 1 DRQIKWFQNRMKWK 17
CC Db :|||||
CC 31 ERQIKWFQNRMKWK 47
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CC RESULT 9
CC ID HXA7_SHEEP STANDARD; PRT; 71 AA.
CC AC Q28600;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-A7 (Fragment).
CC OS HOXA7 OR HOXA-7.
CC GN Ovis aries (Sheep).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Caprinae; Ovis.
CC OX NCBI_TaxID=9940;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Roche P.J.;
CC RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
CC -----
CC EMBL; U61979; AAB04755.1; -.
CC HSSP; P02833; 9ANT.
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DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
KW NON_TER 1 1
FT DNA_BIND 4 63 HOMEBOX.
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8888 MW; 931049FAC1BAACB7 CRC64;
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CC Query Match 58.0%; Score 94; DB 1; Length 71;
CC Best Local Similarity 94.1%; Pred. No. 1.8e-06;
CC Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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CC QY 1 DRQIKWFQNRMKWK 17
CC Db :|||||
CC 45 ERQIKWFQNRMKWK 61
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CC RESULT 10
CC ID HXC5_NOTVI STANDARD; PRT; 71 AA.
CC AC P31262;
CC DT 01-JUL-1993 (Rel. 26, Created)
CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-C5 (NvHox-3.4) (Fragment).
CC OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
CC OC Notophthalmus.
CC OX NCBI_TaxID=8316;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=92290273; PubMed=1351019;
CC RA Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
CC RT "Homeobox-containing genes in the newt are organized in clusters
CC RT similar to other vertebrates.";
CC RL Gene 114:179-186 (1992).
CC CC
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC
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CC
CC -----
CC EMBL; M84001; AAA49397.1; ALT_INIT.
CC PIR; JC1161; JC1161.
CC HSSP; P02833; 1SAN.
CC
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEOBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEOBOX_1; 1.
CC PROSITE; PS50032; ANTENNAPEDIA; PARTIAL.
CC PROSITE; PS50071; HOMEOBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
KW NON_TER 1 1
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FT  DNA BIND      4   63   HOMEBOX.
FT  NON_TER      71   71
SQ  SEQUENCE      71 AA;  8979 MW;  07999FDE8995B42 CRC64;

Query Match      58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 DRQIKWIFQNRMRKWK 17
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DB  45 ERQIKWIFQNRMRKWK 61

RESULT 11
HM90 APIME
ID  HM90 APIME      STANDARD;      PRT;      74 AA.
AC  P15850;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DE  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Homeobox protein H90 (Fragment).
OS  Apis mellifera (Honeybee)
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC  Apidae; Apis.
OX  NCBI_TaxID=7460;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9009384; PubMed=2574865;
RA  Walldorf U., Fleig R., Gehring W.J.;
RT  "Comparison of homeobox-containing genes of the honeybee and
RT  Drosophila.";
RL  Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975 (1989).
CC  -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC  -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC  EMBL; M29493; AAA27728.1; --
CC  PIR; D34510; D34510.
CC  HSP; P02833; IHOM.
CC  InterPro; IPR001356; Homeobox.
CC  Pfam; PF00046; homeobox; 1.
CC  ProDom; PD000010; Homeobox; 1.
CC  SMART; SM00389; HOX; 1.
CC  PROSITE; PS00027; HOMEBOX_1; 1.
CC  PROSITE; PS00071; HOMEBOX_2; 1.
CC  Homeobox; DNA-binding; Developmental protein; Nuclear protein.
CC  NON_TER      1   1
CC  DNA_BIND      74   74   HOMEBOX.
CC  SEQUENCE      74 AA;  9263 MW;  5FC8FB4F73D3B37 CRC64;

Query Match      58.0%; Score 94; DB 1; Length 74;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 DRQIKWIFQNRMRKWK 17
    :|||||
DB  49 ERQIKWIFQNRMRKWK 65

RESULT 12
HX4 RAT
ID  HX4 RAT      STANDARD;      PRT;      76 AA.
AC  P18865;
DT  01-NOV-1990 (Rel. 16, Created)

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DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Homeobox protein Hox-C4 (R3) (Fragment).
GN  HOXC4 OR HOXC-4.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=Sprague-Dawley;
RX  MEDLINE=89231502; PubMed=2907739;
RA  Falzon M., Chung S.Y.;
RT  "The expression of rat homeobox-containing genes is developmentally
RT  regulated and tissue specific.";
RL  Development 103:601-610 (1988).
CC  -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC  A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC  SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- TISSUE SPECIFICITY: PREDOMINANTLY SPINAL CORD AND KIDNEY.
CC  -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC  "DEFORMED" SUBFAMILY.
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CC  EMBL; M37567; AAA41343.1; --
CC  PIR; C43559; C43559.
CC  HSP; P02833; 9ANT.
CC  InterPro; IPR001827; Antennapedia.
CC  InterPro; IPR001356; Homeobox.
CC  InterPro; IPR000047; HTH lambrapressr.
CC  Pfam; PF00046; homeobox; 1.
CC  PRINTS; PR00031; HYHREPRESSR.
CC  ProDom; PD000010; Homeobox; 1.
CC  SMART; SM00389; HOX; 1.
CC  PROSITE; PS00032; ANTENNAPEIDIA; PARTIAL.
CC  PROSITE; PS00027; HOMEBOX_1; 1.
CC  PROSITE; PS00071; HOMEBOX_2; 1.
CC  Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC  Transcription regulation.
CC  NON_TER      1   1
CC  DNA_BIND      11   70   HOMEBOX.
CC  SEQUENCE      76 AA;  9293 MW;  5235F665C0672385 CRC64;

Query Match      58.0%; Score 94; DB 1; Length 76;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 DRQIKWIFQNRMRKWK 17
    :|||||
DB  52 ERQIKWIFQNRMRKWK 68

RESULT 13
HX5 SALSA
ID  HX5 SALSA      STANDARD;      PRT;      78 AA.
AC  P09637;
DT  01-MAR-1989 (Rel. 10, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Homeobox protein Hox-A5 (S12-B) (Fragment).
GN  HOXA5.
OS  Salmo salar (Atlantic salmon).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC  Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

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CC NCBI_TaxID=8030;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=88226009; PubMed=2897318;
CC Fjose A., Molven A., Eiken H.G.;
CC "Molecular cloning and characterization of homeo-box-containing genes
CC from Atlantic salmon.";
CC Gene 62:141-152(1988).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC EMBL; M18904; AAA49560.1; -
CC PIR; I51342; I51342.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
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CC NON_TER 80 80
CC SEQUENCE 78 AA; 9489 MW; 828DEBDDF78AC820 CRC64;
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CC Query Match 58.0%; Score 94; DB 1; Length 78;
CC Best Local Similarity 94.1%; Pred. No. 2e-06;
CC Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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CC QY 1 DROIKIWFQNRKMKWK 17
CC :|||||
CC 42 ERQIKIWFQNRKMKWK 58
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CC RESULT 14
CC HXA4_LINSA
CC ID HXA4_LINSA STANDARD; PRT; 80 AA.
CC AC P81192;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-A4 (Lshox 4) (Fragment).
CC GN HOXA4.
CC OS Lineus sanguineus (Ribbon worm).
CC OC Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;
CC Lineus.
CC NCBI_TaxID=48190;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=98169491; PubMed=9501210;
CC Kmita-Cunisse M., Loosli F., Berner J., Gehring W.J.;
CC "Homeobox genes in the ribbonworm Lineus sanguineus: evolutionary
CC implications.";
CC Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC "DEFORMED" SUBFAMILY.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR00047; HTH lambrapressr.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00071; HOMEBOX 2; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC NON_TER 1 1
CC DNA_BIND 21 80 HOMEBOX.
CC NON_TER 80 80
CC SEQUENCE 80 AA; 9860 MW; P2CE1B01CB8042F1 CRC64;
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CC Best Local Similarity 94.1%; Pred. No. 2.1e-06;
CC Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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CC QY 1 DROIKIWFQNRKMKWK 17
CC :|||||
CC 52 ERQIKIWFQNRKMKWK 68
CC
CC Db
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CC RESULT 15
CC HX5L_BRARE
CC ID HX5L_BRARE STANDARD; PRT; 81 AA.
CC AC P09013;
CC DT 01-NOV-1988 (Rel. 09, Created)
CC DT 01-NOV-1988 (Rel. 09, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-B5 like (ZF-54) (Fragment).
CC GN HOXB5B OR ZF54 OR ZF-54.
CC OS Brachydanio rerio (Zebrafish) (Danio rerio).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
CC Cyprinidae; Danio.
CC NCBI_TaxID=7955;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=89016617; PubMed=2902580;
CC Njollstad P.R., Molven A., Hordvik I., Apold J., Fjose A.;
CC "Primary structure, developmentally regulated expression and
CC potential duplication of the zebrafish homeobox gene ZF-21.";
CC Nucleic Acids Res. 16:9097-9113(1988).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC -----
CC EMBL; X12803; CAA31291.1; -
CC HSSP; P02833; 1SAN.
CC ZFIN; ZDB-GENE-000823-6; hoxb5b.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
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DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT NON_TER 1
 FT DNA_BIND 6 65 HOMEBOX.
 SQ SEQUENCE 81 AA; 9977 MW; B7698AEFFEB3C6B4 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 81;
 Best Local Similarity 94.1%; Pred. No. 2.1e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRMRMKKK 17
 :|||||
 Db 47 ERQIKIWFQNRMRMKKK 63

Search completed: February 18, 2004, 14:28:14
 Job time : 16.5789 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	513	2 Q8VPV8	Q8VPV8 synechococ
2	37	90.2	107	9 Q9FZX5	Q9FZX5 bacterioph
3	37	90.2	274	16 Q8DKQ6	Q8DKQ6 synechococ
4	37	90.2	282	16 Q8D354	Q8D354 wigglewort
5	37	90.2	288	2 Q8VTT4	Q8VTT4 pseudomonas
6	37	90.2	308	2 Q8K2S2	Q8K2S2 acetobacter
7	37	90.2	311	5 Q94380	Q94380 caenorhabdi
8	37	90.2	313	2 Q8VUQ6	Q8VUQ6 pseudomonas
9	37	90.2	318	16 Q8ZC58	Q8ZC58 versinia pe
10	37	90.2	329	16 Q8XVB4	Q8XVB4 ralestonia s
11	37	90.2	331	16 Q91427	Q91427 pseudomonas
12	37	90.2	341	16 Q8G3A8	Q8G3A8 bruceella su
13	37	90.2	344	16 Q8VEH7	Q8VEH7 bruceella me
14	37	90.2	353	16 Q9A7F0	Q9A7F0 caulobacter
15	37	90.2	377	17 Q59445	Q59445 pyrococcus
16	37	90.2	378	17 Q8U022	Q8U022 pyrococcus

17	37	90.2	379	17 Q9V1W1	Q9V1W1 pyrococcus
18	37	90.2	386	16 Q92U27	Q92U27 rhizobium m
19	37	90.2	393	16 Q987Z1	Q987Z1 rhizobium l
20	37	90.2	399	16 Q8PFQ8	Q8PFQ8 xanthomonas
21	37	90.2	404	17 Q57734	Q57734 pyrococcus
22	37	90.2	405	17 Q9UXV2	Q9UXV2 pyrococcus
23	37	90.2	1291	5 Q9VP46	Q9VP46 drosophila
24	37	90.2	1449	5 Q8MVK4	Q8MVK4 dictyosteli
25	37	90.2	1578	5 Q8IBF7	Q8IBF7 plasmodium
26	37	90.2	2283	5 Q8IC35	Q8IC35 plasmodium
27	36	87.8	82	17 Q26213	Q26213 methanobact
28	36	87.8	162	16 Q53756	Q53756 mycobacteri
29	36	87.8	313	16 Q8FU02	Q8FU02 corynabacte
30	36	87.8	322	16 Q8YGV7	Q8YGV7 bruceella me
31	36	87.8	347	16 Q98KR3	Q98KR3 rhizobium l
32	36	87.8	347	16 Q92QP5	Q92QP5 rhizobium m
33	36	87.8	347	16 Q8GIB0	Q8GIB0 bruceella su
34	36	87.8	348	16 Q8UFX0	Q8UFX0 agrobacteri
35	36	87.8	414	16 Q9K194	Q9K194 vibrio chol
36	36	87.8	439	2 Q93Q61	Q93Q61 klebsiella
37	36	87.8	443	16 Q8ZDM7	Q8ZDM7 versinia pe
38	36	87.8	451	16 Q8D0S7	Q8D0S7 versinia pe
39	36	87.8	618	15 Q88284	Q88284 snakehead r
40	36	87.8	740	6 Q95KV1	Q95KV1 bos taurus
41	36	87.8	745	11 Q8CBT3	Q8CBT3 mus musculu
42	36	87.8	756	6 Q95KV0	Q95KV0 bos taurus
43	36	87.8	764	16 Q8U6N1	Q8U6N1 agrobacteri
44	36	87.8	1120	16 Q8ZRA5	Q8ZRA5 salmonella
45	36	87.8	1120	16 Q8Z8T6	Q8Z8T6 salmonella

ALIGNMENTS

RESULT 1

Q8VPV8 PRELIMINARY; PRT; 513 AA.
 ID Q8VPV8; AC Q8VPV8; DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE NADPH dehydrogenase subunit 4.
 GN NDHD3.
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_taxid=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7942;
 RA Maeda S., Badger M.R., Price G.D.;
 RT "Identification of ChpX and ChpY, catalyzing light-dependent CO2
 RT hydration involved in CO2 uptake in Cyanobacteria.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY029338; AAK37764.1; -
 DR InterPro; IPR003918; NADHub_oxred4.
 DR InterPro; IPR001750; Oxidored_q1.
 DR Pfam; PF00361; oxidored_q1; 1.
 DR PRINTS; PR01437; NUOXDRDTASE4.
 DR KW NAD; Oxidoreductase; Plastocyanine.
 SQ SEQUENCE 513 AA; 54237 MW; 27325765E52524AB CRC64;

Query Match 95.1%; Score 39; DB 2; Length 513;

Best Local Similarity 83.3%; Pred.No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6

:|||||

59 IDWEWL 64

RESULT 2

Q9FZX5

ID Q9FZX5 PRELIMINARY; PRT; 107 AA.

AC O9FX5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 12.6 kDa protein.
OS Bacteriophage GA-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=12345;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094855; PubMed=8940089;
RA Freire R., Serrano M., Salas M., Hermoso J.;
RT "Activation of replication origins in phi29-related phages requires
RT the recognition of initiation proteins to specific nucleoprotein
RT complexes";
RL J. Biol. Chem. 271:31000-31007(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97123975; PubMed=8969297;
RA Illana B., Blanco L., Salas M.;
RT "Functional characterization of the genes coding for the terminal
RT protein and DNA polymerase from bacteriophage GA-1. Evidence for a
RT sliding-back mechanism during protein-primed GA-1 DNA replication.";
RL J. Mol. Biol. 264:453-464(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99370049; PubMed=10438592;
RA Horcajadas J.A., Monsalve M., Rojo F., Salas M.;
RT "The switch from early to late transcription in phage GA-1:
RT characterization of the regulatory protein p4G.";
RL J. Mol. Biol. 290:917-928(1999).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20280072; PubMed=10773070;
RA Gascon I., Lazaro J.M., Salas M.;
RT "Differential functional behavior of viral phi29, NF and GA-1 SSB
RT proteins";
RL Nucleic Acids Res. 28:2034-2042(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX MEIJER W.J.J., Horcajadas J.A., Salas M.;
RT "The phi29 family of phages";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Horcajadas J.A., Meijer W.J.J., Rojo F., Salas M.;
RT "Transcriptional map of the Bacillus bacteriophage GA-1. Analysis of
RT the viral C2 promoter";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; X96987; CAC21518.1; -.
KW Hypothetical protein.
SQ SEQUENCE 107 AA; 12636 MW; A8EF24E68A255E02 CRC64;
Query Match 90.2%; Score 37; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWEWL 6
Db 100 DWEWL 104
|||||
RESULT 3
Q8DKQ6 PRELIMINARY; PRT; 274 AA.
AC Q8DKQ6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CbbY family protein.
GN TLR0803.
OS Synechococcus elongatus (Thermosynechococcus elongatus).

OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1";
RL DNA Res. 9:123-130(2002).
DR EMBL; AP005371; BAC08354.1; -.
KW Complete proteome.
SQ SEQUENCE 274 AA; 30329 MW; 021D35F51D8AB77E CRC64;
Query Match 90.2%; Score 37; DB 16; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 5
Db 49 LDWEWL 53
|||||
RESULT 4
Q8D354 PRELIMINARY; PRT; 282 AA.
AC Q8D354;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CyoA protein.
GN CyoA.
OS Wigglesworthia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=164609;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia";
RL Nat. Genet. 32:402-407(2002).
DR EMBL; AB063521; BAC24293.1; -.
KW Complete proteome.
SQ SEQUENCE 282 AA; 32500 MW; 39CCC2862E5F3B35 CRC64;
Query Match 90.2%; Score 37; DB 16; Length 282;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
Db 134 LDWKWL 139
|||||
RESULT 5
Q8VTT4 PRELIMINARY; PRT; 288 AA.
AC Q8VTT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome o ubiquinol oxidase A (Fragment).
GN CyoA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PML1;
RA Svn C.K.C., Liew C.F., Swarup S.;
RT "Pseudomonas putida cytochrome o ubiquinol oxidase A, B, C, and D
genes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321090; AAL37192.1; -.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
FT NON TER
SQ SEQUENCE 288 AA; 31882 MW; 60E40B3A36516BFC CRC64;

Query Match 90.2%; Score 37; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 108 LDWKWL 113

RESULT 6
Q8KZS2 PRELIMINARY; PRT; 308 AA.
AC Q8KZS2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ubiquinol oxidase subunit II.
OS Acetobacter pasteurianus (Acetobacter turbidans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OX NCBI_TaxID=438;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCI 1193;
RA Takakuwa N., Yamane K., Oda Y., Fukaya M., Tsukamoto Y., Ohnishi M.;
RT "Identification of the acetic acid bacterium NCI 1193 and nucleotide
sequences of the genes encoding enzymes related to acetic acid
production.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086015; BAB97173.1; -.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
KW Oxidoreductase.
SQ SEQUENCE 308 AA; 33988 MW; F93006DBE528AD2C CRC64;

Query Match 90.2%; Score 37; DB 2; Length 308;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 135 LDWKWL 140

RESULT 7
Q94380 PRELIMINARY; PRT; 311 AA.
AC Q94380;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ZC47.13 protein.
GN ZC47.13.

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OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z81141; CAB03488.2; -.
DR WormPep; ZC47.13; CE25668.
DR InterPro; IPR002900; DUF38.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01827; FTH; 1.
SQ SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;

Query Match 90.2%; Score 37; DB 5; Length 311;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 295 LEWEWL 300

RESULT 8
Q8VUQ6 PRELIMINARY; PRT; 313 AA.
AC Q8VUQ6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytochrome o oxidase A.
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT2442;
RA Fukumori F., Kishii M.;
RT "Characterization of the toluene-sensitive mutants of Pseudomonas
putida KT2442TOL.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB066295; BAB83593.1; -.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
KW Oxidoreductase.
SQ SEQUENCE 313 AA; 34557 MW; 193E3F7F8EBDA42B CRC64;

Query Match 90.2%; Score 37; DB 2; Length 313;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKWL 138

RESULT 9
Q8ZC58

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ID Q8ZC58 PRELIMINARY; PRT; 318 AA.
AC Q8ZC58;
DT 01-MAR-2002 (TREMREL. 20, Created)
DT 01-MAR-2002 (TREMREL. 20, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-).
GN CYOA OR YPO3164 OR Y1021.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titchall R.W., Holden M.T.G.,
RA Prentice M.B., Sebaiha M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AJ414155; CAC92399.1; -.
DR EMBL; AE013705; AM84602.1; -.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyoA_II.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR Oxidoreductase; Complete proteome.
KW SEQUENCE 318 AA; 35049 MW; E2947941923016D3 CRC64;
Query Match 90.2%; Score 37; DB 16; Length 318;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 135 LDWKWL 140
|||||

RESULT 10
Q8XVB4 PRELIMINARY; PRT; 329 AA.
AC Q8XVB4;
DT 01-MAR-2002 (TREMREL. 20, Created)
DT 01-MAR-2002 (TREMREL. 20, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)
DE Oxidoreductase protein (EC 1.10.3.-).
GN CYOAL OR RSC2917 OR R500308.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

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RA Chandler M., Choiane N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,
RA Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502(2002).
DR EMBL; AL646072; CAD16624.1; -.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyoA_II.
DR InterPro; IPR002429; Cyc_C_ox_2.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;
Query Match 90.2%; Score 37; DB 16; Length 329;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKWL 138
|||||

RESULT 11
Q9I427 PRELIMINARY; PRT; 331 AA.
AC Q9I427;
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Cytochrome o ubiquinol oxidase subunit II.
GN CYOA OR PAI317.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huftnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sajer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004561; AAG04706.1; -.
DR HSP; P18400; 1CYW.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyoA_II.
DR InterPro; IPR002429; Cyc_C_ox_2.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Complete proteome.
SQ SEQUENCE 331 AA; 36623 MW; DC449ED0FF0BB66 CRC64;
Query Match 90.2%; Score 37; DB 16; Length 331;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKWL 138
|||||

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SQ SEQUENCE 344 AA; 38948 MW; B643C91321B600EC CRC64;

Query Match 90.2%; Score 37; DB 16; Length 344;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 141 LDWKWL 146

RESULT 14
Q9A7F0 PRELIMINARY; PRT; 353 AA.
ID Q9A7F0;
AC Q9A7F0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ubiquinol oxidase subunit II.
GN CC1773.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolenay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005851; AAK23749.1; -.
DR HSSP; P18400; 1CYW.
DR TIGR; CC1773; -.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyoA_II.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
KW Complete proteome.
SQ SEQUENCE 353 AA; 38817 MW; 607AF178B2AD184D CRC64;

Query Match 90.2%; Score 37; DB 16; Length 353;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 146 LDWKWL 151

RESULT 15
OS9445 PRELIMINARY; PRT; 377 AA.
ID OS9445;
AC OS9445;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 377AA long hypothetical sarcosine oxidase.
GN PH1751.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;

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RA Kavarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuwa H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 DR ENBL; AP000007; BAA30865.1; -.
 DR InterPro; IPR006076; IPR006076.
 DR InterPro; IPR000205; NAD_binding.
 DR Pfam; PF01266; DAO; 1.
 KW Complete proteome.
 SQ SEQUENCE 377 AA; 42421 MW; FA9B0966328EA097 CRC64;

Query Match 90.2%; Score 37; DB 17; Length 377;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 DB 354 LDWEW 358

Search completed: February 18, 2004, 14:35:59
 Job time : 18.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	501	1 YBQ6_YEAST	P38081 saccharomyc
2	37	90.2	210	1 KTHY_SCHPO	P36590 schizosacch
3	37	90.2	281	1 Y373_MYCPN	P75227 mycoplasma
4	37	90.2	296	1 CYOA_BUCAI	P57544 buchnera ap
5	37	90.2	307	1 COX2_ACERC	P50653 acetobacter
6	37	90.2	314	1 CYOA_PSEPU	Q9wrl1 pseudomonas
7	37	90.2	488	1 YKTL_CABEL	P34312 caenorhabdi
8	37	90.2	1275	1 RFBC_MYXXA	Q50864 myxococcus
9	36	87.8	289	1 Y250_CORGL	P42459 corynebacte
10	36	87.8	290	1 CYOA_BUCAP	Q8k993 buchnera ap
11	36	87.8	745	1 TKKA_HUMAN	O15111 h inhibitor
12	36	87.8	745	1 IKKA_MOUSE	Q60680 m inhibitor
13	36	87.8	756	1 IKKB_MOUSE	O14920 homo sapien
14	36	87.8	757	1 IKKB_MOUSE	O88351 mus musculu
15	36	87.8	757	1 IKKB_MOUSE	Q9qy78 rattus norv
16	35	85.4	385	1 YPSC_BACSU	P50840 bacillus su
17	34	82.9	191	1 GDIR_CABEL	Q20496 caenorhabdi
18	34	82.9	470	1 LAC2_ONCMY	Q92091 oncorhynchu
19	34	82.9	473	1 LACG_LACAC	P50977 lactobacill
20	34	82.9	844	1 AMPN_LACHE	Q10730 lactobacill
21	34	82.9	1113	1 Y140_MYCGE	P47386 mycoplasma
22	34	82.9	1113	1 Y140_MYCPN	P75033 mycoplasma
23	34	82.9	1120	1 KEFA_ECOLI	P77338 escherichia
24	33	80.5	94	1 FIXX_AZOVI	P36588 azotobacter
25	33	80.5	125	1 VG61_BPMD2	O64253 mycobacteri
26	33	80.5	156	1 RNH_PHOLU	Q8gf77 photorhabdu
27	33	80.5	162	1 PHZB_PSEFL	Q51788 pseudomonas
28	33	80.5	223	1 WNT1_STRPU	P28094 strongyloce
29	33	80.5	387	1 INTD_ECOLI	P24218 escherichia
30	33	80.5	418	1 HLT_VIBFA	Q99289 vibrio para
31	33	80.5	468	1 WNTG_DROME	P09615 drosophila
32	33	80.5	483	1 ENGA_BRUME	Q9yfh2 bruceella me
33	33	80.5	547	1 SPAK_HUMAN	Q9uew8 homo sapien

34	33	80.5	553	1 SPAK_RAT	O88506 rattus norv
35	33	80.5	556	1 SPAK_MOUSE	Q921w9 mus musculu
36	33	80.5	725	1 AREA_PENCH	Q01582 penicillium
37	33	80.5	807	1 PHK_RHILLO	Q988v7 rhizobium 1
38	33	80.5	860	1 AREA_PENRO	O13508 penicillium
39	33	80.5	865	1 NRFA_PENUR	Q92269 penicillium
40	33	80.5	866	1 AREA_ASPOR	O13415 aspergillus
41	33	80.5	876	1 AREA_EMENI	P17429 emericella
42	33	80.5	878	1 SYV_METJA	Q58413 methanococc
43	33	80.5	882	1 AREA_ASPNG	O13412 aspergillus
44	33	80.5	891	1 SYV_PYRAB	Q9uy55 pyrococcus
45	33	80.5	891	1 SYV_PYRHO	O58052 pyrococcus

ALIGNMENTS

RESULT 1
YBQ6_YEAST STANDARD; PRT; 501 AA.
ID YBQ6_YEAST
AC P38081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 57.8 kDa protein in PRP6-MUM2 intergenic region.
GN YBR056W OR YBR0510.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95321020; PubMed=7597852;
RA Aljinovic G., Pohl T.M.;
RT "Sequence and analysis of 24 kb on chromosome II of Saccharomyces
cerevisiae."
RL Yeast 11:475-479 (1995).
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
HYDROLASES).
CC -----
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CC -----
CC EMBL; Z35925; CAA84999.1; -;
CC EMBL; Z46260; CAA86399.1; -;
CC PIR; S45914; S45914.
CC DR S0000260; YBR056W.
CC InterPro; IPR001547; Glyco_hydro_5.
CC PROSITE; PS00659; GLYCOSYL_HYDROL_F5; FALSE NEG.
CC Hydrothermal protein; Hydrolase; Glycosidase.
CC ACT_SITE 236 236 PROTON DONOR (BY SIMILARITY).
CC ACT_SITE 333 333 NUCLEOPHILE (BY SIMILARITY).
CC SQ SEQUENCE 501 AA; 57822 MW; 5133A161736ADD3 CRC64;
Query Match 95.1%; Score 39; DB 1; Length 501;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWEWL 6
Db 109 IDWEWL 114
RESULT 2
KTHY_SCHPO STANDARD; PRT; 210 AA.
ID KTHY_SCHPO
AC P36590; O74528;

```

FT CONFLICT 59 59 K -> T (IN REF. 1)...
FT CONFLICT 80 93 TIQIYIEQINKGVT -> PSIIYRANQRCN (IN REF.
FT 1).
FT CONFLICT 125 125 P -> T (IN REF. 1).
FT CONFLICT 164 164 F -> L (IN REF. 1).
FT CONFLICT 186 186 S -> YA (IN REF. 1).
FT CONFLICT 191 191 H -> D (IN REF. 1).
SQ SEQUENCE 210 AA; 24249 MW; 4266144AEDAB68C0 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 210;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEW 5
    |||||
Db 112 LDWEW 116

RESULT 3
Y373 MYCPN
ID Y373 MYCPN STANDARD; PRT; 281 AA.
AC P75227;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG373 homolog (G12_orf281).
DE MFN551 OR MP291.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Hammett-Reich R., Hilbert H., Flaggens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RL pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
CC EMBL; AE000027; AAB95939.1; -.
CC PIR; S73617; S73617.
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 281 AA; 32569 MW; FC70957510D7BEF3 CRC64;
SQ SEQUENCE 281 AA; 32569 MW; FC70957510D7BEF3 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 281;
Best Local Similarity 100.0%; Pred.No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWEWL 6
    |||||
Db 271 DWEWL 275

RESULT 4
CYOA BUCAI
ID CYOA BUCAI STANDARD; PRT; 296 AA.
AC P57544;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA OR BU472.

```

OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.,
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
 GROWN AT HIGH AERATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC -----
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 CC -----
 CC EMBL; AP001119; BAB13169.1; -
 DR HSSP; P18400; 1CYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR006333; CytoA_II.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR InterPro; IPR000437; Prok_LipoProt.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR TIGRFAMs; TIGR01433; CytoA; 1.
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE NEG.
 DR Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 KW Signal; Lipoprotein; Complete proteome.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 54 POTENTIAL.
 FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 79 99 POTENTIAL.
 FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
 SQ SEQUENCE 296 AA; 1AB2B4F0408FFBAC CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 296;
 Best Local Similarity 83.3%; Pred. No. 35;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 125 LDWKWL 130
 RESULT 5
 ID_QOX2_ACEAC STANDARD; PRT; 307 AA.
 AC P30653;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
 DE A1 subunit 2) (Oxidase BA(3) subunit 2).
 GN CYAB.
 OS Acetobacter aceti.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Acetobacter.

OX NCBI_TaxID=435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1023;
 RX MEDLINE=93322308; PubMed=8392509;
 RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
 RA Kawamura Y., Horinouchi S., Beppu T.,
 RT "Characterization of a cytochrome a1 that functions as a ubiquinol
 oxidase in Acetobacter aceti.";
 RL J. Bacteriol. 175:4307-4314(1993).
 CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D13185; BAA02480.1; -
 DR PIR; A36885; A36885.
 DR HSSP; P18400; 1CYW.
 DR InterPro; IPR001505; Copper_CuA.
 DR InterPro; IPR006333; CytoA_II.
 DR InterPro; IPR002429; Cyt_c_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR PRINTS; PR01166; CYCOXIDASEII.
 DR ProDom; PD000131; Copper_CuA; 1.
 DR TIGRFAMs; TIGR01433; CytoA; 1.
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 DR Oxidoreductase; Transmembrane; Respiratory chain; Signal;
 KW Lipoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 SQ SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;
 Query Match 90.2%; Score 37; DB 1; Length 307;
 Best Local Similarity 83.3%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 135 LDWKWL 140
 RESULT 6
 ID_QVOA_PSEPU STANDARD; PRT; 314 AA.
 AC Q9WWE1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase BO(3) subunit 2).
 DE subunit 2).
 GN CYOA.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IH-2000;
 RX MEDLINE=99085656; PubMed=9868765;
 RA Hirayama H., Takami H., Inoue A., Horikoshi K.;

RT "Isolation and characterization of toluene-sensitive mutants from
RT Pseudomonas putida IH-2000.";
RL FEWS Microbiol Lett. 169:219-225(1998).
CC -1- FUNCTION: CYTOCHROME C TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB016787; BAA76356.1; -.
CC HSSP; P18400; ICYW.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CytoA II.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRfam; TIGR01433; CytoA; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Inner membrane; Signal; Lipoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 POTENTIAL.
FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 314 AA; 34702 MW; 96EE04FC3AA77F07 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 314;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 133 LDWKWL 138

RESULT 7
ID YKTL_CABEL STANDARD; PRT; 488 AA.
AC P34312;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein C07A9.1 in chromosome III precursor.
GN C07A9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Favello A., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favellio A., Fraser A.,
RA Fultoon L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,

RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Suleston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z29094; CAA82340.1; -.
CC PIR; S40706; S40706.
DR HSSP; P23807; IIXX.
DR WormPep; C07A9.1; CE00502.
DR InterPro; IPR002619; CX.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR ProDom; PD006744; CX; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.
KW Hypothetical protein; Lectin; Signal.
FT SIGNAL 1 49 POTENTIAL.
FT CHAIN 50 488 HYPOTHETICAL PROTEIN C07A9.1 IN
FT DOMAIN 224 341 CHROMOSOME III.
FT CARBOHYD 187 187 C-TYPE LECTIN.
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 488 AA; 54717 MW; 9022691E47078814 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
DB 287 DWEWL 291

RESULT 8
ID RFBC_MYXXA STANDARD; PRT; 1275 AA.
AC Q50864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE O-antigen biosynthesis protein rfbc.
GN RFBC.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DK6640;
RX MEDLINE=96198166; PubMed=8626291;
RA Guo D., Bowden M.G., Pershad R., Kaplan H.B.;
RT "The Myxococcus xanthus rfABC operon encodes an ATP-binding cassette
RT transporter homolog required for O-antigen biosynthesis and
RT multicellular development.";
RL J. Bacteriol. 178:1631-1639(1996).
CC -1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
CC
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EMBL; U36795; AAB05019.1; -.
 DR PIR; T18556; T18556.
 DR InterPro; IPR0011296; Glyco trans 1.
 DR InterPro; IPR001173; Glyco trans 2.
 DR Pfam; PF00534; Glycos transf 1; 1.
 DR Pfam; PF00535; Glycos transf 2; 2.
 KW Lipopolysaccharide biosynthesis.
 SQ SEQUENCE 1275 AA; 139596 MW; 3AF9662A10A140F1 CRC64;

Query Match 90.2%; Score 37; DB 1; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
 |||||
 Db 349 DWEWL 353

RESULT 9

Y250 CORGL STANDARD; PRT; 289 AA.
 AC P42459;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein Cgl0250 (ORFX).
 GN CGL0250.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RX MEDLINE=94161495; Pubmed=8117072;
 RA Patek M., Krumbach K., Eggeling L., Sahn H.;
 RT "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis."
 RT Appl. Environ. Microbiol. 60:133-140(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59.

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EMBL; X70959; CAA50297.1; ALT FRAME.
 DR EMBL; AP05274; BAB97642.1; -.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 44 64 POTENTIAL.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.

FT TRANSMEM 196 216 POTENTIAL.
 FT TRANSMEM 230 250 POTENTIAL.
 FT TRANSMEM 258 278 POTENTIAL.
 SQ SEQUENCE 289 AA; 31381 MW; 5C7A38DC8BFF078A CRC64;

Query Match 87.8%; Score 36; DB 1; Length 289;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 :|||:
 Db 256 VDWEWL 261

RESULT 10

CYOA_BUCAP STANDARD; PRT; 290 AA.
 ID CYOA_BUCAP
 AC Q8K993;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase subunit 2).
 DE CYOA OR BUSG456.
 GN Buchnera aphidicola (subsp. Schizaphis graminum).
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; Pubmed=12089438;
 RA Tamas I., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
 RA Tarnagge J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria."
 RL Science 296:2376-2379(2002).
 CC -1- FUNCTION: Cytochrome O terminal oxidase complex is the component of the aerobic respiratory chain that predominates when cells are grown at high aeration (By similarity).
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS. BUT LACK HEME-BINDING DOMAIN.

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EMBL; AE014121; AAM67999.1; -.
 DR InterPro; IPR001505; Copper CuA.
 DR InterPro; IPR006333; CyoA II.
 DR InterPro; IPR002429; Cyt C ox 2.
 DR InterPro; IPR000437; Prok_Lipprot.
 DR Pfam; PF00116; COX2; 1.
 DR PRINTS; PR01166; CYCOXIDASEII.
 DR ProDom; PD000131; Copper CuA; 1.
 DR TIGRFAMs; TIGR01433; CyoA; 1.
 DR PROSITE; PS00013; PROKAR_LIPPROTEIN; FALSE NEG.
 KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane; Signal; Lipoprotein; Complete proteome.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290
 FT LIPID 25 25 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 25 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 63 POTENTIAL.
 FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 108 POTENTIAL.
 FT DOMAIN 109 290 EXTRACELLULAR (POTENTIAL).
 SQ SEQUENCE 290 AA; 33730 MW; 3D80A02A84732963 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 290;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 Db 134 LDWRWL 139

RESULT 11

IKKA_HUMAN STANDARD; PRT; 745 AA.
 ID 015111; O14666; Q13132; O92467;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)
 DE (I kappa-B kinase alpha) (IKK- α) (IKK- α) (IKK- α) (IKK- α)
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitinous
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
 GN CHUK OR IKK- α .
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RP TISSUE=T-cell;
 RX MEDLINE=97386461; PubMed=9244310;
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
 RT "Identification and characterization of an IkappaB kinase.";
 RL Cell 90:373-383(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97394468; PubMed=9252186;
 RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RT "A cytokine-responsive IkappaB kinase that activates the transcription
 RT factor NF-kappaB.";
 RL Nature 388:548-554(1997).
 RN [3]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [5]
 RP SEQUENCE OF 32-745 FROM N.A.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of

RT Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RN [8]
 RP IKK- α -IKK β BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delbase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [9]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11]
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; IKK β AND IKK γ .
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKB-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKK β , IKK γ and CREBBP.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF012890; AAC51662.1; -;
 DR EMBL; AF009225; AAC51671.1; -;
 DR EMBL; AF080157; AAC08996.1; -;
 DR EMBL; U22512; AAC50713.1; -;
 DR HSSP; Q63450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -;

GO: GO:0005737; C:cytoplasm; TAS.
 GO: GO:0008384; F:IkappaB kinase activity; TAS.
 GO: GO:0007345; P:embryogenesis and morphogenesis; TAS.
 GO: GO:0007252; P:I-kappaB phosphorylation; TAS.
 GO: GO:0006955; P:immune response; TAS.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR002290; Ser_Thr_kinase.
 Pfam: PF00069; pkinase; 1.
 PRINTS: PR00109; TYRKINASE.
 ProDom: PD000001; Prot_kinase; 1.
 SMART: SM00220; S_TKC; 1.
 PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 PROSITE: PS00108; PROTEIN KINASE ST; 1.
 PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 Transferrase: Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MUTAGEN 176 176 T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->N: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> Y (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS -> DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LDMEWL 6
 Db 738 LDMSWL 743
 RESULT 12
 IKKA_MOUSE
 ID IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9DX33;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)
 DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/c;
 RX MEDLINE=96044444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";

Genomics 27:348-351(1995).
 [2]
 RL SEQUENCE FROM N.A. (ISOFORM 1).
 RN STRAIN=BALB/c;
 RP MEDLINE=96258427; PubMed=8777433;
 RX Connolly M.A., Marcu K.B.;
 RA "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain.";
 RT Cell. Mol. Biol. Res. 41:537-549(1996).
 RL [3]
 RN SEQUENCE FROM N.A. (ISOFORM 3).
 RP STRAIN=C57BL/6J; TISSUE=Colon;
 RC MEDLINE=21085660; PubMed=11217851;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gotjohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL [4]
 RN ALTERNATIVE SPLICING.
 RP MEDLINE=20198447; PubMed=10733566;
 RX McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R., Galeziunas R., Marcu K.B.;
 RA "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements.";
 RT Mol. Cell. Biol. 20:2635-2649(2000).
 RL [5]
 RN PHOSPHORYLATION BY MAP3K14/NIK.
 RP MEDLINE=98188238; PubMed=9520401;
 RX Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H., Okumura K.;
 RA "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RL [6]
 RN IKKA-IKKB BINDING.
 RP MEDLINE=99212141; PubMed=10195894;
 RX Delhase M., Hayakawa M., Chen Y., Karin M.;
 RA "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";
 RT Science 284:309-313(1999).
 RL [7]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RX Nemoto S., DiDonato J.A., Lin A.;
 RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RT Mol. Cell. Biol. 18:7336-7343(1998).
 RL [8]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RX Jobin C., Sartor R.B.;
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal RT inflammation and protection.";
 RT Am. J. Physiol. 278:C451-C462(2000).

CC -|- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC
 CC -|- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC
 CC -|- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKKG and CREBBP (By
 CC similarity).
 CC
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
 CC -|- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -|- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -|- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; U12473; AAC52589.1; -;
 CC DR EMBL; AK018671; BAB31335.1; -;
 CC DR PIR; I49101; I49101.
 CC DR HSSP; O63450; IAO6.
 CC DR MGD; MG1:99484; Chuk.
 CC DR InterPro; IPR000719; Prot_kinase.
 CC DR InterPro; IPR002290; Ser_thr_kinase.
 CC DR Pfam; PF00069; pkinase; 1.
 CC DR PRINTS; PR00109; TYRKINASE.
 CC DR ProDom; PD000001; Prot_kinase; 1.
 CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 CC DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation; Alternative splicing.
 CC KW DOMAIN 15 300 PROTEIN KINASE.
 CC FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 CC FT DOMAIN 738 743 NEMO-BINDING.
 CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 144 144 BY SIMILARITY.
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)
 CC (BY SIMILARITY).
 CC FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
 CC (BY SIMILARITY).
 CC FT VARSPPLIC 452 471 MSLRLYNALTKMKNLTLS -> IPRKNVKSERNGRKGH
 CC SLF (in isoform 2).
 CC FT VARSPPLIC 472 745 /FTId=VSP_004866.
 CC FT Missing (in isoform 2).
 CC FT VARSPPLIC 577 584 /FTId=VSP_004867.
 CC FT Missing (in isoform 3).
 CC FT VARSPPLIC 584 /FTId=VSP_004868.

FT VARSPPLIC 585 745 Missing (in isoform 3).
 FT /FTId=VSP_004869.
 FT CONFLICT 236 236 K -> E (IN REF. 3).
 FT CONFLICT 400 400 S -> Y (IN REF. 3).
 SQ .SEQUENCE 745 AA; 84728 MW; 3BF5582AFF92233 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 Db 738 LDWSWL 743
 RESULT 13
 ID IKKB HUMAN STANDARD; PRT; 756 AA.
 AC O14920; O75327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 GN IKKB OR IKKB
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RX MEDLINE=98008814; PubMed=9346485;
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
 RT IkappaB kinase-alpha and NIK.";
 RL Science 278:866-869(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 RT 8p12--p11 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzjanski M.I., Skalska U., Smailus D.E.,
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN IKK PHOSPHORYLATION.
RP MEDLINE=99038238; PubMed=9819420;
RX Nemoto S., DiDonato J.A., Lin A.,
RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [7]
RN REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.,
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
RN [8]
RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (By similarity).
CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
CC complex. Phosphorylated IKB-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
CC and CREBBP.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.

DR GO: 0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00240; ubiquitin; 1.
DR ProDom: PD000001; Prot kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 PHOSPHORYLATION.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
FT EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT CONFLICT 231 255 WSKVKRKSEVDIVVSEDLNGTVKE -> CVRMWPGTVVHVS
FT CNPSTLGGGRWIT (IN REF. 5).
FT CONFLICT 425 425 Q -> H (IN REF. 1).
SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
Query Match 87.8%; Score 36; DB 1; Length 756;
Best Local Similarity 83.3%; Pred. No. 1-2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDWEWL 6
DB 737 LDWSWL 742
RESULT 14
IKKB_MOUSE
ID IKKB_MOUSE STANDARD; PRT; 757 AA.
AC Q88351; Q9RIJ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.,
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of IKB.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DEVELOPMENTAL STAGE.

RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-ALPHA-P65-P50
 CC complex. Phosphorylated IKB-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBBP (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 CC -I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 CC the mouse embryo, at E9.5 day its expression begins to be
 CC localized to the brain, neural ganglia, neural tube, and in liver
 CC at E12.5 day. At E15.5 day, the expression is further restricted
 CC to specific tissues of the embryo.
 CC -I- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF026524; AAC23557.1; -;
 CC EMBL; AF088910; AAD52095.1; -;
 CC HSSP; Q63450; 1A06.
 CC MGD; MGI:1338071; Ikbb.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_Thr_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00069; pkinase; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation.
 CC DOMAIN 15 300 PROTEIN KINASE.
 CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 CC FT DOMAIN 737 742 NEMO-BINDING.
 CC FT NF_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 145 145 BY SIMILARITY.
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 736 TLDWSLQWDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 DB 737 LDWSWL 742
 RESULT 15
 IKKB RAT STANDARD; PRT; 757 AA.
 ID IKKB RAT AC Q9QV78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-ALPHA-P65-P50
 CC complex. Phosphorylated IKB-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBBP (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----

DR EMBL; AF115282; AAF21978.1; -;
 DR HSSP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN_KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFFE46A7DF91F9C CRC64;

Query Match 87.8%; Score 36; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
 |||||
 Db 737 LDWSWL 742

Search completed: February 18, 2004, 14:28:14
 Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	95.1	501	2 S45914	probable glucan 1,
2	37	90.2	210	2 T41553	thymidylate kinase
3	37	90.2	210	2 S28955	dTMP kinase (EC 2.
4	37	90.2	242	2 T27590	hypothetical prote
5	37	90.2	277	1 JC5900	bo-type ubiquinol
6	37	90.2	281	2 S73617	MG373 homolog G12
7	37	90.2	286	2 A84985	cytochrome o ubiq
8	37	90.2	307	1 A36885	bo-type ubiquinol
9	37	90.2	318	2 AD0384	cytochrome o ubiq
10	37	90.2	331	2 D83480	cytochrome o ubiq
11	37	90.2	344	2 AG3489	cytochrome o ubiq
12	37	90.2	353	2 A87469	ubiquinol oxidase
13	37	90.2	377	2 B71184	probable sarcosine
14	37	90.2	379	2 F75144	sarcosine oxidase,
15	37	90.2	386	2 C96006	probable cytochrom
16	37	90.2	404	2 A71213	alanine-tRNA ligas
17	37	90.2	405	2 G75027	hypothetical prote
18	37	90.2	488	2 S40706	O-antigen biosynt
19	37	90.2	1275	2 T18556	hypothetical prote
20	36	87.8	82	2 C69013	hypothetical prote
21	36	87.8	162	2 C70829	hypothetical prote
22	36	87.8	270	2 I40724	hypothetical prote
23	36	87.8	322	2 AI3395	NADH2 dehydrogen
24	36	87.8	348	2 AE2733	NADH ubiquinone ox
25	36	87.8	348	2 G97514	NADH dehydrogenase
26	36	87.8	414	2 B82408	hypothetical prote
27	36	87.8	443	2 AE0309	probable sugar tra
28	36	87.8	745	1 I49101	conserved helix-lo
29	36	87.8	764	2 AD3144	formate dehydrogen

30	36	87.8	764	2 H98143	cbbBc protein (U60
31	36	87.8	1120	2 AI0561	integral membrane
32	35	85.4	332	2 AH2593	cytochrome o ubiq
33	35	85.4	377	2 B97376	cytochrome ba(3) (
34	35	85.4	378	2 T12895	hypothetical prote
35	35	85.4	385	2 F69941	conserved hypotet
36	35	85.4	420	2 A54759	cytochrome ba(3) c
37	35	85.4	451	2 G82218	sensor histidine k
38	35	85.4	480	2 T24087	hypothetical prote
39	35	85.4	660	2 S66708	probable membrane
40	35	85.4	700	2 T24092	hypothetical prote
41	35	85.4	723	2 T32136	hypothetical prote
42	35	85.4	765	2 T35719	chitinase - Strept
43	35	85.4	783	2 F88808	protein RO9E10.3 [
44	35	85.4	854	2 C83905	hypothetical prote
45	35	85.4	903	2 T20804	hypothetical prote

ALIGNMENTS

RESULT 1

S45914
probable glucan 1,3-beta-glucosidase (EC 3.2.1.58) YBR056w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0510
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S45914; S49511; S55855
R;Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
A;Reference number: S45906
submitted to the Protein Sequence Database, August 1994
A;Accession: S45914
A;Molecule type: DNA
A;Residues: 1-501 <ALJ>
A;Cross-references: EMBL:Z35925; NID:G536292; PID:G536293; MIPS:YBR056w
A;Experimental source: strain S288C
R;Aljinovic, G.
submitted to the EMBL Data Library, October 1994
A;Description: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae
A;Reference number: S49503
A;Molecule type: DNA
A;Residues: 1-501 <AL2>
A;Cross-references: EMBL:Z46260; NID:G559942; PID:G559952
A;Experimental source: strain S288C
R;Aljinovic, G.; Pohl, T.M.
Yeast 11, 475-479, 1995
A;Title: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae.
A;Reference number: S55846; MUID:95321020; PMID:7597852
A;Accession: S55855
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-501 <ALW>
A;Cross-references: EMBL:Z46260; NID:G559942; PID:CAA86399.1; PID:G559952
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
C;Genetics:
A;Cross-references: SGD:S0000260
A;Map position: 2R
C;Keywords: glycosidase; hydrolase

Query Match 95.1%; Score 39; DB 2; Length 501;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
:|||||
Db 109 IDWEWL 114

RESULT 2

T41553
thymidylate kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C:Accession: T41553
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z22001
 A:Accession: T41553
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-210 <WOO>
 A:Cross-references: EMBL:AL023794; PIDN:CAA19357.1; GSPDB:GN00068; SPDB:SPCC70.07C
 A:Experimental source: strain 972h-; cosmid c70
 C:Genetics:
 A:Gene: SPDB:SPCC70.07C
 A:Map position: 3
 A:Introns: 45/1; 110/3
 C:Superfamily: dTMP kinase

Query Match 90.2%; Score 37; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 |||||
 DB 112 LDWEW 116

RESULT 3
 S28955
 dTMP kinase (EC 2.7.4.9) - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jan-2001
 C:Accession: S28955
 R:Abaggar, L.T.; Yeh, Y.I.S.; Jong, A.Y.
 Biochim. Biophys. Acta 1132, 222-224, 1992
 A:Title: Functional and structural conservation of *Schizosaccharomyces pombe* dTMP kinase
 A:Reference number: S28955; MUID:93003330; PMID:1327149
 A:Accession: S28955
 A:Molecule type: mRNA
 A:Residues: 1-210 <ABA>
 A:Cross-references: EMBL:X65868; NID:g4973; PIDN:CAA46698.1; PID:g4974
 C:Superfamily: dTMP kinase
 C:Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase
 F:14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 90.2%; Score 37; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 |||||
 DB 111 LDWEW 115

RESULT 4
 T27590
 hypothetical protein ZC47.13 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T27590
 R:McMurray, A.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z20391
 A:Accession: T27590
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-242 <WIL>
 A:Cross-references: EMBL:Z81141; PIDN:CAB03488.1; CESP:ZC47.13
 A:Experimental source: clone ZC47
 C:Genetics:
 A:Gene: CESP:ZC47.13
 A:Introns: 172/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZC47.9

Query Match 90.2%; Score 37; DB 2; Length 242;
 Best Local Similarity 83.3%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWEWL 6
 |||||
 DB 226 LEWEWL 231

RESULT 5
 JC5900
 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - *Bradyrhizobium japonicum*
 C:Species: *Bradyrhizobium japonicum*
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JC5900
 R:Surpin, M.A.; Luebben, M.; Maier, R.J.
 Gene 183, 201-206, 1996
 A:Title: The *Bradyrhizobium japonicum* coxWYZ gene cluster encodes a bb3-type ubiquinol
 A:Reference number: JC5900; MUID:97149299; PMID:8996107
 A:Accession: JC5900
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-277 <SUR>
 C:Genetics:
 A:Gene: coxW
 C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp

Query Match 90.2%; Score 37; DB 1; Length 277;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 DB 108 LDWKWL 113

RESULT 6
 S73617
 MG373 homolog G12_orf281 - *Mycoplasma pneumoniae* (strain ATCC 29342)
 C:Species: *Mycoplasma pneumoniae*
 A:Variety: ATCC 29342
 C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
 C:Accession: S73617
 R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A:Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*
 A:Reference number: S73327; MUID:97105885; PMID:8948633
 A:Accession: S73617
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-281 <HIM>
 A:Cross-references: EMBL:AE000027; GB:U00089; NID:g1673941; PIDN:AAB95939.1; PID:g167396
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Genetic code: SGC3

Query Match 90.2%; Score 37; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEWL 6
 |||||
 DB 271 DWEWL 275

RESULT 7
 A84985
 cytochrome o ubiquinol oxidase subunit II [imported] - *Buchnera* sp. (strain APS)
 C:Species: *Buchnera* sp.
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
 C:Accession: A84985
 R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: A84985
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <STO>
A;Cross-references: GB:AF000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: cyoA; BU472
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 296;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:|
Db 125 LDWKWL 130

RESULT 8
A36885
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti
N;Alternate names: cytochrome a1 chain II
C;Species: Acetobacter aceti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A36885
R;Fukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horinouchi
J. Bacteriol. 175, 4307-4314, 1993
A;Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A
A;Reference number: A36885; MUID:93322308; PMID:8392509
A;Accession: A36885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <FOK>
A;Cross-references: GB:DL3185; NID:g409064; PIDN:BA02480.1; PID:g433186
A;Experimental source: isolate 1023
C;Genetics:
A;Gene: cyaB
C;Complex: heterotetramer; chains I, II, III and IV
C;Function:
A;Description: terminal oxidase for ethanol oxidation
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>
F;48-64/Domain: transmembrane #status predicted <TM1>
F;89-105/Domain: transmembrane #status predicted <TM2>

Query Match 90.2%; Score 37; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:|
Db 135 LDWKWL 140

RESULT 9
AD0384
Cytochrome O ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Yersinia pestis (stra
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD0384
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AD0384
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92399.1; PID:g15981102; GSPDB:GN00175
C;Genetics:
A;Gene: cyoA
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res;

Query Match 90.2%; Score 37; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:|
Db 135 LDWKWL 140

RESULT 10
D83480
Cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (s
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83480
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <STO>
A;Cross-references: GB:AE004561; GB:AE004091; NID:g9947253; PIDN:AAG04706.1; GSPDB:GN00
A;Experimental source: strain PA01
C;Genetics:
A;Gene: cyoA; PA1317
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 331;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||:|
Db 133 LDWKWL 138

RESULT 11
AG3489
Cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002
C;Accession: AG3489
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL53082.1; PID:g17983945; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1901
A;Map position: I
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res;

Query Match 90.2%; Score 37; DB 2; Length 344;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 Db 141 LDWKWL 146

RESULT 12
 A87469
 ubiquinol oxidase subunit II [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
 C:Accession: A87469
 R:Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87469
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-353 <STO>
 A:Cross-references: GB:AE005673; NID:g13423199; PIDN:NAK23749.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC1773
 C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 353;
 Best Local Similarity 83.3%; Pred. No. 89;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 Db 146 LDWKWL 151

RESULT 13
 B71184
 probable sarcosine oxidase - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
 C:Accession: B71184
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: B71184
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-377 <KAW>
 A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30865.1; PID:g3258182
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1751
 C:Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 |||||
 Db 354 LDWEW 358

RESULT 14

F75144
 sarcosine oxidase, chain beta (soxb) PAB0214 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: F75144
 R:anonymous, Genoscope
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
 A:Reference number: A75001
 A:Accession: F75144
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-379 <KAW>
 A:Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49237.1; PID:g545774
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: soxB; PAB0214
 C:Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEW 5
 |||||
 Db 356 LDWEW 360

RESULT 15
 C96006
 probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] - Sinc
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C96006
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C96006
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-386 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:gi5141202; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Galibert, P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 C:Contents: annotation
 C:Genetics:
 A:Gene: cyoA; SMD21487
 A:Genome: plasmid
 C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
 C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res

Query Match 90.2%; Score 37; DB 2; Length 386;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 Db 141 LDWKWL 146

Search completed: February 18, 2004, 14:38:52
 Job time : 6.5921 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	6	10	US-09-847-940B-17
2	41	100.0	6	11	US-09-847-946A-17
3	41	100.0	6	11	US-09-847-946A-45
4	41	100.0	6	11	US-09-847-946A-117
5	41	100.0	7	11	US-09-847-946A-121
6	41	100.0	8	11	US-09-847-946A-114
7	41	100.0	8	11	US-09-847-946A-122
8	41	100.0	9	11	US-09-847-946A-113
9	41	100.0	9	11	US-09-847-946A-116
10	41	100.0	9	11	US-09-847-946A-119
11	41	100.0	9	11	US-09-847-946A-120
12	41	100.0	10	11	US-09-847-946A-115
13	41	100.0	10	11	US-09-847-946A-118
14	41	100.0	11	11	US-09-847-946A-112
15	39	95.1	471	12	US-10-369-493-12414

16	37	90.2	20	12	US-09-962-756-939	Sequence 939, App
17	37	90.2	20	12	US-10-253-471-939	Sequence 939, App
18	37	90.2	70	9	US-09-864-761-46514	Sequence 46514, A
19	37	90.2	219	12	US-10-369-493-19572	Sequence 19572, A
20	37	90.2	259	12	US-10-369-493-22800	Sequence 22800, A
21	37	90.2	280	12	US-10-369-493-3354	Sequence 3354, App
22	37	90.2	354	15	US-10-166-087-6	Sequence 6, Appl
23	37	90.2	462	12	US-10-369-493-8244	Sequence 8244, App
24	36	87.8	6	10	US-09-847-940B-2	Sequence 2, Appl
25	36	87.8	6	11	US-09-847-946A-2	Sequence 2, Appl
26	36	87.8	6	11	US-09-847-946A-33	Sequence 33, Appl
27	36	87.8	7	11	US-09-847-946A-37	Sequence 37, Appl
28	36	87.8	8	11	US-09-847-946A-30	Sequence 30, Appl
29	36	87.8	8	11	US-09-847-946A-38	Sequence 38, Appl
30	36	87.8	9	11	US-09-847-946A-29	Sequence 29, Appl
31	36	87.8	9	11	US-09-847-946A-32	Sequence 32, Appl
32	36	87.8	9	11	US-09-847-946A-35	Sequence 35, Appl
33	36	87.8	9	11	US-09-847-946A-36	Sequence 36, Appl
34	36	87.8	10	11	US-09-847-946A-31	Sequence 31, Appl
35	36	87.8	10	11	US-09-847-946A-34	Sequence 34, Appl
36	36	87.8	11	11	US-09-847-946A-28	Sequence 28, Appl
37	36	87.8	11	11	US-09-847-946A-132	Sequence 132, App
38	36	87.8	11	11	US-09-847-946A-140	Sequence 140, App
39	36	87.8	13	11	US-09-847-946A-143	Sequence 143, App
40	36	87.8	13	11	US-09-847-946A-144	Sequence 144, App
41	36	87.8	13	11	US-09-847-946A-145	Sequence 145, App
42	36	87.8	13	11	US-09-847-946A-148	Sequence 148, App
43	36	87.8	17	11	US-09-847-946A-141	Sequence 141, App
44	36	87.8	17	11	US-09-847-946A-142	Sequence 142, App
45	36	87.8	17	11	US-09-847-946A-146	Sequence 146, App

ALIGNMENTS

RESULT 1
US-09-847-940B-17
; Sequence 17, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-17

Query Match 100.0%; Score 41; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 2
US-09-847-946A-17
; Sequence 17, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-17

Query Match 100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 3
US-09-847-946A-45
; Sequence 45, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-45

Query Match 100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 4
US-09-847-946A-117
; Sequence 117, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-117

Query Match 100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 5
US-09-847-946A-121
; Sequence 121, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-121

Query Match 100.0%; Score 41; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 1 LDWEWL 6

RESULT 6

US-09-847-946A-114
; Sequence 114, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114

; LENGTH: 8
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence

US-09-847-946A-114

Query Match 100.0%; Score 41; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6

Db 3 LDWEWL 8

RESULT 7

US-09-847-946A-122

; Sequence 122, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 122

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-122

Query Match 100.0%; Score 41; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6

Db 1 LDWEWL 6

RESULT 8

US-09-847-946A-113

; Sequence 113, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 113

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence

US-09-847-946A-113

Query Match 100.0%; Score 41; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6

Db 1 LDWEWL 6

RESULT 9

US-09-847-946A-116

; Sequence 116, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 116

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-116

Query Match 100.0%; Score 41; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||||
Db 1 LDWEWL 6

RESULT 10

US-09-847-946A-119
; Sequence 119, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-119

Query Match 100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||||
Db 3 LDWEWL 8

RESULT 11

US-09-847-946A-120
; Sequence 120, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-120

Query Match 100.0%; Score 41; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||||
Db 2 LDWEWL 7

RESULT 12

US-09-847-946A-115
; Sequence 115, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-115

Query Match 100.0%; Score 41; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
|||||
Db 2 LDWEWL 7

RESULT 13

US-09-847-946A-118
; Sequence 118, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-118

US-09-847-946A-118

Query Match 100.0%; Score 41; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
Db 3 LDWEWL 8

RESULT 14

US-09-847-946A-112
; Sequence 112, Application US/09847946A
; Publication No. US2003054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PRI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-112

Query Match 100.0%; Score 41; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
Db 3 LDWEWL 8

RESULT 15

US-10-369-493-12414
; Sequence 12414, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12414
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(471)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12414

Query Match 95.1%; Score 39; DB 12; Length 471;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6
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Db 119 IDWEWL 124

Search completed: February 18, 2004, 15:42:01
Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-17
Perfect score: 41
Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	90.2	334	4	US-09-252-991A-22395
2	36	87.8	439	4	US-09-172-952-14
3	36	87.8	745	2	US-08-887-518-3
4	36	87.8	745	2	US-09-023-321-3
5	36	87.8	745	2	US-08-890-853-4
6	36	87.8	745	2	US-09-032-475-3
7	36	87.8	745	2	US-09-099-125A-4
8	36	87.8	745	2	US-09-099-124A-4
9	36	87.8	745	3	US-09-032-476-4
10	36	87.8	745	3	US-08-890-854-4
11	36	87.8	745	3	US-09-023-324-4
12	36	87.8	745	3	US-09-168-629-2
13	36	87.8	745	3	US-08-910-820-10
14	36	87.8	745	3	US-08-810-131A-2
15	36	87.8	745	4	US-09-109-986-4
16	36	87.8	745	4	US-09-844-908-10
17	36	87.8	745	4	US-09-868-758-3
18	36	87.8	756	2	US-08-887-518-4
19	36	87.8	756	2	US-09-023-321-4
20	36	87.8	756	2	US-08-890-853-2
21	36	87.8	756	2	US-09-032-475-4
22	36	87.8	756	2	US-09-099-125A-2
23	36	87.8	756	2	US-09-099-124A-2
24	36	87.8	756	3	US-09-032-476-2
25	36	87.8	756	3	US-08-890-854-2
26	36	87.8	756	3	US-09-023-324-2
27	36	87.8	756	3	US-09-168-629-15

28	36	87.8	756	3	US-08-910-820-9	Sequence 9, Appli
29	36	87.8	756	4	US-09-109-986-2	Sequence 2, Appli
30	36	87.8	756	4	US-09-844-908-9	Sequence 9, Appli
31	36	87.8	756	4	US-09-868-758-4	Sequence 4, Appli
32	36	87.8	996	4	US-09-417-197-123	Sequence 123, App
33	36	87.8	997	4	US-09-417-197-121	Sequence 121, App
34	34	82.9	38	2	US-08-488-161-55	Sequence 55, Appl
35	34	82.9	38	3	US-09-273-685-55	Sequence 55, Appl
36	34	82.9	38	5	PCr-US95-11934-55	Sequence 55, Appl
37	34	82.9	138	1	US-08-686-878A-33	Sequence 33, Appl
38	34	82.9	138	4	US-09-175-928-33	Sequence 33, Appl
39	34	82.9	470	4	US-09-107-532A-4517	Sequence 4517, Ap
40	33	80.5	25	3	US-09-082-279B-1275	Sequence 1275, Ap
41	33	80.5	25	4	US-09-315-304B-1275	Sequence 1275, Ap
42	33	80.5	25	4	US-09-834-784-1275	Sequence 1275, Ap
43	33	80.5	162	4	US-09-199-637A-161	Sequence 161, App
44	33	80.5	162	4	US-09-199-637A-162	Sequence 162, App
45	33	80.5	177	4	US-09-252-991A-20614	Sequence 20614, A

ALIGNMENTS

RESULT 1
US-09-252-991A-22395
; Sequence 22395, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22395
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22395

Query Match 90.2%; Score 37; DB 4; Length 334;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWEWL 6
Db 136 LDKWL 141

RESULT 2
US-09-172-952-14
; Sequence 14, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 439
; TYPE: PRT
; ORGANISM: YiaX2
US-09-172-952-14

Query Match 87.8%; Score 36; DB 4; Length 439;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 171 LDWRWL 176

RESULT 3
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 738 LDWSWL 743

RESULT 4
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
DB 738 LDWSWL 743

RESULT 5
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: IKK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
||| ||
Db 738 LDWSWL 743

RESULT 6

US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
||| ||
Db 738 LDWSWL 743

RESULT 7

US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760

;
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
||| ||
Db 738 LDWSWL 743

RESULT 8

US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE: 08/08/890,853
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 87.8%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
||| |||
DB 738 LDWSWL 743

RESULT 9
US-09-032-476-4
Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDWEWL 6
||| |||
DB 738 LDWSWL 743
RESULT 10
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
||| |||
DB 738 LDWSWL 743

RESULT 11
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/09/023,324
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/890,854
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-023-324-4

Query Match 87.8%; Score 36; DB 3; Length 745;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
 |||||
 DB 738 LDWSWL 743

RESULT 12
 US-09-168-629-2
 ; Sequence 2, Application US/09168629
 ; Patent No. 6242253
 ; GENERAL INFORMATION:
 ; APPLICANT: Karin, Michael
 ; APPLICANT: DiDonato, Joseph A.
 ; APPLICANT: Rothwarf, David M.
 ; APPLICANT: Hayakawa, Makio
 ; APPLICANT: Zandi, Ebrahim
 ; TITLE OF INVENTION: 1kB Kinase, Subunits Thereof, and Methods of Using Same
 ; FILE REFERENCE: P-UD 3295
 ; CURRENT FILING DATE: 1998-10-08
 ; EARLIER APPLICATION NUMBER: 60/061,470
 ; EARLIER FILING DATE: 1997-10-09
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 745
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-168-629-2

Query Match 87.8%; Score 36; DB 3; Length 745;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
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 DB 738 LDWSWL 743

RESULT 13
 US-08-910-820-10
 ; Sequence 10, Application US/08910820
 ; Patent No. 6258579
 ; GENERAL INFORMATION:
 ; APPLICANT: Mercurio, Frank
 ; APPLICANT: Zhu, Hengyi
 ; APPLICANT: Barbosa, Miguel
 ; APPLICANT: Li, Gian
 ; APPLICANT: Murray, Brion W.
 ; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
 ; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,820
 ; FILING DATE: 12-AUG-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 860098.413C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 745 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 US-08-910-820-10

Query Match 87.8%; Score 36; DB 3; Length 745;
 Best Local Similarity 83.3%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
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 DB 738 LDWSWL 743

RESULT 14
 US-08-810-131A-2
 ; Sequence 2, Application US/08810131A
 ; Patent No. 6268194
 ; GENERAL INFORMATION:
 ; APPLICANT: Karin, Michael
 ; APPLICANT: DiDonato, Joseph A.
 ; APPLICANT: Rothwarf, David M.
 ; APPLICANT: Hayakawa, Makio
 ; APPLICANT: Zandi, Ebrahim
 ; TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
 ; TITLE OF INVENTION: Same
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California

COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-131A-2

Query Match 87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 738 LDWSWL 743

RESULT 15
US-09-109-986-4
Sequence 4, Application US/09109986
Patent No. 649266
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-109-986-4

Query Match 87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWEWL 6
Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:51
Job time : 7.06579 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	745	1 IKKA HUMAN	O15111 h inhibitor
2	37	92.5	745	1 IKKA MOUSE	Q06080 m inhibitor
3	37	92.5	756	1 IKXB HUMAN	O14920 homo sapien
4	37	92.5	757	1 IKXB MOUSE	O88351 mus musculus
5	37	92.5	757	1 IKXB RAT	Q99778 rattus norv
6	36	90.0	524	1 CP72 CATRO	Q05047 catharanthu
7	36	90.0	656	1 VEXE SALT1	P43112 salmonella
8	36	90.0	840	1 VP01 YEAST	P32563 saccharomyc
9	35	87.5	290	1 CYOA BUCAP	Q8k993 buchnera ap
10	35	87.5	296	1 CYOA_BUCAI	P57544 buchnera ap
11	35	87.5	307	1 COX2_ACAC	P50653 acetobacter
12	35	87.5	314	1 CYOA_PSPFU	Q9wri1 pseudomonas
13	34	85.0	99	1 NOS3 SHEEP	P79209 ovis aries
14	34	85.0	262	1 LY4A MOUSE	P20937 mus musculus
15	34	85.0	263	1 KLR4 MOUSE	Q06051 mus musculus
16	34	85.0	914	1 GUX2_CLOSR	P50900 clostridium
17	34	85.0	1167	1 ITAE_MOUSE	Q06077 mus musculus
18	34	85.0	1201	1 NOS3_MOUSE	P70313 mus musculus
19	34	85.0	1202	1 NOS3_HUMAN	P29474 homo sapien
20	34	85.0	1204	1 NOS3_BOVIN	P29473 bos taurus
21	34	85.0	1204	1 NOS3_PIG	Q28969 sus scrofa
22	33	82.5	220	1 Y132_METJA	O57596 methanococc
23	33	82.5	300	1 Y223_HASIN	P44579 haemophilus
24	33	82.5	362	1 DCUP_YEAST	P32347 saccharomyc
25	33	82.5	411	1 CYB_CHRVI	Q1215 chromatium
26	33	82.5	480	1 MTH6_DROME	Q9v877 drosophila
27	33	82.5	501	1 YBQ6_YEAST	P38081 saccharomyc
28	33	82.5	578	1 YC20_METJA	Q58617 methanococc
29	33	82.5	983	1 EPB3_CHICK	P29318 gallus gall
30	33	82.5	983	1 EPB3_HUMAN	P29320 homo sapien
31	33	82.5	983	1 EPB3_MOUSE	P29319 mus musculus
32	33	82.5	984	1 EPB3_RAT	Q08680 rattus norv
33	33	82.5	1002	1 EPB5_CHICK	Q07497 gallus gall

34 33 82.5 1039 1 GUNB_CALSA
35 32 80.0 83 1 VG41_BPML5
36 32 80.0 94 1 VG41_BPMD2
37 32 80.0 269 1 BASI_HUMAN
38 32 80.0 315 1 T2S1_STRAL
39 32 80.0 336 1 NOSO_BACSU
40 32 80.0 339 1 RFAI_ECOLI
41 32 80.0 343 1 ZDH4_MOUSE
42 32 80.0 344 1 ZDH4_HUMAN
43 32 80.0 366 1 GCST_SYNEL
44 32 80.0 380 1 APJ_MACMU
45 32 80.0 387 1 MANA_RHIME

ALIGNMENTS

RESULT 1
IKKA_HUMAN STANDARD; PRT; 745 AA.
AC O15111: O14666; Q13132: Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK α) (IKK-alpha) (IkappaB kinase)
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitouse
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
DE CHUK OR IKK α .
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkappaB kinase.";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
RT factor NF-kappaB.";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=96258427; PubMed=877433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain.";

Cell. Mol. Biol. Res. 41:537-549(1995)...

[6] PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179 AND SER-180.

RA MEDLINE=98188283; PubMed=9520446;

XX Ling L., Cao Z., Goeddel D.V.;

RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

[7] PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.

RA MEDLINE=99413720; PubMed=10485710;

XX Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M., Donner D.B.;

RT "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";

RL Nature 401:82-85(1999).

[8] IKK-KAPPA BINDING.

RA MEDLINE=99212141; PubMed=10195894;

XX Dalhase M., Hayakawa M., Chen Y., Karin M.;

RT "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";

RL Science 284:309-313(1999).

[9] IKK PHOSPHORYLATION.

RA MEDLINE=99038238; PubMed=9819420;

XX Nemoto S., DiDonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343(1998).

[10] REVIEW.

RA MEDLINE=20178139; PubMed=10712233;

XX Joblin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462(2000).

[11] SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, IKKB AND IKKKG.

RA MEDLINE=21968797; PubMed=11971985;

XX Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.;

RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase.";

RL Mol. Cell. Biol. 22:3549-3561(2002).

CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.

CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated when dephosphorylated.

CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-GAMMA/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: Widely expressed.

CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEK1, and dephosphorylated by PP2A. Autophosphorylated.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.

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CC

DR EMBL; AF012890; AAC51662.1; --

DR EMBL; AF009225; AAC51671.1; --

DR EMBL; AF080157; AAC08996.1; --

DR EMBL; U22512; AAC50713.1; --

DR HSSP; G63450; 1A06.

DR Gnew; HGNC:1974; CHUK.

DR MIM; 600664; --

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0008384; P:IkappaB kinase activity; TAS.

DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.

DR GO; GO:0006955; P:immune response; TAS.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002290; Ser Thr kinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.

KW DOMAIN 15 302 PROTEIN KINASE.

FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).

FT NP_BIND 21 29 ATP (BY SIMILARITY).

FT BINDING 44 44 ATP (BY SIMILARITY).

FT ACT_SITE 144 144 BY SIMILARITY.

FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).

FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).

FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.

FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.

FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.

FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.

FT MUTAGEN 176 176 S->E: FULL ACTIVATION.

FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.

FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.

FT CONFLICT 543 543 E -> G (IN REF. 2).

FT CONFLICT 604 604 L -> R (IN REF. 5).

FT CONFLICT 679 680 TS -> AY (IN REF. 5).

FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).

FT CONFLICT 686 687 TS -> DL (IN REF. 5).

SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 92.5%; Score 37; DB 1; Length 745;

Best Local Similarity 83.3%; Pred No. 76;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6

Db 738 LDWSML 743

RESULT 2

IKKA MOUSE

ID IKKA MOUSE STANDARD; PRT; 745 AA.

AC Q60680; Q9D2X3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)

DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)

DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).

GN CHUK OR IKKA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OX

[1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=BALB/c;
 RX MEDLINE=9604444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RL chromosome 10 and mouse chromosome 19.";
 RN Genomics 27:348-351(1995).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=BALB/c;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RL family of interacting proteins, contains a serine-threonine kinase
 RL catalytic domain.";
 RN Cell. Mol. Biol. Res. 41:537-549(1996).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 3).
 RP STRAIN=CS7BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S.,
 RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirni L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RN Nature 409:685-690(2001).
 [4]
 RN ALTERNATIVE SPLICING.
 RP MEDLINE=20198447; PubMed=10733566;
 RA McKenzie P.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Galeziunas R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RL leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RL IKKbeta have different activation requirements.";
 RN Mol. Cell. Biol. 20:2635-2649(2000).
 [5]
 RN PHOSPHORYLATION BY MAP3K14/NIK.
 RP MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RL upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RL protein kinase/ERK kinase kinase-1.";
 RN Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 [6]
 RN IKK-IKKB BINDING.
 RP MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RL IKKbeta subunit phosphorylation.";
 RN Science 284:309-313(1999).
 [7]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RL kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RN Mol. Cell. Biol. 18:7336-7343(1998).

[8]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RA Tobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RL inflammation and protection.";
 RN Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKKG and CREBBP (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
 CC -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; U12473; AAC52589.1; -;
 DR EMBL; AK018671; BAB31335.1; -;
 DR PIR; I49101; I49101.
 DR HSSP; Q63450; IAO6.
 DR MGD; MGI:99484; Chuk.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Alternative splicing.
 FT DOMAIN 15 300 PROTEIN_KINASE.
 FT DOMAIN 455 476 LEUCINE_ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
 FT (BY SIMILARITY).

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FT VARSPLIC 452 471 MSLRLRYNANLTKMKNLTLS -> IPRKNVKSMEGRNGRKGH
FT SLF (in isoform 2).
FT /FTId=VSP 004866.
FT VARSPLIC 472 745 Missing (in isoform 2).
FT /FTId=VSP 004867.
FT VARSPLIC 577 584 DHLTSDST -> GKTQSQY (in isoform 3).
FT /FTId=VSP 004868.
FT VARSPLIC 585 745 Missing (in isoform 3).
FT /FTId=VSP 004869.
FT CONFLICT 236 236 K -> E (IN REF. 3).
FT CONFLICT 400 400 S -> Y (IN REF. 3).
SQ SEQUENCE 745 AA; 84728 MW; 3FEP5582AF9F2233 CRC64;

Query Match 92.5%; Score 37; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6
|||:|
Db 738 LDWSWL 743

RESULT 3
IKKB HUMAN
ID IKKB HUMAN STANDARD; PRT; 756 AA.
AC O14920; O75327;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (IC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:866-866 (1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RA "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40 (1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RA "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
RT 8p12-->p11 by in situ hybridization.";
RL Cytogenet. Cell Genet. 82:32-33 (1998).
RN [5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerfeld A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343 (1998).
RN [7]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462 (2000).
RN [8]
RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKBG.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561 (2002).
CC -! FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (By similarity).
CC -! SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
CC complex. Phosphorylated IKB-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP.
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -! PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC -----
CC EMBL; AF029684; AAC51860.1; -
CC EMBL; AF080158; AAD08997.1; -
CC EMBL; AF031416; AAC64675.1; -
CC EMBL; BC006231; AAB06231.1; -

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DR HSP; Q63450; 1A06.
DR Genew; HGNC:5960; IKKB.
DR MW; 603258; -.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0005224; F:ATP binding activity; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; F:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN_KINASE.
FT DOMAIN 458 479 LEUCINE_ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 PHOSPHORYLATION.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT CONFLICT 231 255 WSKVRQKSEVDIVSDNGTVKF -> CVRMPGTVANS
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FT CONFLICT 425 425 Q -> H (IN REF. 1).
FT CONFLICT 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;

Query Match 92.5%; Score 37; DB 1; Length 756;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAWL 6
|||:|
Db 737 LDMSWL 742

RESULT 4
ID IKKB_MOUSE STANDARD; PRT; 757 AA.
AC Q88351; Q9R1J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
DE IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542 (1998).
RN [2]

SEQUENCE FROM N.A.
RP Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RA "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of Ikb."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=99455228; PubMed=10523828;
RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT pathway activates ikappaB kinases (IKK-alpha/beta) and IKK-beta is a
RT developmentally regulated protein kinase."
RL Oncogene 18:5514-5524 (1999).
RN [4]
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase 1 and NF-kappaB-inducing kinase."
RL Mol. Cell. Biol. 18:7336-7343 (1998).
RN [5]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection."
RL Am. J. Physiol. 278:C451-C462 (2000).
CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC -I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
CC the mouse embryo, at E9.5 day its expression begins to be
CC localized to the brain, neural ganglia, neural tube, and in liver
CC at E12.5 day. At E15.5 day, the expression is further restricted
CC to specific tissues of the embryo.
CC -I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
-----
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-----
DR EMBL; AF026524; AAC23557.1; -.
DR EMBL; AF088910; AAD52095.1; -.
DR HSP; Q63450; 1A06.
DR MGD; MGI:1338071; Ikbb.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.

```

FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 737 TLDSWLQMEDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred.No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 737 LDWSWL 742
 RESULT 5
 IKKB_RAT
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9078;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase regulation 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF115282; AAF21978.1; -.
 DR HSSP; Q63450; IA06.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR01245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFFE46A7DF91F9C CRC64;
 Query Match 92.5%; Score 37; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred.No. 77;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWAWL 6
 Db 737 LDWSWL 742
 RESULT 6
 CP72_CATRO
 ID CP72_CATRO STANDARD; PRT; 524 AA.
 AC Q05047;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase)
 DE (SLS).
 GN CYP72A1 OR CYP72 OR P450CR3.
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
 OC Catharanthus.
 OX NCBI_TaxID=4058;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. CP3A;
 RA Vetter H.-P., Mangold U., Schroeder G., Marner F.-J.,
 RA Werck-Reichardt D., Schroeder J.;
 RT "Molecular analysis and heterologous expression of an inducible
 RT cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
 RL Plant Physiol. 100:998-1007(1992).
 RN [2]
 RN SEQUENCE OF 469-524 FROM N.A.

RC STRAIN=cv. G. Don;
 RA MEDLINE=93283641; PubMed=8507838;
 RX Meijer A.H., Souer E., Verpoorte R., Hoge J.H.C.;
 RT "Isolation of cytochrome P-450 cDNA clones from the higher plant
 RT Catharanthus roseus by a PCR strategy.";
 RL Plant Mol. Biol. 22:379-383(1993).
 RN [3]
 RP FUNCTION.
 RC STRAIN=cv. CP3A;
 RX MEDLINE=20575722; PubMed=1135113;
 RA Imler S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
 RA Schmidt J., Strack D., Materin U., Schroeder J.;
 RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme
 RT activities and identification of cytochrome P450 CYP72A1 as
 RT secologanin synthase.";
 RL Plant J. 24:797-804(2000).
 CC -1- FUNCTION: Converts loganin into secologanin.
 CC -1- CATALYTIC ACTIVITY: Loganin + NADPH + O(2) = secologanin + NADP(+) + 2 H(2O).
 CC -1- PATHWAY: Indole alkaloids biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
 CC -1- TISSUE SPECIFICITY: Upper and lower leaf epidermis.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -----
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 CC -----
 DR EMBL; L10081; AAA33106.1; -;
 DR EMBL; X69775; CAA49430.1; -;
 DR PIR; S35168; S35168.
 DR PIR; T09944; T09944.
 DR HSSP; P14779; IJZP.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450.1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
 FT NADP; Heme; Alkaloid metabolism.
 FT TRANSMEM 12 32 POTENTIAL.
 FT METAL 470 470 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT VARIANT 190 190 I -> L.
 FT VARIANT 194 194 Q -> E.
 FT VARIANT 223 223 E -> D.
 FT VARIANT 312 312 K -> R.
 FT VARIANT 318 318 S -> T.
 FT VARIANT 403 403 V -> I.
 FT VARIANT 405 405 K -> E.
 FT VARIANT 411 411 S -> P.
 SQ SEQUENCE 524 AA; 60557 MW; EF5D864E43C751E8 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAW 5
 |||||
 Db 28 LDWAW 32

RESULT 7

VEXE SALTI
 ID VEXE SALTI STANDARD; PRT; 656 AA.
 AC P43112;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vi polysaccharide export protein vexE.
 GN VEXE OR STY4651 OR T4344.

OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_taxid=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GIFU 10007;
 RX MEDLINE=93323234; PubMed=8331073;
 RA Hashimoto Y., Li N., Yokoyama H., Ezaki T.;
 RT "Complete nucleotide sequence and molecular characterization of Viab
 RT region encoding Vi antigen in Salmonella typhi.";
 RL J. Bacteriol. 175:4456-4465(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner P.R.;
 RT "Comparative genomics of Salmonella enterica serovar typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSLOCATION OF THE VI ANTIGEN.
 CC -----
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 CC -----
 DR EMBL; D14156; BAA03200.1; -;
 DR EMBL; AL627283; CAD06771.1; -;
 DR EMBL; AE016848; AAO71797.1; -;
 DR PIR; A56975; A56975.
 DR InterPro; IPR001440; TPR.
 KW Polysaccharide transport; Transport; Complete proteome.
 SQ SEQUENCE 656 AA; 73652 MW; 26097F9D6F51EED CRC64;

Query Match 90.0%; Score 36; DB 1; Length 656;

Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAW 5
 |||||
 Db 411 LDWAW 415

RESULT 8

VPH1 YEAST
 ID VPH1 YEAST STANDARD; PRT; 840 AA.
 AC P32563;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Vacuolar ATP synthase 95 kDa subunit (Vacuolar ATPase 95 kDa subunit).
 GN VPH1 OR YOR270C.
 OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92332542; PubMed=1385813;
RA Manolson M.F., Proteau D., Preston R.A., Stenbit A., Roberts B.T.,
RA Hoyt M.A., Preuss D., Mulholland J., Botstein D., Jones E.W.;
RT "The VP1 gene encodes a 95-kDa integral membrane polypeptide
RT required for in vivo assembly and activity of the yeast vacuolar
RT H(+)-ATPase.";
RL J. Biol. Chem. 267:14294-14303(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=93147685; PubMed=1491220;
RA Manolson M.F., Proteau D., Jones E.W.;
RT "Evidence for a conserved 95-120 kDa subunit associated with and
RT essential for activity of V-ATPases.";
RL J. Exp. Biol. 172:105-112(1992).
RN [3]
RN SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=97051594; PubMed=8896271;
RA Cheret G., Bernard A., Sor F.J.;
RT "DNA sequence analysis of the VP1-SNF2 region on chromosome XV of
RT Saccharomyces cerevisiae.";
RL Yeast 12:1059-1064(1996).
RN [4]
RN SEQUENCE FROM N.A.
RX STRAIN=S288C / FY1679;
RX MEDLINE=97298311; PubMed=9153759;
RA Poirey R., Jauniaux J.C.;
RT "Sequencing analysis of a 36. kb fragment of yeast chromosome XV
RT reveals 26 open reading frames including SEC3, CDC31, SUG2, GCD1,
RT RBL2, PNT1, PAC1 and VP1.";
RL Yeast 13:483-487(1997).
RN [5]
RN FUNCTION: REQUIRED FOR ASSEMBLY AND ACTIVITY OF THE VACUOLAR
RN ATPASE. POTENTIAL ROLE IN DIFFERENTIAL TARGETING AND REGULATION OF
RN THE ENZYME FOR A SPECIFIC ORGANELLE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC -1- SIMILARITY: BELONGS TO THE V-ATPASE 116 kDa SUBUNIT FAMILY.
CC
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CC
CC EMBL; M89778; AAA35211.1; -;
CC EMBL; X89633; CAA61776.1; -;
CC EMBL; M75178; CAA99494.1; -;
CC EMBL; M75179; CAA99496.1; -;
CC PIR; A42970; A42970.
CC SGD; S0005796; VP1.
CC GO; GO:0006797; P:polysphosphate metabolism; IMP.
DR InterPro; IPR002490; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_sub_a; 1.
KW Hydrogen ion transport; Transmembrane; Glycoprotein.
FT DOMAIN 1 411
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 412 432
FT DOMAIN 433 462
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 463 483
FT DOMAIN 484 540
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 541 561
FT DOMAIN 562 571
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 572 592
FT DOMAIN 593 635
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 636 656
FT DOMAIN 657 760
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 761 787
FT DOMAIN 788 840
FT EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 840 AA; 95528 MW; 77709A914410CD4D CRC64;
Query Match 90.0%; Score 36; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMAW 5
DB 518 LDMAW 522
RESULT 9
CYOA_BUCAP STANDARD; PRT; 290 AA.
AC CYOA_BUCAP Q8K993;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase Bo(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA OR BUSG456.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamas L., Klason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.U., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -1- FUNCTION: Cytochrome O terminal oxidase complex is the component
CC of the aerobic respiratory chain that predominates when cells are
CC grown at high aeration (By similarity).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC
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CC
CC EMBL; AE014121; AAM67999.1; -;
CC InterPro; IPR001505; Copper_Cua.
CC InterPro; IPR006333; Cyoa_II.
CC InterPro; IPR002429; Cyt_C_ox_2.
CC InterPro; IPR000437; Prok_Lipoprot.
CC Pfam; PF00116; COX2; 1.
CC PRINTS; PR01166; CYCOXIDASEII.
CC ProDom; PD000131; Copper_Cua; 1.
CC TIGRFAMs; TIGR01433; Cyoa; 1.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE NEG.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Signal; Lipoprotein; Complete proteome.
FT SIGNAL 1 24
FT CHAIN 25 290
FT LIPID 25 25
FT DOMAIN 25 42
FT TRANSMEM 43 63
FT DOMAIN 64 87
FT TRANSMEM 88 108
FT DOMAIN 109 290
FT EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 290 AA; 33730 MW; 3D80A02A84732963 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 290;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDRAWL 6
||| ||
DB 134 LDMRWL 139

RESULT 10
ID_CXOA_BUCAI STANDARD; PRT; 296 AA.
AC P57544;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
subunit 2).
DE subunit 2).
GN CYOA OR BU472.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RT Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.

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CC EMBL; AP001119; BABL3169.1; -.
CC HSP; P18400; LCYW
CC InterPro; IPR001505; Copper Cua.
CC InterPro; IPR006333; CyoA II.
CC InterPro; IPR002429; Cyt_c ox 2.
CC InterPro; IPR000437; Prok_LipoProt.
CC Pfam; PF00116; COX2; 1.
CC ProDom; PD000131; Copper Cua; 1.
CC TIGRFAMs; TIGR01433; CyoA; 1.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE NEG.
CC Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
CC Signal; Lipoprotein; Complete proteome.
CC SIGNAL 1 15 POTENTIAL.
CC CHAIN 16 296 UBQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 34 54 POTENTIAL.
CC FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 79 99 POTENTIAL.
CC FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
CC SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FFBAC CRC64;

Query Match 87.5%; Score 35; DB 1; Length 296;

Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDRAWL 6
||| ||
DB 125 LDMRWL 130

RESULT 11
ID_QOX2_ACEAC STANDARD; PRT; 307 AA.
AC P50653;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
A1 subunit 2) (Oxidase BA(3) subunit 2).
GN CYAB.
OS Acetobacter aceti.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OX NCBI_TaxID=435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1023;
RX MEDLINE=93322308; PubMed=8392509;
RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
RA Kawamura Y., Horinouchi S., Beppu T.;
RT "Characterization of a cytochrome a1 that functions as a ubiquinol
oxidase in Acetobacter aceti.";
RL J. Bacteriol. 175:4307-4314(1993).
CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.

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CC EMBL; D13185; BAA02480.1; -.
CC PIR; A36885; A36885.
CC HSP; P18400; LCYW.
CC InterPro; IPR001505; Copper Cua.
CC InterPro; IPR006333; CyoA II.
CC InterPro; IPR002429; Cyt_c ox 2.
CC Pfam; PF00116; COX2; 1.
CC PRINTS; PD00166; CYCOXIDASEII.
CC ProDom; PD000131; Copper Cua; 1.
CC TIGRFAMs; TIGR01433; CyoA; 1.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
CC Oxidoreductase; Transmembrane; Respiratory chain; Signal;
CC Lipoprotein.
CC SIGNAL 1 23 POTENTIAL.
CC CHAIN 24 307 UBQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT TRANSMEM 46 66 POTENTIAL.
CC FT TRANSMEM 87 107 POTENTIAL.
CC SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;

Query Match 87.5%; Score 35; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDRAWL 6
||| ||
DB 135 LDMRWL 140

```

RESULT 12
CYOA_PSEPU STANDARD; PRT; 314 AA.
AC Q9WRI;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
DE CYOA.
GN Pseudomonas putida.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH-2000;
RX MEDLINE=99085656; PubMed=9868765;
RA Hirayama H., Takami H., Inoue A., Horikoshi K.;
RT Isolation and characterization of toluene-sensitive mutants from
RT Pseudomonas putida IH-2000.;
RL FEMS Microbiol. Lett. 169:219-225(1998).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC -----
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CC -----
DR EMBL; AB016787; BAA76356.1; -.
DR HSSP; P18400; 1CYW.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyoA II.
DR InterPro; IPR002429; Cyt_cox_2.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR PROSITE; PS00013; PROKARY LIPOPROTEIN; 1.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Inner membrane; Signal; Lipoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 43 63 POTENTIAL.
FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 107 POTENTIAL.
FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
SQ SEQUENCE 314 AA; 34702 MW; 96EE04FC3AA77F07 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 314;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWAWL 6
Db 133 LDWKWL 138

RESULT 13
NOS3_SHEEP
ID NOS3_SHEEP STANDARD; PRT; 99 AA.

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P79209;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE I1) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS)
DE (Fragment).
DE NOS3 OR ENOS.
GN Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RT "Effect of hypoxia on the microvasculature of developing fetal
RT brain of sheep: a studies on the expression pattern of
RT constitutive forms of nitric oxide synthase.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A GMP-MEDIATED SIGNAL
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
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CC -----
DR EMBL; U76738; AAB40705.1; -.
DR HSSP; P29473; IDOC.
DR InterPro; IPR004030; NO synthase.
DR Pfam; PF02898; NO synthase; 1.
DR PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
KW Heme; Multigene family.
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 85.0%; Score 34; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
Db 66 DWAWI 70

RESULT 14
LY4A_MOUSE
ID LY4A_MOUSE STANDARD; PRT; 262 AA.
AC P20337;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein YE1/48 (T lymphocyte antigen A1) (LY49-A

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DE antigen).
GN KLRA1 OR LY49A OR LY-49A OR LY49 OR LY-49.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89140367; PubMed=2783949;
RA Chan P.-Y., Takei F.;
RT "Molecular cloning and characterization of a novel murine T cell
RT surface antigen, YEL/48.";
RL J. Immunol. 142:1727-1736(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89309828; PubMed=2787364;
RA Yokoyama W.M., Jacobs L., Kanagawa O., Shevach E.M., Cohen D.I.;
RT "A murine T lymphocyte antigen belongs to a supergene family of type
RT II integral membrane proteins.";
RL J. Immunol. 143:1379-1386(1989).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR H-2D
CC ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: HIGH, IN T LYMPHOMA LINES, VERY LOW IN
CC NORMAL LYMPHOCYTES.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M25775; AAA40578.1; ALT_SEQ.
DR EMBL; M25812; AAA37242.1; --
DR PIR; A30573; A30573.
DR PIR; A45813; A45813.
DR PDB; 1QO3; 02-JAN-00.
DR MGD; MGI:101907; Klra1.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c.1.
DR SMART; SM00034; CLECT.1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family; 3D-structure.
FT DOMAIN 1 44 CYTOPLASMIC (PROBABLE).
FT TRANSMEM 45 66 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 67 262 EXTRACELLULAR (PROBABLE).
FT DOMAIN 138 257 C-TYPE LECTIN (LONG FORM).
FT DISULFID 167 253 BY SIMILARITY.
FT DISULFID 232 245 BY SIMILARITY.
FT SITE 137 139 CELL ATTACHMENT SITE.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 76 78 NCE -> KIQ (IN REF. 2).
FT CONFLICT 106 106 I -> M (IN REF. 2).
FT CONFLICT 166 166 A -> T (IN REF. 2).
FT CONFLICT 223 223 G -> R (IN REF. 2).
SQ SEQUENCE 262 AA; 30498 MW; 3C3328D265F71B5E CRC64;

Query Match

Best Local Similarity 85.0%; Score 34; DB 1; Length 262;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DWAWL 6

||||

Db 207 DWAWI 211
RESULT 15
KLRA_MOUSE STANDARD; PRT; 263 AA.
ID KUR4_MOUSE
AC Q60651; O78026; Q9EPAS;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Killer cell lectin-like receptor 4 (T-cell surface glycoprotein
DE LY-49D) (LY49-D antigen).
GN KLRA4 OR LY49D OR LY-49D OR LY49-D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM D2).
RX STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=94300068; PubMed=8027540;
RA Smith H.R.C., Karlihofer F.M., Yokoyama W.M.;
RT "Ly-49 multigene family expressed by IL-2-activated NK cells.";
RL J. Immunol. 153:1068-1079(1994).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX STRAIN=C57BL/6.
RX MEDLINE=96421544; PubMed=8824161;
RA Silver E.T., Elliott J.F., Kane K.P.;
RT "Alternatively spliced Ly-49D and H transcripts are found in IL-2-
RT activated NK cells.";
RL Immunogenetics 44:478-482(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM D1).
RX STRAIN=NOD, and NOR;
RX MEDLINE=20384764; PubMed=10925254;
RA Silver E.T., Gong D.-E., Chang C.S., Amrani A., Santamaria P.,
RA Kane K.P.;
RT "Ly-49P activates NK-mediated lysis by recognizing H-2Dd.";
RL J. Immunol. 165:1771-1781(2000).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=D1;
CC IsoId=Q60651-1; Sequence=Displayed;
CC Name=D2;
CC IsoId=Q60651-2; Sequence=VSP 003068;
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; U10090; AAA50218.1; --
DR EMBL; L78247; AAC32667.1; --
DR EMBL; AF218079; AAF99592.1; --
DR EMBL; AF218078; AAF99591.1; --
DR PIR; I49049; I49049.
DR MGD; MGI:101904; Klra4.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c.1.
DR SMART; SM00034; CLECT.1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family;
KW Alternative splicing; Polymorphism.

FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 65 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 66 263 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 139 258 C-TYPE LECTIN (LONG FORM).
FT DISULFID 168 254 BY SIMILARITY.
FT DISULFID 233 246 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 39 41 Missing (in isoform D2).
FT /FTid=vsp 003068.
FT VARIANT 5 5 E -> K (IN STRAINS NOD AND NOR).
FT VARIANT 29 29 R -> W (IN STRAINS NOD AND NOR).
FT VARIANT 32 32 E -> Q (IN STRAINS NOD AND NOR).
FT VARIANT 35 35 R -> G (IN STRAINS NOD AND NOR).
FT VARIANT 45 45 L -> F (IN STRAINS NOD AND NOR).
FT VARIANT 60 60 T -> I (IN STRAINS NOD AND NOR).
FT VARIANT 79 79 K -> Q (IN STRAINS NOD AND NOR).
FT VARIANT 132 132 Y -> S (IN STRAINS NOD AND NOR).
FT VARIANT 189 189 L -> F (IN STRAINS NOD AND NOR).
SQ SEQUENCE 263 AA; 30872 MW; D0A940A089A9F42D CRC64;

Query Match 85.0%; Score 34; DB 1; Length 263;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DWAWL 6
| | | |
Db 208 DWAWI 212

Search completed: February 18, 2004, 14:28:13
Job time : 3.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	745	1 I49101	conserved helix-loop-helix
2	36	90.0	215	2 D75215	probable phosphorib
3	36	90.0	251	2 E70521	probable phosphor
4	36	90.0	304	2 F83632	probable cytochrom
5	36	90.0	316	2 AB2931	hypothetical prote
6	36	90.0	316	2 D98351	diptide ABC tran
7	36	90.0	516	2 T10000	cytochrome P450 (C
8	36	90.0	524	2 T09999	cytochrome P450 -
9	36	90.0	524	2 T09944	probable cytochrom
10	36	90.0	656	2 A56975	Vi polysaccharide
11	36	90.0	656	2 AF1040	Vi polysaccharide
12	36	90.0	840	1 A42970	H-exporting Apas
13	36	90.0	1212	2 F83153	probable two-compo
14	36	90.0	1575	2 T18545	lysobactin synthet
15	35	87.5	162	2 C70829	hypothetical prote
16	35	87.5	204	2 C83748	hypothetical prote
17	35	87.5	277	1 JC5900	bo-type ubiquinol
18	35	87.5	296	2 A84985	cytochrome o ubiq
19	35	87.5	299	2 B83243	hypothetical prote
20	35	87.5	307	1 A36885	bo-type ubiquinol
21	35	87.5	318	2 AD0384	cytochrome o ubiq
22	35	87.5	331	2 D83480	cytochrome o ubiq
23	35	87.5	337	2 AG2946	hypothetical prote
24	35	87.5	337	2 C98336	probable integral
25	35	87.5	344	2 AG3489	cytochrome o ubiq
26	35	87.5	353	2 A87469	ubiquinol oxidase
27	35	87.5	386	2 C96006	probable cytochrom
28	35	87.5	394	2 C85064	hypothetical prote
29	35	87.5	418	2 D85064	hypothetical prote

30 35 87.5 443 2 AE0309 probable sugar tra
31 35 87.5 1139 2 AI0379 probable potassium
32 34 85.0 260 2 I49049 Ly-49D-GE antigen
33 34 85.0 262 2 I43261 natural killer cel
34 34 85.0 262 2 A30573 T-cell surface gly
35 34 85.0 262 2 A45813 T-cell surface gly
36 34 85.0 267 2 I55686 LGL-1 - mouse
37 34 85.0 322 2 AI3395 NADH2 dehydrogenas
38 34 85.0 348 2 AE2733 NADH ubiquinone ox
39 34 85.0 348 2 G97514 NADH dehydrogenase
40 34 85.0 395 2 E90438 hypothetical prote
41 34 85.0 395 2 B96610 type I restriction
42 34 85.0 616 2 C69226 nitric-oxide synth
43 34 85.0 1202 2 S71424 nitric-oxide synth
44 34 85.0 1203 1 A47501 nitric-oxide synth
45 34 85.0 1205 1 A38943

ALIGNMENTS

RESULT 1

I49101
conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I49101
R;Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
A;Reference number: I49101; MUID:96044444; PMID:7558004
A;Accession: I49101
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-745 <RES>
A;Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C;Genetics:
A;Gene: CHUK
C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homol
C;Keywords: ATP; phosphotransferase
F;13-283/Domain: protein kinase homology <KIN>

RESULT 2

D75215
purine phosphoribosyltransferase PAB2405 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D75215
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A;Reference number: A75001
A;Accession: D75215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-215 <RAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49171.1; PID:e15150
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: gptA; PAB2405

Query Match 90.0%; Score 36; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
Db 141 IDRAWI 146

RESULT 3
E70521
C:Accession: E70521
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70521
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-251 <COL>
A:Cross-references: GB:Z97188; GB:AL123456; NID:G3261805; PIDN:CAB10016.1; PID:G2224828
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv3817
C:Superfamily: kanamycin kinase

Query Match 90.0%; Score 36; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DRAWL 6
Db 86 DRAWL 90

RESULT 4
F83632
C:Accession: F83632
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83632
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <STO>
A:Cross-references: GB:AE004449; GB:AE004091; NID:G9945928; PIDN:AAG03503.1; GSPDB:GN00117
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0113
C:Superfamily: heme O synthase

Query Match 90.0%; Score 36; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5
Db 259 LDRAW 263

RESULT 5
AB2931
C:Species: Agrobacterium tumefaciens (strain C58, Dupont)

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AB2931
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Y.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB2931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL43864.1; PID:gl7741409; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3048
A:Map position: linear chromosome

Query Match 90.0%; Score 36; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5
Db 67 LDRAW 71

RESULT 6
D98351
C:Accession: D98351
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: D98351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90334.1; PID:gl5160371; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_3514
A:Map position: linear chromosome

Query Match 90.0%; Score 36; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAW 5
Db 67 LDRAW 71

RESULT 7
T10000
C:Accession: T10000
C:Species: Catharanthus roseus (Madagascar periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
R;Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-Reichmann, D.; Plant Sci. 96, 129-136, 1994
A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanthus roseus
A:Reference number: Z16915
A:Accession: T10000
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-516 <MAN>
A:Cross-references: EMBL:U19075; NID:G404689; PID:G404690

A;Experimental source: cv. cp3

C;Genetics:

A;Gene: CYP72C

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;318-481/Domain: cytochrome P450 homology <P45>

F;459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 17 LDMAW 21

RESULT 8

T09999

Cytochrome P450 - Madagascar periwinkle

C;Species: Catharanthus roseus (Madagascar periwinkle)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001

C;Accession: T09999

R;Wangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-

Plant Sci. 96, 129-136, 1994

A;Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth

A;Reference number: Z16915

A;Accession: T09999

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-524 <MAN>

A;Cross-references: EMBL:L19074; NID:g404687; PID:g404688

A;Experimental source: cv. cp3

C;Genetics:

A;Gene: CYP72B

A;Introns: 96/1; 170/3; 252/2; 381/3

C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;329-492/Domain: cytochrome P450 homology <P45>

F;470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 524;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 28 LDMAW 32

RESULT 9

T09944

Probable cytochrome P450 protein - Madagascar periwinkle

N;Alternate names: CYP72 protein

C;Species: Catharanthus roseus (Madagascar periwinkle)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001

C;Accession: T09944

R;Vetter, H.P.; Mangold, U.; Schroeder, G.; Warner, F.J.; Werck-Reichhart, D.; Schroeder

Plant Physiol. 100, 998-1007, 1992

A;Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450

A;Reference number: Z16902

A;Accession: T09944

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-524 <VET>

A;Cross-references: EMBL:L10081; NID:g167483; PID:g167484

C;Genetics:

A;Gene: CYP72

C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;329-492/Domain: cytochrome P450 homology <P45>

F;470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 28 LDMAW 32

RESULT 10

A56975

Vi polysaccharide capsule transporter VexE - Salmonella typhi

C;Species: Salmonella typhi

C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 11-Jan-2000

C;Accession: A56975

R;Hashimoto, Y.; Li, N.; Yokoyama, H.; Ezaki, T.

J. Bacteriol. 175, 4456-4465, 1993

A;Title: Complete nucleotide sequence and molecular characterization of ViaB region enc

A;Reference number: A36892; MUID:93322324; PMID:8331073

A;Accession: A56975

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-656 <HAS>

A;Cross-references: GB:D14156; NID:g426443; PIDN:BAA03200.1; PID:d1003709; PID:g426453

C;Genetics:

A;Gene: vexE

C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat h

F;284-317/Domain: tetratricopeptide repeat homology <TT1>

F;318-351/Domain: tetratricopeptide repeat homology <TT2>

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 656;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 411 LDMAW 415

RESULT 11

AF1040

Vi polysaccharide export protein [imported] - Salmonella enterica subsp. enterica serov

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AF1040

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AF1040

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-656 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD06771.1; PID:g16505421; GSPDB:GN00176

C;Genetics:

A;Gene: vexE

C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat h

Query Match

Best Local Similarity 90.0%; Score 36; DB 2; Length 656;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 411 LDMAW 415

RESULT 12

A42970

H+-exporting ATPase (EC 3.6.3.6) 95K chain, vacuolar - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein O5430c; protein YOR270c
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 C:Accession: A42970; S67167; S67172; S72041
 R:Manolson, M.F.; Proteau, D.; Preston, R.A.; Stenbit, A.; Roberts, B.T.; Hoyt, M.A.; P
 J. Biol. Chem. 267, 14294-14303, 1992
 A:Title: The VP1 gene encodes a 95-kDa integral membrane polypeptide required for in vi
 A:Reference number: A42970; MUID:92332542; PMID:1385813
 A:Accession: A42970
 A:Molecule type: DNA
 A:Residues: 1-840 <JAU>
 A:Cross-references: GB:M89778; NID:G173172; PIDN:AAA35211.1; PID:G173173
 A:Experimental source: strain X2180-1b; vacuolar acidification-defective mutants
 A>Note: sequence extracted from NCBI backbone (NCBIN:108529, NCBI:P:108530)
 R:Jauniaux, J.C.; Poirey, R.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67143
 A:Accession: S67167
 A:Molecule type: DNA
 A:Residues: 1-840 <JAU>
 A:Cross-references: EMBL:Z75178; NID:G1420605; PIDN:CAA99494.1; PID:G1420606; GSPDB:GN00
 A:Experimental source: strain S288C
 R:Cheret, G.; Sor, F.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67169
 A:Accession: S67172
 A:Molecule type: DNA
 A:Residues: 1-840 <CHE>
 A:Cross-references: EMBL:Z75178; NID:G1420605; PIDN:CAA99494.1; PID:G1420606; GSPDB:GN00
 A:Experimental source: strain S288C
 R:Cheret, G.; Bernardi, A.; Sor, F.
 Yeast 12, 1059-1064, 1996
 A:Title: DNA sequence analysis of the VP1-SNF2 region on chromosome XV of *Saccharomyces*
 A:Reference number: S72039; MUID:97051594; PMID:8896271
 A:Accession: S72041
 A:Molecule type: DNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Residues: 1-840 <CHW>
 A:Cross-references: EMBL:X89633; NID:G1279694; PIDN:CAA61776.1; PID:G1279697
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
 C:Genetics:
 A:Gene: SGD:VP1; MIPS:YOR270c
 A:Cross-references: MIPS:YOR270c; SGD:S0005796
 A:Map position: 15R
 C:Function:
 A:Description: hydrogen ion transport; hydrolase; required for assembly and activity of
 C:Superfamily: vacuolar ATP synthase 95K chain
 C:Keywords: ATP; glycoprotein; hydrogen ion transport; hydrolase; membrane-associated co
 F:407-441/Domain: transmembrane #status predicted <TM1>
 F:457-478/Domain: transmembrane #status predicted <TM2>
 F:539-558/Domain: transmembrane #status predicted <TM3>
 F:565-591/Domain: transmembrane #status predicted <TM4>
 F:635-656/Domain: transmembrane #status predicted <TM5>
 F:733-795/Domain: transmembrane #status predicted <TM6>

Query Match 90.0%; Score 36; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
 DB 518 LDMAW 522

RESULT 13

F83153
 A:Title: Probable two-component sensor PA3946 [imported] - *Pseudomonas aeruginosa* (strain PAO1)
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83153
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: F83153
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1212 <STO>
 A:Cross-references: GB:AE004812; GB:AE004091; NID:G9950125; PIDN:AA07333.1; GSPDB:GN001
 A:Experimental source: strain PAO1
 C:Genetics:
 A:Gene: PA3946
 C:Superfamily: evgS protein; response regulator homology

Query Match 90.0%; Score 36; DB 2; Length 1212;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAWL 6
 DB 47 DWAWL 51

RESULT 14

T18545
 A:Title: Lysobactin synthetase - *Lysobacter* sp. (ATCC 53042) (fragment)
 C:Species: *Lysobacter* sp.
 A:Variety: ATCC 53042
 C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000
 C:Accession: T18545
 R:Bernhard, F.

submitted to the EMBL Data Library, March 1996
 A:Description: Identification of genes encoding for peptide synthetases from Gram-negati
 A:Reference number: Z18962
 A:Accession: T18545
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-1575 <BER>
 A:Cross-references: EMBL:X96558; NID:e991096; PID:e236566; PIDN:CAA65394.1
 A:Experimental source: ATCC 53042
 C:Superfamily: acyl carrier protein homology; acetate-CoA ligase homology
 C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
 F:468-924/Domain: acetate-CoA ligase homology <ACL>
 F:942-1010/Domain: acyl carrier protein homology <ACP>
 F:974/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 1575;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5
 DB 601 LDMAW 605

RESULT 15

C70829
 A:Title: Hypothetical protein Rv0471c - *Mycobacterium tuberculosis* (strain H37RV)
 C:Species: *Mycobacterium tuberculosis*
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
 C:Accession: C70829
 R:Coale, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: C70829

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-162 <COL>
 A:Cross-references: GB:AL021933; GB:AL123456; NID:G3261529; PIDN:CAA17426.1; PID:e125254

A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0471c
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0471c

Query Match 87.5%; Score 35; DB 2; Length 162;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWAWL 6
||| |
Db 63 LDMRWL 68

Search completed: February 18, 2004, 14:38:52
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-16
Perfect score: 40
Sequence: 1 LDMAWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	223	4	US-09-107-532A-5762
2	37	92.5	745	2	US-08-887-518-3
3	37	92.5	745	2	US-09-023-321-3
4	37	92.5	745	2	US-08-890-853-4
5	37	92.5	745	2	US-09-032-475-3
6	37	92.5	745	2	US-09-099-125A-4
7	37	92.5	745	2	US-09-099-124A-4
8	37	92.5	745	3	US-09-032-476-4
9	37	92.5	745	3	US-08-890-854-4
10	37	92.5	745	3	US-09-032-324-4
11	37	92.5	745	3	US-09-168-629-2
12	37	92.5	745	3	US-08-910-820-10
13	37	92.5	745	3	US-08-810-131A-2
14	37	92.5	745	4	US-09-109-986-4
15	37	92.5	745	4	US-09-844-908-10
16	37	92.5	745	4	US-09-868-758-3
17	37	92.5	745	2	US-08-887-518-4
18	37	92.5	745	2	US-09-023-321-4
19	37	92.5	745	2	US-08-890-853-2
20	37	92.5	745	2	US-09-032-475-4
21	37	92.5	745	2	US-09-099-125A-2
22	37	92.5	745	2	US-09-099-124A-2
23	37	92.5	745	3	US-09-032-476-2
24	37	92.5	745	3	US-08-890-854-2
25	37	92.5	745	3	US-09-023-324-2
26	37	92.5	745	3	US-09-168-629-15
27	37	92.5	745	3	US-08-910-820-9

28	37	92.5	756	4	US-09-109-986-2	Sequence 2, Appli
29	37	92.5	756	4	US-09-844-908-9	Sequence 9, Appli
30	37	92.5	756	4	US-09-868-758-4	Sequence 4, Appli
31	37	92.5	996	4	US-09-417-197-123	Sequence 123, App
32	37	92.5	997	4	US-09-417-197-121	Sequence 121, App
33	36	90.0	316	4	US-09-252-991A-17312	Sequence 17312, A
34	36	90.0	1627	4	US-09-252-991A-20395	Sequence 20395, A
35	35	87.5	302	4	US-09-252-991A-21655	Sequence 21655, A
36	35	87.5	334	4	US-09-252-991A-22395	Sequence 22395, A
37	35	87.5	439	4	US-09-172-952-14	Sequence 14, Appli
38	34	85.0	1205	1	US-07-908-245-2	Sequence 2, Appli
39	34	85.0	1205	2	US-08-319-866-10	Sequence 10, Appli
40	34	85.0	1205	3	US-09-123-708-6	Sequence 6, Appli
41	34	85.0	1205	3	US-09-123-624-6	Sequence 6, Appli
42	34	85.0	1257	2	US-08-750-152A-2	Sequence 2, Appli
43	33	82.5	100	1	US-08-241-853-28	Sequence 28, Appli
44	33	82.5	100	1	US-08-241-853-29	Sequence 29, Appli
45	33	82.5	100	2	US-08-850-917-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1
US-09-107-532A-5762
; Sequence 5762, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5762:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...223
; SEQUENCE DESCRIPTION: SEQ ID NO: 5762:
US-09-107-532A-5762

Query Match 95.0%; Score 38; DB 4; Length 223;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
184 LDRAWI 189

RESULT 2
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
738 LDRAWL 743

RESULT 3
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO

; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
738 LDRAWL 743

RESULT 4
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
Db 738 LDMSWL 743

RESULT 5

US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003

; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
Db 738 LDMSWL 743

RESULT 6

US-09-099-125A-4
; Sequence 4, Application US/09099125A

; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDRAWL 6
Db 738 LDMSWL 743

RESULT 7

US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302

; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A

;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/890,853
; APPLICATION NUMBER: 92.5%; Score 37; DB 2; Length 745;
; FILING DATE: 83.3%; Pred. No. 3.4e+02;
; ATTORNEY/AGENT INFORMATION: Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 92.5%; Score 37; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 738 LDWSWL 743

RESULT 8
US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-032-476-4

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 738 LDWSWL 743

RESULT 9
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-854-4

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 738 LDWSWL 743

RESULT 10
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 08/890,854
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||:|
Db 738 LDWSWL 743

RESULT 11
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 745
TYPE: PRT
ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||:|

Db 738 LDWSWL 743
RESULT 12
US-08-910-820-10
Sequence 10, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gian
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
|||:|
Db 738 LDWSWL 743

RESULT 13
US-08-810-131A-2
Sequence 2, Application US/08810131A
Patent No. 6268194
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/810,131A
; APPLICATION NUMBER: US/08/810,131A
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-810-131A-2

Query Match 92.5%; Score 37; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 738 LDWSWL 743

RESULT 14
US-09-109-986-4
; Sequence 4, Application US/09109986
; Patent No. 6479266
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-109-986-4

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 738 LDWSWL 743

RESULT 15
US-09-844-908-10
; Sequence 10, Application US/09844908
; Patent No. 6576437
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; Zhu, Hengyi
; Barbosa, Miguel
; Li, Gian
; Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,908
; FILING DATE: 27-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
; US-09-844-908-10

Query Match 92.5%; Score 37; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDRAWL 6
DB 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:51
Job time : 7.06579 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-15
Perfect score: 36
Sequence: 1 LDWSYL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	94.4	98	1 YDAS_ECOLI	P76063 escherichia
2	33	91.7	330	1 YETK_BACSU	O31540 bacillus su
3	32	88.9	265	1 FAD1_SCHPO	O74841 schizosacch
4	32	88.9	445	1 YKAB_BACFI	P30268 bacillus fi
5	32	88.9	476	1 CLS_CLOPE	O92nc6 clostridium
6	32	88.9	517	1 SEST_CABEL	Q9n4d6 caenorhabdi
7	32	88.9	707	1 ORCL_SCHPO	P54789 schizosacch
8	32	88.9	734	1 GYS1_RABIT	P13834 oryctolagus
9	32	88.9	737	1 GYS1_HUMAN	P13807 homo sapien
10	32	88.9	737	1 GYS1_MACMU	O8mj26 macaca mula
11	32	88.9	737	1 GYS3_MOUSE	P54859 mus musculu
12	32	88.9	738	1 GYS1_MOUSE	Q921e4 mus musculu
13	32	88.9	2245	1 MYSJ_DICDI	P54697 dictyosteli
14	31	86.1	223	1 RM49_CABEL	Q21939 caenorhabdi
15	31	86.1	385	1 O46A_DROME	P81919 drosophila
16	31	86.1	506	1 POFB_SCHPO	Q09855 schizosacch
17	31	86.1	703	1 GYS2_HUMAN	P54840 homo sapien
18	31	86.1	703	1 GYS2_RAT	P17625 rattus norv
19	31	86.1	745	1 IKKA_HUMAN	O15111 h inhibitor
20	31	86.1	745	1 IKKA_MOUSE	Q60680 m inhibitor
21	31	86.1	756	1 IKKB_HUMAN	O14920 homo sapien
22	31	86.1	757	1 IKKB_MOUSE	O88351 mus musculu
23	31	86.1	757	1 IKKB_RAT	Q9qy78 rattus norv
24	31	86.1	758	1 VKGC_BOVIN	Q07175 bos taurus
25	31	86.1	758	1 VKGC_HUMAN	P38435 homo sapien
26	31	86.1	758	1 VKGC_RAT	O88496 rattus norv
27	31	86.1	1161	1 CYGE_DROME	O84496 rattus norv
28	30	83.3	97	1 FIXX_RHLSN	Q07553 drosophila
29	30	83.3	121	1 YCP2_VICFA	O53207 rhizobium s
30	30	83.3	121	1 UPK_FUSNN	P15821 vicia faba
31	30	83.3	266	1 UPK_FUSNN	Q8ri86 fusobacteri
32	30	83.3	364	1 KITH_ILTVT	P23983 infectious
33	30	83.3	365	1 ALF_NEUCR	P53444 neurospora
34	30	83.3	417	1 CPB2_HUMAN	P48052 homo sapien

ALIGNMENTS

RESULT 1
YDAS_ECOLI
ID YDAS_ECOLI STANDARD; PRT; 98 AA.
AC P76063;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydas precursor.
GN YDAS OR B1357.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
EMBL: A5000233; AAC74439.1; -
PIR: H64885; H64885.
Ecogene; EGI3361; ydas.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 98 HYPOTHETICAL PROTEIN YDAS.
SQ SEQUENCE 98 AA; 10975 MW; 397F00BA459F3BC4 CRC64;
Query Match 94.4%; Score 34; DB 1; Length 98;
Best Local Similarity 83.3%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWSYL 6
Db 67 IDWSYL 72
RESULT 2
YETK_BACSU
ID YETK_BACSU STANDARD; PRT; 330 AA.
AC O31540;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

P00730 bos taurus
P48752 human adeno
P12540 human adeno
Q22431 caenorhabdi
Q921k6 mus musculu
O95376 homo sapien
Q16924 drosophila
Q11038 mycobacteri
O87906 bacillus th
P40310 saccharomyc
Q91502 arabidopsi8
Q57595 methanococc

34 30 83.3 419 1 CBPA_BOVIN
35 30 83.3 446 1 PIV2_ADE40
36 30 83.3 452 1 PIV2_ADE12
37 30 83.3 482 1 ARI2_CABEL
38 30 83.3 492 1 ARI2_MOUSE
39 30 83.3 493 1 ARI2_HUMAN
40 30 83.3 509 1 ARI2_DROME
41 30 83.3 528 1 YC79_MYCTU
42 30 83.3 675 1 CPAA_BACTJ
43 30 83.3 691 1 TOKI_YEAST
44 30 83.3 1179 1 ATX1_ARATH
45 29 80.6 103 1 Y131_METJA

DE Hypothetical transport protein yetk.
GN YETK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Arevedo V., Bertero M.G., Bessieres P., Bolocin A., Borchert S.,
RA Borrill R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaers-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Maeda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassaretti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE EMA TRANSPORTER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; Z99107; CAB12540.1; --
CC PIR; H69798; H69798.
CC Subtilist; BG12867; yetk.
CC InterPro; IPR000620; DUF6.
CC Pfam; PF00892; DUF6; 2.
KW Hypothetical protein; Transport; Transmembrane; Complete proteome.
FT TRANSMEM 27 47 POTENTIAL.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 270 290 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 330 AA; 35758 MW; 7C6C65F1EDB276B5 CRC64;
Query Match 91.7%; Score 33; DB 1; Length 330;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DE Hypothetical transport protein yetk.
GN YETK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Arevedo V., Bertero M.G., Bessieres P., Bolocin A., Borchert S.,
RA Borrill R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaers-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Maeda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassaretti A.,
RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE EMA TRANSPORTER FAMILY.
CC -----
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CC -----
CC ENBL; Z99107; CAB12540.1; --
CC PIR; H69798; H69798.
CC Subtilist; BG12867; yetk.
CC InterPro; IPR000620; DUF6.
CC Pfam; PF00892; DUF6; 2.
KW Hypothetical protein; Transport; Transmembrane; Complete proteome.
FT TRANSMEM 27 47 POTENTIAL.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 206 226 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 270 290 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 330 AA; 35758 MW; 7C6C65F1EDB276B5 CRC64;
Query Match 91.7%; Score 33; DB 1; Length 330;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSYL 6
Db 239 LDMSYV 244
ID FAD1 SCHPO STANDARD; PRT; 265 AA.
AC O74841.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable FAD synthetase (EC 2.7.2) (FAD adenylyltransferase) (FAD
DE pyrophosphorylase) (Flavin adenine dinucleotide synthetase).
GN SPCC1235.04C
DE Schizosaccharomyces pombe (Fission yeast).
OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
ON NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe".
RL Nature 415:871-880(2002).
CC -!- FUNCTION: ADENYLATES FMN TO FAD (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + FMN = diphosphate + FAD.
CC -!- SIMILARITY: BELONGS TO THE PAPS REDUCTASE FAMILY. FAD1 SUBFAMILY.
CC -----
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CC -----
CC ENBL; AL031764; CAA21108.1; --
CC PIR; T40878; T40878.
CC GenesDB SPombe; SPCC1235.04C; --
CC InterPro; IPR002500; PAPS_reduct.
CC Pfam; PF01507; PAPS_reduct; 1.
KW Transferase; Nucleotidyltransferase; FAD; FMN.
SQ SEQUENCE 265 AA; 30608 MW; BC6C662E6F43A6F3 CRC64;
Query Match 88.9%; Score 32; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY      1 LDMSY 5
DB      173 LDMSY 177

RESULT 4
YKAB BACFI
ID YKAB BACFI STANDARD; PRT; 445 AA.
AC P30268;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Probable aminotransferase in ktaA 3'region (EC 2.6.-.-) (ORF B).
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1399;
RN [1]
RP SEQUENCE FROM N.A.
RA Quirk P.G., Krulwich T.A.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: Pyridoxal phosphate (Potential).
CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L02548; AAA22560.1; --
CC PIR; S27492; S27492.
CC HSP; P12995; IQ3.
CC InterPro; IPR005814; AminoTrans_3.
CC Pfam; PF00202; aminotran_3; 1.
CC PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
KW Hypothetical protein; Aminotransferase; Transferase;
KW Pyridoxal phosphate.
FT BINDING 280 280 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 445 AA; 48849 MW; 5C9211998C2E24BC CRC64;

Query Match 88.9%; Score 32; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DMSYL 6
DB      4 DMSYL 8

RESULT 5
CLS_CLOPE
ID CLS_CLOPE STANDARD; PRT; 476 AA.
AC Q9ZNC6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardiolipin synthetase (EC 2.7.8.-) (Cardiolipin synthase) (CL
DE synthase).
DE CLS OR CLSD OR CPE1430.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCT 8237 / ATCC 13124 / CN 1491 / Type A;
RX MEDLINE=20049836; PubMed=10585141;
RA Koyama M., Katayama S., Kaji M., Taniguchi Y., Matsushita O.,
RA Minami J., Morita S., Okabe A.;

RT "A Clostridium perfringens hem gene cluster contains a cysG(B)
RT homologue that is involved in cobalamin biosynthesis.";
RL Microbiol. Immunol. 43:947-957(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
CC from one phosphatidylglycerol molecule to another to form
CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =
CC diphosphatidylglycerol + glycerol.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY. CARDIOLIPIN
CC SYNTHASE SUBFAMILY.
CC -1- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
CC -----
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CC -----
CC EMBL; AB017186; BAA74786.1; --
CC PIR; T43863; T43863.
CC HAMAP; MF_00190; --; 1.
CC InterPro; IPR001736; PLD.
CC Pfam; PF00614; PLDC; 2.
CC SMART; SM00155; PLDC; 2.
CC PROSITE; PS50035; PLD; 2.
KW Transferase; Phospholipid biosynthesis; Transmembrane;
KW Repeat; Complete proteome.
FT TRANSMEM 2 22 POTENTIAL.
FT TRANSMEM 31 51 POTENTIAL.
FT DOMAIN 207 234 PLD PHOSPHODIESTERASE 1.
FT DOMAIN 389 416 PLD PHOSPHODIESTERASE 2.
FT ACT_SITE 212 212 POTENTIAL.
FT ACT_SITE 394 394 POTENTIAL.
FT CONFLICT 469 469 T -> I (IN REF. 1).
SQ SEQUENCE 476 AA; 55040 MW; 8EC32FC113F0A9CB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
DB      265 LDMSY 269

RESULT 6
SEST CAEEL
ID SEST CAEEL STANDARD; PRT; 517 AA.
AC Q9N4J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SBP-2003 (Rel. 42, Last annotation update)
DE Putative sestrin.
DE Y74C9A.5.
GN Y74C9A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du H., Wohlmann P., Ames M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN CONCEPTUAL TRANSLATION.
RA Axelsson K., Baloch A.;
RL Unpublished observations (MAR-2001).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the sestrin family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
CC EMBL; AC024206; AAF36051.1; ALT_SEQ.
CC WormPep; Y74C9A.5; CE24663.
CC InterPro; IPR006730; PA26.
CC Pfam; PF04636; PA26; 1.
KW Hypothetical protein; Nuclear protein.
SQ SEQUENCE 517 AA; 60881 MW; D7BC041916D0E205 CRC64;
Query Match 88.9%; Score 32; DB 1; Length 517;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSYL 6
DB 156 IDWSYM 161
:|||||
RESULT 7
ID_ORCL1_SCHPO STANDARD; PRT; 707 AA.
AC P54789;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Origin recognition complex subunit 1.
GN ORC1 OR ORP1 OR SPBC29A10.15.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96099401; PubMed=7502077;
RX Gavin K.A., Hidak M., Stillman B.D.;
RA "Conserved initiator proteins in eukaryotes";
RL Science 270:1667-1671(1995).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=96109289; PubMed=8618924;
RA Muzi-Falconi M., Kelly T.J.;
RT "Orp1, a member of the Cdc18/Cdc6 family of S-phase regulators, is
RT homologous to a component of the origin recognition complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:12475-12479(1995).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RX Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
[4]
RN SUBUNIT.
RP MEDLINE=20006240; PubMed=10535928;
RX Moon K.Y., Kong D., Lee J.K., Raychaudhuri S., Hurwitz J.;
RA "Identification and reconstitution of the origin recognition complex
RT from Schizosaccharomyces pombe";
RL Proc. Natl. Acad. Sci. U.S.A. 96:12367-12372(1999).
CC -!- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
CC BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
CC REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
CC THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.
CC -!- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY DURING THE CELL
CC CYCLE.
CC -!- SIMILARITY: BELONGS TO THE ORC1 FAMILY.
CC -----
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CC -----
CC EMBL; U40378; AAC49141.1; -.
CC EMBL; U43392; AAB38247.1; -.
CC EMBL; U38522; AAC49129.1; -.
CC EMBL; AL034463; CAA22443.1; -.
CC F1R; T40070; T40070.
CC GenesDB_Spombe; SPBC29A10.15; -.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003959; AAA_ATPase_cent.
CC InterPro; IPR000637; AT_Hook.
CC InterPro; IPR001025; BAH.
CC Pfam; PF00004; AAA; 1.
CC Pfam; PF02178; AT_hook; 1.
CC Pfam; PF01426; BAH; 1.
CC SMART; SM00382; AAA; 1.
CC SMART; SM00384; AT_hook; 1.
CC SMART; SM00433; BAH; 1.
CC SMART; SM00433; BAH; 1.
KW DNA replication; Nuclear protein; DNA-binding; ATP-binding.
FT NP_BIND 368 375 ATP (POTENTIAL).
SQ SEQUENCE 707 AA; 80514 MW; D056018159A40A44 CRC64;
Query Match 88.9%; Score 32; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSY 5
|||||

Db 193 LDMSY 197

RESULT 8

YGS1_RABIT STANDARD; PRT; 734 AA.

AC P13834; O18817;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glycogen [starch] synthase, muscle (EC 2.4.1.11).
GN GYS1 OR GYS.

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Skeletal muscle;
RX MEDLINE=90033911; PubMed=2509275;
RA Zhang W.M., Browner M.F., Fletterick R.J., Depaoli-Roach A.A.,
Roach P.J.;
RT "Primary structure of rabbit skeletal muscle glycogen synthase deduced
RT from cDNA clones.";
RL FASEB J. 3:2532-2536(1989).
RN [2]
RP SEQUENCE OF 1-29 AND 611-734.
RX MEDLINE=86242253; PubMed=3087361;
RA Cohen P., Holmes C.F.B.;
RT "Identification of the C-terminus of rabbit skeletal muscle glycogen
RT synthase.";
RL Biochem. Biophys. Res. Commun. 137:542-545(1986).
RN [3]
RP SEQUENCE OF 1-29, AND PHOSPHORYLATION SITES.
RX MEDLINE=80246030; PubMed=6772446;
RA Rylatt D.B., Aitken A., Bilham T., Condon G.D., Embl N., Cohen P.;
RT "Glycogen synthase from rabbit skeletal muscle. Amino acid sequence
RT at the sites phosphorylated by glycogen synthase kinase-3, and
RT extension of the N-terminal sequence containing the site
RT phosphorylated by phosphorylase kinase.";
RL Eur. J. Biochem. 107:529-537(1980).
RN [4]
RP SEQUENCE OF 1-15.
RX MEDLINE=79148665; PubMed=107043;
RA Huang T.S., Kreba E.G.;
RT "Effect of proteases on the structure and activity of rabbit skeletal
RT muscle glycogen synthetase.";
RL FEBS Lett. 98:66-70(1979).
RN [5]
RP PARTIAL SEQUENCE, AND PHOSPHORYLATION SITES.
RX MEDLINE=85285012; PubMed=3928373;
RA Kuret J., Woodgett J.R., Cohen P.;
RT "Multisite phosphorylation of the glycogen synthase from rabbit skeletal
RT muscle. Identification of the sites phosphorylated by casein
RT kinase-1.";
RL Eur. J. Biochem. 151:39-48(1985).
RN [6]
RP SEQUENCE OF 664-682, AND PHOSPHORYLATION SITES.
RX MEDLINE=88326353; PubMed=3137939;
RA Mahrenholz A.M., Votaw P., Roach P.J., Depaoli-Roach A.A.,
Zioncheck T.F., Harrison M.L., Geahlen R.L.;
RT "Phosphorylation of glycogen synthase by a bovine thymus protein-
RT tyrosine kinase, p40.";
RL Biochem. Biophys. Res. Commun. 155:52-58(1988).
CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
CC nonreducing end of alpha-1,4-glucan.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
CC -1- AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
CC -1- PATHWAY: Glycogen biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
CC FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF017114; AAB69872.1; -.
CC FIR; A33369; A33369.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Allosteric enzyme; Phosphorylation.
FT INIT MET 0 0
FT BINDING 38 38 UDP-GLUCOSE (BY SIMILARITY).
FT MOD_RES 7 7 PHOSPHORYLATION (BY PKA).
FT MOD_RES 10 10 PHOSPHORYLATION.
FT MOD_RES 640 640 PHOSPHORYLATION.
FT MOD_RES 644 644 PHOSPHORYLATION.
FT MOD_RES 648 648 PHOSPHORYLATION.
FT MOD_RES 652 652 PHOSPHORYLATION.
FT MOD_RES 656 656 PHOSPHORYLATION.
FT MOD_RES 697 697 PHOSPHORYLATION.
FT CONFLICT 691 691 E -> Q (IN REF. 2).
FT CONFLICT 725 725 P -> S (IN REF. 2).
FT CONFLICT 727 727 S -> P (IN REF. 2).
SQ SEQUENCE 734 AA; 83470 MW; 781BA6C435048C56 CRC64;
Query Match 88.9%; Score 32; DB 1; Length 734;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDMSYL 6
DB 595 LDMSYL 600
RESULT 9
YGS1_HUMAN STANDARD; PRT; 737 AA.
AC P13807;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glycogen [starch] synthase, muscle (EC 2.4.1.11).
GN GYS1 OR GYS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=89160794; PubMed=2493642;
RA Browner M.F., Nakano K., Bang A.G., Fletterick R.J.;
RT "Human muscle glycogen synthase cDNA sequence: a negatively charged
RT protein with an asymmetric charge distribution.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1443-1447(1989).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT NIDDM SER-464.
RX MEDLINE=95385856; PubMed=7657035;
RA Orho M., Nikula-Ijas P., Schallin-Jantti C., Permutt M.A., Groop L.C.;
RT "Isolation and characterization of the human muscle glycogen synthase
RT gene.";
RL Diabetes 44:1099-1105(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RX MEDLINE=97163531; PubMed=9010351;
RA Su X., Schuler L., Shapiro S.S.;
RT "Cloning and characterization of a glycogen synthase cDNA from human
RT endometrium.";
RL J. Steroid Biochem. Mol. Biol. 59:459-465(1996).

CC -|- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
 CC nonreducing end of alpha-1,4-glucan.
 CC -|- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
 CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
 CC -|- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
 CC -|- PATHWAY: Glycogen biosynthesis.
 CC -|- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; J04501; AAA88046.1; --
 CC EMBL; Z33622; CAAB3916.1; --
 CC EMBL; Z33623; CAAB3916.1; JOINED.
 CC EMBL; Z33624; CAAB3916.1; JOINED.
 CC EMBL; Z33625; CAAB3916.1; JOINED.
 CC EMBL; Z33626; CAAB3916.1; JOINED.
 CC EMBL; Z33610; CAAB3916.1; JOINED.
 CC EMBL; Z33627; CAAB3916.1; JOINED.
 CC EMBL; Z33628; CAAB3916.1; JOINED.
 CC EMBL; Z33629; CAAB3916.1; JOINED.
 CC EMBL; Z33630; CAAB3916.1; JOINED.
 CC EMBL; Z33631; CAAB3916.1; JOINED.
 CC EMBL; Z33633; CAAB3916.1; JOINED.
 CC EMBL; U32573; AAB60385.1; --
 CC PIR; A32156; A32156.
 CC Genew; HGNC:4706; GYS1.
 CC GK; P13807; --
 CC MIM; 138570; --
 CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
 CC Allosteric enzyme; Phosphorylation; Disease mutation;
 CC Diabetes mellitus; Polymorphism.
 CC BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
 CC FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
 CC FT VARIANT 130 130 K->E (IN dBSNP:5456).
 CC FT VARIANT 283 283 N->S (IN dBSNP:5461).
 CC FT VARIANT 359 359 E->G (IN dBSNP:5478).
 CC FT VARIANT 416 416 M->V (IN dBSNP:5465).
 CC FT VARIANT 464 464 G->S (IN dBSNP:5447).
 CC FT VARIANT 619 619 G->S (IN dBSNP:5450).
 CC FT VARIANT 691 691 P->A (IN dBSNP:5453).
 CC FT CONFLICT 136 136 T->I (IN REF. 1 AND 3).
 CC FT CONFLICT 462 462 MISSING (IN REF. 3).
 CC FT CONFLICT 608 608 A->D (IN REF. 3).
 CC FT CONFLICT 706 706 S->R (IN REF. 1 AND 3).
 CC SEQUENCE 737 AA; 83785 MW; 0E321BBFDEB0BD7F CRC64;
 CC -----
 CC Query Match 88.9%; Score 32; DB 1; Length 737;
 CC Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 CC Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDW5YL 6
 Db 596 LDW5YL 601

 RESULT 10
 GYS1 MACMU STANDARD; PRT; 737 AA.
 AC Q8MJ26;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycogen [starch] synthase, muscle (EC 2.4.1.11).
 GN GYS1 OR GYS.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]_TaxID=9544;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Ortmeier H.K., Marciani K.R., Hansen B.C.;
 RT "Monkey skeletal muscle glycogen synthase sequence.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
 CC nonreducing end of alpha-1,4-glucan (By similarity).
 CC -|- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
 CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
 CC -|- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
 CC -|- PATHWAY: Glycogen biosynthesis.
 CC -|- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF529178; AAM93267.1; --
 CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
 CC Allosteric enzyme; Phosphorylation.
 CC BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
 CC FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 CC FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
 CC SEQUENCE 737 AA; 83786 MW; BB80B3114C58F56C CRC64;
 CC -----
 CC Query Match 88.9%; Score 32; DB 1; Length 737;
 CC Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 CC Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDW5YL 6
 Db 596 LDW5YL 601

 RESULT 11
 GYS3 MOUSE STANDARD; PRT; 737 AA.
 AC P54859;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycogen [etarch] synthase, brain (EC 2.4.1.11).
 GN GYS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OF1 Albinos; TISSUE=Brain;
 RX MEDLINE=96385248; PubMed=8793107;
 RA Pellagri G., Rossier C., Magistretti P.J., Martin J.L.;
 RT "Cloning, localization and induction of mouse brain glycogen
 synthase.";
 RL Brain Res. Mol. Brain Res. 38:191-199(1996).
 CC -|- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
 CC nonreducing end of alpha-1,4-glucan.
 CC -|- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -|- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
 CC -|- PATHWAY: Glycogen biosynthesis.
 CC -|- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; X94616; CAA64322.1; -.
 DR MGD; MGI:107378; GYS3.
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KW Allosteric enzyme; Phosphorylation.
 FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
 FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 640 640 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 644 644 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 648 648 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 652 652 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 656 656 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 697 697 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 737 AA; 83824 MW; 891A0614C8F6C085 CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 737;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 |||||
 Db 595 LDKYL 600
 RESULT 12
 GYS1_MOUSE
 ID GYS1_MOUSE STANDARD; PRT; 738 AA.
 AC Q921E4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycogen [etarch] synthase, muscle (EC 2.4.1.11).
 GN GYS1 OR GYS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Seldin M.F., Xue Z., Rochelle J.M., DeBry R., Surwit R.;
 RT "Mouse glycogen synthase gene.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
 CC nonreducing end of alpha-1,4-glucan (by similarity).
 CC -|- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -|- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE (BY SIMILARITY).
 CC -|- PATHWAY: Glycogen biosynthesis.
 CC -|- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; U53218; AAD09457.1; -.
 DR MGD; MGI:101805; GYS1.
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KW Allosteric enzyme; Phosphorylation.
 FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
 FT MOD_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
 FT MOD_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 738 AA; 83955 MW; 6C2C8B5D5004F1D1 CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 738;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LDMSYL 6
 |||||
 Db 596 LDKYL 601
 RESULT 13
 MYSJ_DICDI
 ID MYSJ_DICDI STANDARD; PRT; 2245 AA.
 AC P54657;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Myosin IJ heavy chain.
 GN MYOJ.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=96215148; PubMed=8636147;
 RA Hammer J.A. III, Jung G.;
 RT "The sequence of the dictyostelium myo J heavy chain gene predicts a
 RT novel, dimeric, unconventional myosin with a heavy chain molecular
 RT mass of 258 kDa.";
 RL J. Biol. Chem. 271:7120-7127(1996).
 RN [2]
 RP SEQUENCE OF 1-1021 FROM N.A.
 RX MEDLINE=97039016; PubMed=8884597;
 RA Peterson M.D., Urioste A.S., Titus M.A.;
 RT "Dictyostelium discoideum myoJ: a member of a broadly defined myosin
 RT V class or a class XI unconventional myosin?";

RL J. Muscle Res. Cell Motil. 17:411-424 (1996).
 RN [3]
 RP SEQUENCE OF 182-298 FROM N.A.
 RX MEDLINE=95023928; PubMed=7937787;
 RA Titus M.A., Kuspa A., Loomis W.F.;
 RT "Discovery of myosin genes by physical mapping in Dictyostelium";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9446-9450 (1994).
 CC -!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE
 CC -!- ACTIVITY THAT IS ACTIVATED BY ACTIN.
 CC
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -!- SIMILARITY: Contains 1 dilute domain.
 CC -!- SIMILARITY: Contains 3 IQ domains.
 CC
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 CC
 CC EMBL; U42409; AAA85186.1; -;
 DR EMBL; L35322; AAA79858.1; -;
 DR PIR; T18278; T18278.
 DR HSSP; P08799; 1MND.
 DR DictyDb; DDO1095; myoJ.
 DR InterPro; IPR002710; DIL.
 DR InterPro; IPR000048; IQ region.
 DR InterPro; IPR001609; myosin head.
 DR InterPro; IPR004009; Myosin_N.
 DR Pfam; PF01843; DIL; 1.
 DR Pfam; PF00612; IQ; 6.
 DR Pfam; PF00063; myosin head; 2.
 DR Pfam; PF02736; Myosin_N; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD003376; DIL; 1.
 DR ProDom; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 3.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS0096; IQ; 3.
 KW Myosin; ATP-binding; Actin-binding; Calmodulin-binding; Repeat;
 KW Coiled coil.
 FT DOMAIN 1 809 MYOSIN HEAD-LIKE.
 FT DOMAIN 824 851 IQ 1.
 FT DOMAIN 872 901 IQ 2.
 FT DOMAIN 943 972 IQ 3.
 FT DOMAIN 973 1812 COILED COIL (POTENTIAL).
 FT DOMAIN 2060 2220 DILUTE.
 FT NP BIND 174 181 ATP (POTENTIAL).
 FT DOMAIN 669 749 ACTIN-BINDING.
 FT CONFLICT 191 191 L -> F (IN REF. 2).
 FT CONFLICT 284 284 A -> T (IN REF. 2).
 FT CONFLICT 291 291 G -> R (IN REF. 2).
 FT CONFLICT 332 347 NKGCFEIGVSDDEH -> IEWPFELKYRMKS (IN
 FT REF. 2).
 FT CONFLICT 550 550 N -> K (IN REF. 2).
 FT CONFLICT 865 866 HH -> QQ (IN REF. 2).
 SQ SEQUENCE 2245 AA; 258478 MW; 615SEFID1AB45BE CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 2245;
 Best Local Similarity 66.7%; Pred. No. 5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 530 IDWSYI 535
 RESULT 14
 RM49_CABEL
 ID RM49_CABEL
 AC Q21939;
 PRT; 223 AA.

DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Potential mitochondrial 60s ribosomal protein L49 (MRP-L49).
 GN R1D1.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Steward C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE L49EM FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 CC EMBL; Z75547; CAA99906.1; -;
 DR PIR; T24188; T24188.
 DR WormPep; R1D1.9; CE06314.
 DR Pfam; PF05046; Img2; 1.
 KW Hypothetical protein; Ribosomal protein; Mitochondrion.
 SQ SEQUENCE 223 AA; 25862 MW; 2A8DC95C813CBA3F CRC64;
 Query Match 86.1%; Score 31; DB 1; Length 223;
 Best Local Similarity 66.7%; Pred. No. 78;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSYL 6
 DB 90 IDWSIV 95
 RESULT 15
 O46A DROME
 ID O46A DROME STANDARD; PRT; 385 AA.
 AC P81519; Q906X9; Q9VSH3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Odorant receptor 46a.
 GN OR46A OR OR46F.1 OR DOR46F.1 OR AN9 OR CG17849.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99389723; PubMed=10458908;
 RA Gao Q., Chess A.;
 RT "Identification of candidate Drosophila olfactory receptors from
 RT genomic DNA sequence."
 RL Genomics 60:31-39 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.G.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirski R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RA Science 287:2185-2195(2000).
RA [3]
RP REVISIONS.
RC STRAIN=Berkely;
RX MEDLINE=22426063; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RX MEDLINE=99166868; PubMed=10069338;
RA Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
RT "A novel family of divergent seven-transmembrane proteins: candidate
RT odorant receptors in *Drosophila*.";
RL Neuron 22:327-338(1999).
CC -1- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF 17 OLFACTORY RECEPTOR
CC NEURONS IN THE MAXILLARY PALP.
CC -1- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
CC RECEPTORS.
CC -----
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CC -----
CC EMBL; AE003830; AAF58834.2; -;
CC FlyBase; FBgn026388; Or46a.
CC InterPro; IPR004117; 7tm_6.
CC Pfam; PF02949; 7tm_6; 1.
CC Transmembrane; G-protein coupled receptor; Olfaction; Glycoprotein;
KW

KW Multigene family.
FT DOMAIN 1 37
FT TRANSMEM 28 58
FT DOMAIN 59 65
FT TRANSMEM 66 86
FT DOMAIN 87 127
FT TRANSMEM 128 148
FT DOMAIN 149 170
FT TRANSMEM 171 191
FT DOMAIN 192 255
FT TRANSMEM 256 287
FT DOMAIN 277 287
FT TRANSMEM 288 308
FT DOMAIN 309 354
FT TRANSMEM 355 375
FT DOMAIN 376 385
SQ SEQUENCE 385 AA; 44483 MW; BB062862B7A59310 CRC64;
Query Match 86.1%; Score 31; DB 1; Length 385;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSYL 6
DB 148 LMSHL 153
Search completed: February 18, 2004, 14:28:13
Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-14
Perfect score: 35
Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	91.4	404	1 YCFD_HASIN	P44683 haemophilus
2	31	88.6	135	1 VAL2_CLVK	P14976 cassava lat
3	31	88.6	135	1 VAL2_CLVN	P14968 cassava lat
4	31	88.6	135	1 VAL2_TYLCV	P27262 tomato yell
5	31	88.6	204	1 HIS2_YERPE	Q8zfvl versinia pe
6	31	88.6	240	1 LSCS_VATMA	P81371 vatairea ma
7	31	88.6	355	1 CXAS_RAT	P28234 rattus norv
8	31	88.6	356	1 CXAS_CANFA	P33725 canis famil
9	31	88.6	357	1 CXAS_HUMAN	P36382 homo sapien
10	31	88.6	357	1 CXAS_MOUSE	Q01231 mus musculu
11	31	88.6	368	1 CXAS_CHICK	P18860 gallus gall
12	31	88.6	382	1 LYS1_CANAL	P43085 candida alb
13	31	88.6	383	1 PZC4_SCHPO	O14156 schizosacch
14	31	88.6	399	1 CXAC_CHICK	P36381 gallus gall
15	31	88.6	400	1 NUCM_PROWI	Q37619 prototheca
16	31	88.6	406	1 CXAS_BOVIN	P1987 bos taurus
17	31	88.6	415	1 CXAS_RAT	P29414 rattus norv
18	31	88.6	416	1 CXAS_MOUSE	Q4448 mus musculu
19	31	88.6	432	1 CXAS_HUMAN	P48165 homo sapien
20	31	88.6	434	1 CXAS_HUMAN	Q9y688 homo sapien
21	31	88.6	439	1 CXAS_MOUSE	P28236 mus musculu
22	31	88.6	439	1 CXAS_SHEEP	P5917 ovis aries
23	31	88.6	510	1 CX56_CHICK	P29415 gallus gall
24	31	88.6	1363	1 ILPR_BRALA	Q02466 branchiosto
25	30	85.7	98	1 YDAS_ECOLI	P76063 escherichia
26	30	85.7	225	1 TRPF_CANAL	P43073 candida alb
27	30	85.7	570	1 MKKS_HUMAN	Q9npj1 homo sapien
28	30	85.7	654	1 CBP1_YEAST	P07252 saccharomyc
29	30	85.7	709	1 KPPI_SCHPO	Q09175 schizosacch
30	30	85.7	745	1 IKKA_HUMAN	Q05111 h inhibitor
31	30	85.7	745	1 IKKA_MOUSE	Q06080 m inhibitor
32	30	85.7	751	1 TALA_POVHA	P03075 hamster pol
33	30	85.7	756	1 IKKB_HUMAN	O14920 homo sapien

34 30 85.7 757 1 IKKB_MOUSE
35 30 85.7 757 1 IKKB_RAT
36 30 85.7 3746 1 ACVS_PENCH
37 30 85.7 3791 1 ACVT_PENCH
38 29 82.9 139 1 YOR2_ADEGI
39 29 82.9 179 1 Y256_SULSO
40 29 82.9 228 1 Y268_MYCGE
41 29 82.9 233 1 CR29_ENTHI
42 29 82.9 284 1 YK62_SULTO
43 29 82.9 328 1 NIR3_AZOB
44 29 82.9 330 1 YETK_BACSU
45 29 82.9 344 1 METE_THEVO

ALIGNMENTS

RESULT 1

YCFD_HASIN STANDARD; PRT; 404 AA.
AC P44683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein HI0396.
GN HI0396.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512 (1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429 (2000).
CC -1- SIMILARITY: STRONG, TO E.COLI YCFD.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U32723; AAC22055.1; -;
DR PIR; A64151; A64151.
DR TIGR; HI0396; -;
DR InterPro; IPR003347; TF_JmJc.
DR SMART; SM00558; JmJc; 1.
KW Complete proteome.
SQ SEQUENCE 404 AA; 46419 MW; A3FF26064D3F8B4C CRC64;

Query Match 91.4%; Score 32; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 70;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 366 LDWAF 371

RESULT 2
VAL2_CLVW STANDARD; PRT; 135 AA.
AC P14976;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (15.2 kDa protein).
GN AC2.
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RA Stanley J., Gay M.R.;
RT "Nucleotide sequence of cassava latent virus DNA.";
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.

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CC EMBL; J02057; -; NOT ANNOTATED CDS.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini AL2; 1.
SQ SEQUENCE 135 AA; 15159 MW; 75D24A8CD6368848 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
Db 128 DWSFL 132

RESULT 3
VAL2_CLVW STANDARD; PRT; 135 AA.
AC P14968;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (15.2 kDa protein).
GN AC2.
OS Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174930; PubMed=2308831;
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.

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DR EMBL; X17095; CAA34952.1; -;
DR PIR; S07593; S07593.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini AL2; 1.
SQ SEQUENCE 135 AA; 15178 MW; 2825C2F42E5E1F49 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
Db 128 DWSFL 132

RESULT 4
VAL2_TYLCV STANDARD; PRT; 135 AA.
ID VAL2_TYLCV
AC P27262;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL2 protein (C2 protein).
GN C2.
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Fichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 185:151-161(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.

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DR EMBL; X15656; CAA33689.1; -;
DR PIR; C40779; QQCVC4.
DR InterPro; IPR000942; Gemini AL2.
DR Pfam; PF01440; Gemini AL2; 1.
DR PRINTS; PR00230; GEMCOATL2.
DR ProDom; PD001117; Gemini AL2; 1.
SQ SEQUENCE 135 AA; 15611 MW; F111C8C2F7E9DD32 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
Db 128 DWSFL 132

RESULT 5
HIS2 YERPE STANDARD; PRT; 204 AA.
ID HIS2 YERPE
AC Q82FY1;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histidine biosynthesis bifunctional protein HISIE [includes:
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].
 GN HISI OR HISIE OR YPO1542 OR Y2628.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
 RA "Genome sequence of Yersinia pestis, the causative agent of plague."
 RT Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-
 CC phosphoribosyl)-AMP + diphosphate.
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-
 CC phosphoribosyl)-5-(1-(5-phosphoribosyl)amino)imidazole-4-carboxamide.
 CC -1- PATHWAY: Histidine biosynthesis; second step.
 CC -1- PATHWAY: Histidine biosynthesis; third step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH
 CC FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PRA-PH
 CC FAMILY.
 CC -----
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 CC -----
 CC ENBL; AJ414149; CAC90365.1; -;
 CC ENBL; AE013864; AM86182.1; -;
 CC PIR; AB0188; AB0188.
 CC HAMAP; MF 01019; -; 1.
 CC InterPro; IPR002496; PRA-CH.
 CC InterPro; IPR002497; PRA-PH.
 CC Pfam; PF01502; PRA-CH; 1.
 CC Pfam; PF01503; PRA-PH; 1.
 CC ProDom; PD002610; PRA-CH; 1.
 CC ProDom; PD002611; PRA-PH/CH; 1.
 CC Histidine biosynthesis; Multifunctional enzyme; Hydrolase;
 KW Complete proteome.
 FT DOMAIN 1 114 PHOSPHORIBOSYL-AMP CYCLOHYDROLASE.
 FT DOMAIN 115 204 PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE.
 SQ SEQUENCE 204 AA; 22807 MW; BF3328DF1C0A8C79 CRC64;

Query Match

88.6%; Score 31; DB 1; Length 204;

Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSFL 6
 DB 111 DWSFL 115
 RESULT 6
 LECS_VATMA
 ID LECS_VATMA STANDARD; PRT; 240 AA.
 AC P81371;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Seed lectin (VWL).
 OS Vatairea macrocarpa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Dalbergieae; Vatairea.
 OX NCBI_TaxID=77050;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=98218569; PubMed=9559667;
 RA Calvete J.J., Santos C.F., Mann K., Grangeiro T.B., Nimitz M.,
 RA Urbankc C., Sousa-Cavada B.;
 RT "Amino acid sequence, glycan structure, and proteolytic processing of
 RL the lectin of Vatairea macrocarpa seeds.";
 RL FEBS Lett. 425:286-292(1998).
 CC -1- FUNCTION: LECTIN THAT BINDS GALACTOSE.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- TISSUE SPECIFICITY: Seed.
 CC -1- PTM: PARTIALLY N-GLYCOSYLATED AT POSITIONS 111 AND 183 WITH
 CC THE HEPTASACCHARIDE [(BETA-XYLOSYL-1,2) (ALPHA-MANNOSYL-1,6) (ALPHA-
 CC MANNOsyl-1,3)](BETA-MANOSYL-1,4-GLCNAC-BETA-1,4-GLCNAC-BETA-1,4
 CC [ALPHA-FUCOSYL-1,3]GLCNAC. A SMALL PROPORTION OF ALPHA CHAINS ARE
 CC PROTEOLYTICALLY CLEAVED AT 114-115 INTO GAMMA AND BETA CHAINS.
 CC THIS IS PROBABLY DEPENDENT ON THE DEGLYCOSYLATION OF N-111.
 CC -1- MISCELLANEOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION
 CC AND ONE CALCIUM ION. THE METAL IONS ARE ESSENTIAL FOR THE
 CC SACCHARIDE-BINDING AND CELL-AGGLUTINATING ACTIVITIES (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
 CC HSSP; P19588; 1LUL.
 CC GlycoSuiteDB; P81371; -;
 CC InterPro; IPR000985; Lectin_legA.
 CC InterPro; IPR001220; Lectin_legB.
 CC Pfam; PF00138; lectin_legA; 1.
 CC Pfam; PF00139; lectin_legB; 1.
 CC ProDom; PD000671; Lectin_legA; 1.
 CC ProDom; PD000711; Lectin_legB; 1.
 CC PROSITE; PS00307; LECTIN LEGUME BETA; 1.
 CC PROSITE; PS00308; LECTIN LEGUME ALPHA; 1.
 KW Lectin; Calcium; Manganese; Glycoprotein.
 FT CHAIN 1 240 SEED LECTIN ALPHA CHAIN.
 FT CHAIN 1 114 SEED LECTIN GAMMA CHAIN.
 FT CHAIN 115 239 SEED LECTIN BETA CHAIN.
 FT METAL 123 123 MANGANESE (BY SIMILARITY).
 FT METAL 125 125 MANGANESE AND CALCIUM (BY SIMILARITY).
 FT METAL 129 129 CALCIUM (BY SIMILARITY).
 FT METAL 132 132 MANGANESE AND CALCIUM (BY SIMILARITY).
 FT METAL 137 137 MANGANESE (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .).
 FT VARIANT 117 117 I -> V.
 FT VARIANT 148 148 M -> K.
 FT VARIANT 154 154 G -> A.
 FT VARIANT 168 168 E -> Q.
 FT UNSURE 239 240
 SQ SEQUENCE 240 AA; 26197 MW; C17DF6B2568C65C1 CRC64;

Query Match

88.6%; Score 31; DB 1; Length 240;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
|||||
Db 224 LDWSF 228

RESULT 7

CKA5_RAT STANDARD; PRT; 355 AA.
AC P28234;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
GN GJA5 OR CXN-40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=92112940; PubMed=1370487;
RA Haefliger J.-A., Bruzzone R., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Paul D.U.;
RT "Four novel members of the connexin family of gap junction proteins.
RT Molecular cloning, expression, and chromosome mapping.";
RL J. Biol. Chem. 267:2057-2064(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021055; PubMed=1328644;
RA Beyer E.C., Reed K.E., Westphale E.M., Kanter H.L., Larson D.M.;
RT "Molecular cloning and expression of rat connexin40, a gap junction
RT protein expressed in vascular smooth muscle.";
RL J. Membr. Biol. 127:69-76(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98066770; PubMed=9403066;
RA Seul K.H., Tadmor P.N., Beyer E.C.;
RT "Mouse connexin40: gene structure and promoter analysis.";
RL Genomics 46:120-126(1997).
CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -!- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung.
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.

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EMBL; M76535; AAA41000.1; -
DR EMBL; M83092; AAA41194.1; -
DR EMBL; AF021806; AAC53502.1; -
DR EMBL; AF022136; AAC53503.1; -
DR PIR; A42053; A42053.
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 40 POTENTIAL.
FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 76 98 POTENTIAL.
FT DOMAIN 99 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 177 POTENTIAL.
FT DOMAIN 178 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 227 POTENTIAL.
FT DOMAIN 228 355 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 355 AA; 40102 MW; 4F85943868600B9 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
|||||
Db 2 DWSFL 6

RESULT 8

CKA5_CANFA STANDARD; PRT; 356 AA.
AC P33725;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
GN GJA5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92136511; PubMed=1310450;
RA Kanter H.L., Saffitz J.E., Beyer E.C.;
RT "Cardiac myocytes express multiple gap junction proteins.";
RL Circ. Res. 70:438-444(1992).
CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -!- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.

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EMBL; M81347; AAA30838.1; -
DR PIR; A49024; A49024.
DR InterPro; IPR000500; Connexin.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 40 POTENTIAL.
FT DOMAIN 41 76 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 77 99 POTENTIAL.
FT DOMAIN 100 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 177 POTENTIAL.
FT DOMAIN 178 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 227 POTENTIAL.

FT DOMAIN 228 356 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 356 AA; 39801 MW; C8431D65CF9E78FE CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 356;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
 |||||
 DB 2 DWSFL 6

RESULT 9
 CXAS HUMAN STANDARD; PRT; 357 AA.
 AC P363E2;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
 GN GJA5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95055780; PubMed=7966354;
 RA Kanter H.L., Saffitz J.E., Beyer E.C.;
 RT "Molecular cloning of two human cardiac gap junction proteins,
 RT connexin40 and connexin45.";
 RT J. Mol. Cell. Cardiol. 26:861-868(1994).
 RN [2]
 RP REVISIONS.
 RA Beyer E.C., Christensen E.A.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lin H.H., Jin N., Kiang D.T.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Heffliger J.-A., Goy J.J., Waerber G.;
 RT "Sporadic cases of dilated cardiomyopathies associated with
 RT atrioventricular conduction defects are not linked to mutation within
 RT the connexins 40 and 43 genes.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zieberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which

CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; U03486; AAA60457.2; -;
 CC EMBL; L34954; AAA91833.1; -;
 CC EMBL; AF151979; AAD37801.1; -;
 CC EMBL; BC013313; AAH13313.1; -;
 CC Genew; HGNC:4279; GJA5.
 CC MIM; 121013; -;
 CC GO; GO:0015285; F:connexon channel activity; TAS.
 CC GO; GO:0007043; P:intercellular junction assembly; TAS.
 CC GO; GO:0006936; P:muscle contraction; TAS.
 CC InterPro; IPR000500; Connexin.
 CC Pfam; PF00029; connexin; 1.
 CC PRINTS; PR00206; CONNEXIN.
 CC SMART; SM00037; CNX; 1.
 CC PROSITE; PS00407; CONNEXINS_1; 1.
 CC PROSITE; PS00408; CONNEXINS_2; 1.
 KW Gap junction; Transmembrane.
 FT INIT MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 40 POTENTIAL.
 FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 76 98 POTENTIAL.
 FT DOMAIN 99 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 POTENTIAL.
 FT DOMAIN 184 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 POTENTIAL.
 FT DOMAIN 229 357 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 357 AA; 40249 MW; 63FF9AA3CAED760 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 357;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
 |||||
 DB 2 DWSFL 6

RESULT 10
 CXAS MOUSE STANDARD; PRT; 357 AA.
 ID CXAS_MOUSE
 AC Q01231;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).
 GN GJA5 OR CXN-40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RC MEDLINE=92259686; PubMed=1318884;
 RA Hennemann J., Suchyna T., Lichtenberg-Frate H., Jungbluth S.,
 RA Dahl E., Schwarz J., Nicholson B.J., Willecke K.;
 RT "Molecular cloning and functional expression of mouse connexin40, a
 RT second gap junction gene preferentially expressed in lung.";
 RL J. Cell Biol. 117:1299-1310(1992).

CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which
 CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -!- SUBUNIT: A connexon is composed of a hexamer of connexins.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Kidney, heart and skin, but most abundant
 CC in lung.
 CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; X61675; CAA43850.1; -.
 CC PIR; S23111; S23111.
 CC MGD; MGI:95716; Gja5.
 CC InterPro; IPR000500; Connexin.
 CC Pfam; PF00029; connexin; 1.
 CC PRINTS; PR00206; CONNEXIN.
 CC SMART; SM00037; CNX; 1.
 CC PROSITE; PS00407; CONNEXINS_1; 1.
 CC PROSITE; PS00408; CONNEXINS_2; 1.
 CC Gap junction; Transmembrane.
 CC INIT MET 0 0 BY SIMILARITY.
 CC DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 23 40 POTENTIAL.
 CC DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 76 98 POTENTIAL.
 CC DOMAIN 99 155 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 156 178 POTENTIAL.
 CC DOMAIN 179 205 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 206 228 POTENTIAL.
 CC DOMAIN 229 357 CYTOPLASMIC (POTENTIAL).
 CC SEQUENCE 357 AA; 40282 MW; 7823CDA57A9C7C90 CRC64;
 CC
 CC Query Match 88.6%; Score 31; DB 1; Length 357;
 CC Best Local Similarity 100.0%; Pred. No. 94;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 DWSFL 6
 CC DB 2 DWSFL 6
 CC
 CC RESULT 11
 CC CXA5_CHICK
 CC ID CXA5_CHICK STANDARD; PRT; 368 AA.
 CC AC P18860;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Gap junction alpha-5 protein (Connexin 42) (Cx42).
 CC OS Gallus gallus (Chicken).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC OC Gallus.
 CC OX NCBI_TaxID=9031;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=90354434; PubMed=2167316;
 CC RA Beyer E.C.;
 CC RT "Molecular cloning and developmental expression of two chick embryo
 CC gap junction proteins."
 CC J. Biol. Chem. 265:14439-14443 (1990).
 CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which
 CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -!- SUBUNIT: A connexon is composed of a hexamer of connexins.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Mostly in heart, and in the whole embryo,
 CC liver, stomach, and pectoral muscle.
 CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; M35043; AAA48716.1; -.
 CC PIR; B37819; B37819.
 CC InterPro; IPR000500; Connexin.
 CC Pfam; PF00029; connexin; 1.
 CC PRINTS; PR00206; CONNEXIN.
 CC SMART; SM00037; CNX; 1.
 CC PROSITE; PS00407; CONNEXINS_1; 1.
 CC PROSITE; PS00408; CONNEXINS_2; 1.
 CC Gap junction; Transmembrane.
 CC INIT MET 0 0 BY SIMILARITY.
 CC DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 23 45 POTENTIAL.
 CC DOMAIN 46 75 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 76 98 POTENTIAL.
 CC DOMAIN 99 159 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 160 182 POTENTIAL.
 CC DOMAIN 183 210 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 211 233 POTENTIAL.
 CC DOMAIN 234 368 CYTOPLASMIC (POTENTIAL).
 CC SEQUENCE 368 AA; 41613 MW; 853A042FDF51DABC CRC64;
 CC
 CC Query Match 88.6%; Score 31; DB 1; Length 368;
 CC Best Local Similarity 100.0%; Pred. No. 97;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 DWSFL 6
 CC DB 2 DWSFL 6
 CC
 CC RESULT 12
 CC LYS1_CANAL
 CC ID LYS1_CANAL STANDARD; PRT; 382 AA.
 CC AC P43065;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Saccharopine dehydrogenase [NAD+, L-lysine forming] (EC 1.5.1.7)
 CC DE (lysine--2-oxoglutarate reductase) (SDH).
 CC GN LYS1.
 CC OS Candida albicans (Yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 CC OX NCBI_TaxID=5476;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=95012722; PubMed=7927784;
 CC RA Garrad R.C., Schmidt T.M., Bhattacharjee J.K.;
 CC RT "Molecular and functional analysis of the LYS1 gene of Candida
 CC albicans."
 CC Infect. Immun. 62:5027-5031 (1994).
 CC -!- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+) + H(2)O = L-lysine + 2-oxoglutarate + NADH.
 CC -!- PATHWAY: Lysine biosynthesis; alpha-aminoacidic acid pathway;
 CC eighth (last) step.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: TO OTHER FUNGAL SACCHAROPINE DEHYDROGENASE.
 CC -----
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CC -----
 CC EMBL; U13233; AAA21362.1; -
 DR InterPro; IPR004002; AlaDh_PNT.
 DR Pfam; PF01262; AlaDh_PNT_C; 1.
 DR Pfam; PF05222; AlaDh_PNT_N; 1.
 KW Lysine biosynthesis; Oxidoreductase; NAD.
 FT ACT_SITE 217 217 BY SIMILARITY.
 SQ SEQUENCE 382 AA; 42394 MW; A3620191DF04B88F CRC64;

Query Match 88.6%; Score 31; DB 1; Length 382;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSF 5
 DB 151 LDMSF 155

RESULT 13

P2C4 SCHPO STANDARD; PRT; 383 AA.
 AC O14156; O9U02;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein phosphatase 2C homolog 4 (EC 3.1.3.16) (PP2C-4).
 GN PTC4 OR SPAC4A8.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION.
 RC STRAIN=972;
 RX MEDLINE=99365157; PubMed=10436019;
 RA Gaits F., Russell P.;
 RT "Vacuole fusion regulated by protein phosphatase 2C in fission
 yeast.";
 RL Mol. Biol. Cell 10:2647-2654 (1999).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkert G., Aert R., Robben J., Gymnopoulos B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J.L., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880 (2002).
 CC -1- FUNCTION: HAS A ROLE IN THE REGULATION OF VACUOLE FUSION.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.

CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. VACUOLAR.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AF140285; AAD27651.1; -
 DR EMBL; Z98762; CAB58554.1; -
 DR PIR; T38772; T38772
 DR GenedB_SPombe; SPAC4A8.03C; -
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR000222; PP2C.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolyase; Magnesium; Manganese; Membrane; Multigene family.
 FT METAL 92 92 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 308 308 MANGANESE 2 (BY SIMILARITY).
 FT METAL 347 347 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 383 AA; 43569 MW; 88E00C2BDAE4B9BF CRC64;

Query Match 88.6%; Score 31; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6
 DB 299 DMSFL 303

RESULT 14

CX38_CHICK STANDARD; PRT; 399 AA.
 AC P36381; Q92144;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gap junction alpha-8 protein (Connexin 45.6) (Cx45.6).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lens;
 RX MEDLINE=94325567; PubMed=8049527;
 RA Jiang J.X., White T.W., Goodenough D.A., Paul D.L.;
 RT "Molecular cloning and functional characterization of chick lens
 fiber connexin 45.6.";
 RL Mol. Biol. Cell 5:363-373 (1994).
 RN [2]
 RP SEQUENCE OF 1-235 FROM N.A.
 RC TISSUE=Lens fibers;
 RX MEDLINE=96437509; PubMed=8840185;
 RA Sawada K., Agata K., Eguchi G.;
 RT "Characterization of terminally differentiated cell state by
 categorizing cDNA clones derived from chicken lens fibers.";
 RL Int. J. Dev. Biol. 40:531-535 (1996).

CC -!- FUNCTION: One gap junction consists of a cluster of closely packed
 CC pairs of transmembrane channels, the connexons, through which
 CC materials of low mw diffuse from one cell to a neighboring cell.
 CC -!- SUBUNIT: A connexon is composed of a hexamer of connexins.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
 CC SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL; L24799; AAA57134.1; -;
 DR EMBL; D26333; BAA05381.1; -;
 DR PIR; I50219; I50219.
 DR InterPro; IPR000500; Connexin.
 DR InterPro; IPR002266; Connexin50.
 DR Pfam; PF03509; Connexin50; 1.
 DR Pfam; PF00029; connexin; 1.
 DR PRINTS; PR00206; CONNEXIN.
 DR SMART; SM00037; CNX; 1.
 DR PROSITE; PS00407; CONNEXINS_1; 1.
 DR PROSITE; PS00408; CONNEXINS_2; 1.
 KW Gap junction; Transmembrane.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 19 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 20 42 POTENTIAL.
 FT DOMAIN 43 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 96 POTENTIAL.
 FT DOMAIN 97 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 174 POTENTIAL.
 FT DOMAIN 175 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 POTENTIAL.
 FT DOMAIN 230 399 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 145 146 EG -> DL (IN REF. 2).
 FT CONFLICT 187 188 WP -> D (IN REF. 2).
 FT CONFLICT 233 235 IRR -> SEL (IN REF. 2).
 SQ SEQUENCE 399 AA; 45485 MW; 4197392ADB6CB5CA CRC64;

Query Match 88.6%; Score 31; DB 1; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
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 Db 2 DWSFL 6

RESULT 15
 NUCM_PROWI
 ID NUCM_PROWI STANDARD; PRT; 400 AA.
 AC Q37619;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 49 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (NADH dehydrogenase subunit 7).
 GN NAD7.
 OS Prototheca wickerhamii.
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorrellales;
 OC Chlorrellaceae; Prototheca.
 OX NCBI_TaxID=3111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=263-11;
 RX MEDLINE=94180393; PubMed=8133522;
 RA Wolff G., Plante I., Lang B.F., Kueck U., Burger G.;
 RT "Complete sequence of the mitochondrial DNA of the chlorophyte alga

RT Prototheca wickerhamii. Gene content and genome organization.";
 RL J. Mol. Biol. 237:75-86 (1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
 CC THE ENZYME.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 49 kDa SUBUNIT FAMILY.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U02970; AAD12640.1; -;
 DR PIR; T11921; T11921.
 DR InterPro; IPR001135; Oxidored_49kDa.
 DR Pfam; PF0346; complex1_49kDa; 1.
 DR PROSITE; PS00535; COMPLEX1_49K; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 400 AA; 45810 MW; 7227458FE90BC9D2 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSP 5
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 Db 221 LDWSP 225

Search completed: February 18, 2004, 14:28:12
 Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	10	US-09-847-940B-14
2	35	100.0	6	11	US-09-847-946A-14
3	33	94.3	218	12	US-10-032-189-107
4	33	94.3	218	12	US-09-863-776-50
5	33	94.3	218	12	US-09-981-151A-91
6	33	94.3	827	12	US-10-347-470A-26
7	32	91.4	6	10	US-09-847-940B-15
8	32	91.4	6	11	US-09-847-946A-15
9	32	91.4	56	10	US-09-764-877-1782
10	32	91.4	56	12	US-10-242-515-1782
11	32	91.4	743	12	US-10-104-047-2340
12	31	88.6	124	9	US-09-925-302-460
13	31	88.6	157	10	US-09-738-626-4783
14	31	88.6	184	15	US-10-078-770-86
15	31	88.6	238	15	US-10-078-770-96

16	31	88.6	264	12	US-10-097-111-300
17	31	88.6	305	15	US-10-078-770-90
18	31	88.6	317	12	US-10-032-189-32
19	31	88.6	358	12	US-10-438-537-4
20	31	88.6	358	12	US-10-295-027-1228
21	31	88.6	413	12	US-10-032-189-106
22	31	88.6	416	12	US-10-032-189-105
23	31	88.6	417	12	US-10-032-189-104
24	31	88.6	433	12	US-09-863-776-48
25	31	88.6	435	12	US-10-032-189-102
26	31	88.6	435	12	US-10-032-189-103
27	31	88.6	515	12	US-10-108-260A-3041
28	31	88.6	1025	12	US-10-345-072-7
29	31	88.6	1025	15	US-10-195-144-7
30	31	88.6	1285	12	US-10-369-493-12354
31	30	85.7	6	10	US-09-847-940B-2
32	30	85.7	6	11	US-09-847-946A-2
33	30	85.7	6	11	US-09-847-946A-33
34	30	85.7	7	11	US-09-847-946A-37
35	30	85.7	8	11	US-09-847-946A-30
36	30	85.7	8	11	US-09-847-946A-38
37	30	85.7	9	11	US-09-847-946A-32
38	30	85.7	9	11	US-09-847-946A-35
39	30	85.7	9	11	US-09-847-946A-36
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41	30	85.7	10	11	US-09-847-946A-34
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ALIGNMENTS

RESULT 1

US-09-847-940B-14

; Sequence 14, Application US/09847940B

; Patent No. US20020156000A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J.

; APPLICANT: Ghosh, Sankar

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-117CP

; CURRENT APPLICATION NUMBER: US/09/847,940B

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants

US-09-847-940B-14

Query Match 100.0%; Score 35; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6

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Db 1 LDWSFL 6

RESULT 2

US-09-847-946A-14

; Sequence 14, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

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; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
; US-09-847-946A-14

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Query Match 100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDWSFL 6
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Db 1 LDWSFL 6

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RESULT 3
US-10-032-189-107
; Sequence 107, Application US/10032189
; Publication No. US20030170630A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zertusjan, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgees, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grosse, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Bieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20

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; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Connexin
; OTHER INFORMATION: Consensus Sequence
; US-10-032-189-107

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Query Match 94.3%; Score 33; DB 12; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDWSFL 6
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Db 1 MDWSFL 6

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RESULT 4
US-09-863-776-50
; Sequence 50, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Mishra, Vishnu
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Li, Li
; APPLICANT: Taupier, Raymond J
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-020
; CURRENT APPLICATION NUMBER: US/09/863,776
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/206,679
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,688
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,829
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/207,748
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/207,798
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/208,263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/208,831
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/209,451

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; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/210,060
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/219,507
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/221,337
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/221,927
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/263,135
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,688
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,694
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Connexin
; OTHER INFORMATION: Consensus Sequence
US-09-863-776-50

Query Match 94.3%; Score 33; DB 12; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 1 MDWSFL 6

RESULT 5

US-09-981-151A-91
; Sequence 91, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shinkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981.151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243

; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Connexin
; OTHER INFORMATION: Consensus Sequence
US-09-981-151A-91

Query Match 94.3%; Score 33; DB 12; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 1 MDWSFL 6

RESULT 6

US-10-347-470A-26
; Sequence 26, Application US/10347470A
; Publication No. US20040002054A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hwang, Ho Yon
; TITLE OF INVENTION: SQV NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 01997/542003
; CURRENT APPLICATION NUMBER: US/10/347,470A
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/349,630
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/390,930
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-347-470A-26

Query Match 94.3%; Score 33; DB 12; Length 827;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
:|||||
Db 370 LDWSFI 375

RESULT 7

US-09-847-940B-15
; Sequence 15, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-15

Query Match 91.4%; Score 32; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 1 LDWSYL 6

RESULT 8
US-09-847-946A-15
; Sequence 15, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15

Query Match 91.4%; Score 32; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 1 LDWSYL 6

RESULT 9
US-09-764-877-1782
; Sequence 1782, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1782
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1782

Query Match 91.4%; Score 32; DB 10; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
| | | | |
Db 27 LDWNFL 32

RESULT 10
US-10-242-515-1782
; Sequence 1782, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,896
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1782
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1782

Query Match 91.4%; Score 32; DB 12; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||:|
Db 27 LDWNFL 32

RESULT 11

US-10-104-047-2340
; Sequence 2340, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2340
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2340

Query Match 91.4%; Score 32; DB 12; Length 743;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||:|
Db 98 VDWSFL 103

RESULT 12

US-09-925-302-460
; Sequence 460, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 460
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-460

Query Match 88.6%; Score 31; DB 9; Length 124;
Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
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Db 50 DWSFL 54

RESULT 13

US-09-738-626-4783
; Sequence 4783, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4783
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4783

Query Match 88.6%; Score 31; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
|||:|
Db 72 LDWSF 76

RESULT 14

US-10-078-770-86
; Sequence 86, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01

;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 86
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Zea mays
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: (98)
;; NAME/KEY: UNSURE
;; LOCATION: (104)..(105)
;; NAME/KEY: UNSURE
;; LOCATION: (115)
;; NAME/KEY: UNSURE
;; LOCATION: (117)
;; NAME/KEY: UNSURE
;; LOCATION: (123)
;; NAME/KEY: UNSURE
;; LOCATION: (126)..(127)
;; NAME/KEY: UNSURE
;; LOCATION: (136)
;; NAME/KEY: UNSURE
;; LOCATION: (159)
;; NAME/KEY: UNSURE
;; LOCATION: (174)..(175)
US-10-078-770-86

Query Match 88.6%; Score 31; DB 15; Length 184;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
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Db 18 LDWSF 22

RESULT 15
US-10-078-770-96
;; Sequence 96, Application US/10078770
;; Publication No. US20030003471A1
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Miao, Guo-Hua
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides
;; FILE REFERENCE: BB-1365 US NA
;; CURRENT APPLICATION NUMBER: US/10/078,770
;; CURRENT FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 09/614,188
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 96
;; LENGTH: 238
;; TYPE: PRT

;; ORGANISM: Zea mays
US-10-078-770-96
Query Match 88.6%; Score 31; DB 15; Length 238;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSF 5
|||
Db 26 LDWSF 30
Search completed: February 18, 2004, 15:42:00
Job time : 17.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-14
Perfect score: .35
Sequence: 1 LDWSFL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	91.4	829	4	US-09-252-991A-27150
2	31	88.6	86	4	US-09-107-532A-7054
3	31	88.6	277	1	US-08-118-270-68
4	31	88.6	277	5	PCT-US93-08528-68
5	31	88.6	382	2	US-08-360-606B-30
6	30	85.7	177	4	US-09-328-352-5063
7	30	85.7	365	4	US-09-328-352-7147
8	30	85.7	397	4	US-09-107-532A-4918
9	30	85.7	413	4	US-08-328-352-7815
10	30	85.7	745	2	US-08-887-518-3
11	30	85.7	745	2	US-09-023-321-3
12	30	85.7	745	2	US-08-890-853-4
13	30	85.7	745	2	US-09-032-475-3
14	30	85.7	745	2	US-09-099-125A-4
15	30	85.7	745	2	US-09-099-124A-4
16	30	85.7	745	3	US-09-032-476-4
17	30	85.7	745	3	US-08-890-854-4
18	30	85.7	745	3	US-09-023-324-4
19	30	85.7	745	3	US-09-168-629-2
20	30	85.7	745	3	US-08-910-820-10
21	30	85.7	745	3	US-08-100-131A-2
22	30	85.7	745	4	US-09-109-986-4
23	30	85.7	745	4	US-09-844-908-10
24	30	85.7	745	4	US-09-868-758-3
25	30	85.7	756	2	US-08-887-518-4
26	30	85.7	756	2	US-09-023-321-4
27	30	85.7	756	2	US-08-890-853-2

28	85.7	756	2	US-09-032-475-4	Sequence 4, Appli
29	85.7	756	2	US-09-099-125A-2	Sequence 2, Appli
30	85.7	756	2	US-09-099-124A-2	Sequence 2, Appli
31	85.7	756	3	US-09-032-476-2	Sequence 2, Appli
32	85.7	756	3	US-08-890-854-2	Sequence 2, Appli
33	85.7	756	3	US-09-023-324-2	Sequence 2, Appli
34	85.7	756	3	US-09-168-629-15	Sequence 15, Appli
35	85.7	756	3	US-08-910-820-9	Sequence 9, Appli
36	85.7	756	4	US-09-109-986-2	Sequence 9, Appli
37	85.7	756	4	US-09-844-908-9	Sequence 9, Appli
38	85.7	756	4	US-09-868-758-4	Sequence 4, Appli
39	85.7	768	2	US-08-222-617A-5	Sequence 5, Appli
40	85.7	996	4	US-09-417-197-123	Sequence 123, App
41	85.7	997	4	US-09-417-197-121	Sequence 121, App
42	85.7	3666	2	US-08-222-617A-12	Sequence 12, Appl
43	85.7	3727	2	US-08-222-617A-27	Sequence 27, Appl
44	85.7	3778	2	US-08-222-617A-2	Sequence 2, Appli
45	82.9	70	3	US-09-242-050-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-27150
; Sequence 27150, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27150
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27150

Query Match 91.4%; Score 32; DB 4; Length 829;
Best Local Similarity 83.3%; Pred. NO. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||:|
Db 486 LDWSYL 491

RESULT 2
US-09-107-532A-7054
; Sequence 7054, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC

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; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7054:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 86 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...86
; SEQUENCE DESCRIPTION: SEQ ID NO: 7054:
US-09-107-532A-7054

Query Match      88.6%; Score 31; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSF 5
        |||||
Db      42 LDWSF 46

RESULT 3
US-08-118-270-68
; Sequence 68, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 09-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-68

Query Match      88.6%; Score 31; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSFL 6
        |||||
Db      81 DWSFL 85

PCT-US93-08528-68
; Sequence 68, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-08528-68

Query Match      88.6%; Score 31; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSFL 6
        |||||
Db      81 DWSFL 85
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RESULT 5

US-08-360-606B-30
; Sequence 30, Application US/08360606B
; Patent No. 5919617
; GENERAL INFORMATION:
; APPLICANT: Jnanendra K. Bhattacharjee
; APPLICANT: Richard C. Garrod
; APPLICANT: Paul L. Skatrud
; APPLICANT: Robert P. Peery
; TITLE OF INVENTION: Methods and Reagents for
; TITLE OF INVENTION: Detecting Fungal Pathogens in a
; TITLE OF INVENTION: Biological Sample
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive Suite 3200
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,606B
; FILING DATE: December 21, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berghoff, Paul H.
; REGISTRATION NUMBER: 30,243
; REFERENCE/DOCKET NUMBER: 94,319
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: Yes
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
US-08-360-606B-30

Query Match 88.6%; Score 31; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSF 5
|||
DB 151 LDWSF 155

RESULT 6

US-09-328-352-5063
; Sequence 5063, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5063
; LENGTH: 177
; TYPE: PRT

; ORGANISM: Acinetobacter baumannii
US-09-328-352-5063

Query Match 85.7%; Score 30; DB 4; Length 177;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||
DB 137 IDWTF 142

RESULT 7

US-09-328-352-7147
; Sequence 7147, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7147
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7147

Query Match 85.7%; Score 30; DB 4; Length 365;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
|||
DB 23 LDWNFM 28

RESULT 8

US-09-107-532A-4918
; Sequence 4918, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4918:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...397
SEQUENCE DESCRIPTION: SEQ ID NO: 4918:
US-09-107-532A-4918

Query Match 85.7%; Score 30; DB 4; Length 397;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 233 IDWTF 238

RESULT 9
US-09-328-352-7815
; Sequence 7815, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7815
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7815

Query Match 85.7%; Score 30; DB 4; Length 413;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 183 IDWTF 188

RESULT 10
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 11
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 12

US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4341
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 13

US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NTK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO

; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSWL 743

RESULT 14

US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:

Search completed: February 18, 2004, 14:41:50
Job time : 7.06579 secs

; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-125A-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSL 743

RESULT 15

US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 85.7%; Score 30; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSFL 6
Db 738 LDWSL 743

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-13
Perfect score: 33
Sequence: 1 LDWSAL 6

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/6CTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	31	93.9	502	4	US-09-636-077A-13
3	30	90.9	118	4	US-08-311-731A-240
4	30	90.9	516	4	US-09-277-262-2
5	30	90.9	735	4	US-09-252-991A-32240
6	30	90.9	1891	2	US-08-804-227C-12
7	30	90.9	1891	2	US-08-804-198-6
8	29	87.9	201	1	US-07-929-580B-5
9	29	87.9	223	1	US-07-708-885B-3
10	29	87.9	223	1	US-07-714-386-3
11	29	87.9	223	1	US-07-708-888A-3
12	29	87.9	268	4	US-09-252-991A-30879
13	29	87.9	297	4	US-09-172-952-30
14	29	87.9	345	3	US-08-858-003-34
15	29	87.9	345	3	US-09-078-166-34
16	29	87.9	345	3	US-08-997-467-34
17	29	87.9	352	4	US-09-198-452A-702
18	29	87.9	464	4	US-09-252-991A-29305
19	29	87.9	480	4	US-09-252-991A-17687
20	29	87.9	529	4	US-09-252-991A-29757
21	29	87.9	703	4	US-09-252-991A-17865
22	29	87.9	1580	2	US-08-804-227C-11
23	29	87.9	1580	2	US-08-804-198-5
24	29	87.9	3729	2	US-08-804-227C-4
25	28	84.8	208	1	US-08-631-607-3
26	28	84.8	208	4	US-09-098-358B-3
27	28	84.8	536	4	US-09-252-991A-31124

28	28	84.8	1151	4	US-09-252-991A-23596	Sequence 23596, A
29	28	84.8	1843	3	US-09-413-814-50	Sequence 50, Appl
30	28	84.8	2595	3	US-09-036-987A-2	Sequence 2, Appl
31	28	84.8	2595	3	US-09-370-700-2	Sequence 2, Appl
32	28	84.8	2595	4	US-09-603-207-2	Sequence 2, Appl
33	28	84.8	3248	1	US-08-353-700-1	Sequence 1, Appl
34	28	84.8	3248	5	PCT-US95-16216-1	Sequence 1, Appl
35	27	81.8	29	3	US-09-082-279B-1276	Sequence 1276, Ap
36	27	81.8	29	4	US-09-315-304B-1276	Sequence 1276, Ap
37	27	81.8	29	4	US-09-834-784-1276	Sequence 1276, Ap
38	27	81.8	35	3	US-09-082-279B-1427	Sequence 1427, Ap
39	27	81.8	35	4	US-09-315-304B-1427	Sequence 1427, Ap
40	27	81.8	35	4	US-09-834-784-1427	Sequence 1427, Ap
41	27	81.8	45	3	US-09-040-285A-9	Sequence 9, Appl
42	27	81.8	80	3	US-09-040-285A-3	Sequence 3, Appl
43	27	81.8	111	4	US-09-107-532A-5707	Sequence 5707, Ap
44	27	81.8	209	3	US-09-040-285A-8	Sequence 8, Appl
45	27	81.8	229	3	US-09-040-285A-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-635-872A-13
; Sequence 13, Application US/09635872A
; Patent No. 6534300
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 195613USO
; CURRENT APPLICATION NUMBER: US/09/635,872A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-635-872A-13

Query Match 93.9%; Score 31; DB 4; Length 502;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
|||
Db 372 LDWSAM 377

RESULT 2

US-09-636-077A-13
; Sequence 13, Application US/09636077A
; Patent No. 6537785
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; FILE REFERENCE: 195612USO
; CURRENT APPLICATION NUMBER: US/09/636,077A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-636-077A-13

Query Match 93.9%; Score 31; DB 4; Length 502;

Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
| | | | |
Db 372 LDWSAM 377

RESULT 3
US-08-311-731A-240
; Sequence 240, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 240:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
; US-08-311-731A-240

Query Match 90.9%; Score 30; DB 4; Length 118;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
| | | | |
Db 93 LDWSAV 98

RESULT 4
US-09-277-262-2
; Sequence 2, Application US/09277262
; Patent No. 6395482
; GENERAL INFORMATION:
; APPLICANT: Karayiorgou, Maria
; APPLICANT: Gogos, Joseph A.
; TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
; TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: 600-1-223 CIP

; CURRENT APPLICATION NUMBER: US/09/277,262
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 09/229,530
; EARLIER FILING DATE: 1999-01-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-277-262-2

Query Match 90.9%; Score 30; DB 4; Length 516;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
| | | | |
Db 231 LDWSSL 236

RESULT 5
US-09-252-991A-32240
; Sequence 32240, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32240
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-32240

Query Match 90.9%; Score 30; DB 4; Length 735;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6
| | | | |
Db 379 VDWSAL 384

RESULT 6
US-08-804-227C-12
; Sequence 12, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-227C-12

Query Match 90.9%; Score 30; DB 2; Length 1891;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 904 LDWAAL 909

RESULT 7
US-08-804-198-6
Sequence 6, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgett, Stanley G.
APPLICANT: Kuhatoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-6

Query Match 90.9%; Score 30; DB 2; Length 1891;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWSAL 6
Db 904 LDWAAL 909

RESULT 8
US-07-929-580B-5
Sequence 5, Application US/07929580B
Patent No. 5426181
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Lee, Gene W.
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
NUMBER OF SEQUENCES: 5
TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, NW
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,580B
FILING DATE: 19920814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/640,492
FILING DATE: 14-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Guy Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: LEE25\VILCEK-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-929-580B-5

Query Match 87.9%; Score 29; DB 1; Length 201;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 180 LDWQAL 185

RESULT 9
US-07-708-885B-3
Sequence 3, Application US/07708885B
Patent No. 5245017
GENERAL INFORMATION:
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
APPLICANT: Toth, Carol A.
APPLICANT: Thomas, Peter
TITLE OF INVENTION: Method for Isolating
TITLE OF INVENTION: CEA-Binding Protein

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,885B
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zon, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
AUTHORS: Goldmann, Neil D.
TITLE: Genomic Sequence for Human
JOURNAL: J. of Biological Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-708-885B-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
||| ||
Db 202 LDWQAL 207

RESULT 10
US-07-714-386-3
Sequence 3, Application US/07714386
Patent No. 5278290
GENERAL INFORMATION:
APPLICANT: Thomas, Peter
APPLICANT: Toth, Carol A.
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
TITLE OF INVENTION: Binding Protein for
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,386
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zon, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
AUTHORS: Goldmann, Neil D.
TITLE: Genomic Sequence for Human
JOURNAL: J. of Biological Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-714-386-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
||| ||
Db 202 LDWQAL 207

RESULT 11
US-07-708-888A-3
Sequence 3, Application US/07708888A
Patent No. 5281697
GENERAL INFORMATION:
APPLICANT: Toth, Carol A.
APPLICANT: Thomas, Peter
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
TITLE OF INVENTION: CEA-Binding Protein
TITLE OF INVENTION: and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb
MEDIUM TYPE: storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,888A
FILING DATE: 19910531
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Lei, Ke-Jian
AUTHORS: Liu, Teresa
AUTHORS: Zou, Gerald
AUTHORS: Soravis, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
TITLE: Genomic Sequence for Human
TITLE: C-reactive Protein
JOURNAL: Journal of Biological
JOURNAL: Chemistry
VOLUME: 260
ISSUE: 24
PAGES: 13377-83
DATE: 25 OCT 1985
US-07-708-888A-3

Query Match 87.9%; Score 29; DB 1; Length 223;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDWSAL 6
Db 202 LDWQAL 207

RESULT 12

US-09-252-991A-30879
Sequence 30879, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30879
LENGTH: 268
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30879

Query Match 87.9%; Score 29; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSA 5
Db 135 LDWSA 139

RESULT 13

US-09-172-952-30
Sequence 30, Application US/09172952
Patent No. 6368793

GENERAL INFORMATION:
APPLICANT: Hoch, James
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 297
TYPE: PRT
ORGANISM: Yiar-Ec
US-09-172-952-30

Query Match 87.9%; Score 29; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSA 5
Db 59 LDWSA 63

RESULT 14

US-08-858-003-34
Sequence 34, Application US/08858003
Patent No. 6060234

GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaocan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,003
FILING DATE: 16-MAY-1979
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6060234e
US-08-858-003-34

Query Match 87.9%; Score 29; DB 3; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
| | | | |
Db 43 LDWSVL 48

RESULT 15
US-09-078-166-34
; Sequence 34, Application US/09078166
; Patent No. 6063561
; GENERAL INFORMATION:
; APPLICANT: Katz, Leonard
; APPLICANT: Stassi, Diane L.
; APPLICANT: Summers Jr., Richard G.
; APPLICANT: Ruan, Xiaocan
; APPLICANT: Pereda-Lopez, Ana
; APPLICANT: Kakavas, Stephan J.
; TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd.
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,166
; FILING DATE: 16-MAY-1979
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne Casuto
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 4952.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847)-938-3137
; TELEFAX: (847)-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6063561e
US-09-078-166-34

Query Match 87.9%; Score 29; DB 3; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSAL 6
| | | | |
Db 43 LDWSVL 48

Search completed: February 18, 2004, 14:41:50
Job time : 8.06579 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriapi:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	94.4	241	Q98D63	Q98D63 rhizobium 1
2	34	94.4	281	Q8NVL6	Q8NVL6 staphylococ
3	34	94.4	282	Q932C8	Q932C8 staphylococ
4	34	94.4	282	Q06551	Q06551 mycobacteri
5	33	91.7	195	Q8BRE0	Q8BRE0 mus musculu
6	33	91.7	237	Q9JMF2	Q9JMF2 mus musculu
7	33	91.7	263	Q9CRS3	Q9CRS3 mus musculu
8	33	91.7	392	Q99KPS	Q99KPS mus musculu
9	32	88.9	66	Q8CKQ2	Q8CKQ2 versinia pe
10	32	88.9	93	O70791	O70791 rice yellow
11	32	88.9	107	O68455	O68455 ancylobacte
12	32	88.9	138	Q8GBK5	Q8GBK5 uncultured
13	32	88.9	138	Q8GBK0	Q8GBK0 uncultured
14	32	88.9	138	Q8GBJ4	Q8GBJ4 uncultured
15	32	88.9	153	Q8XBY6	Q8XBY6 escherichia
16	32	88.9	168	Q9I265	Q9I265 pseudomonas

17	32	88.9	179	11	Q8BZU5	Q8BZU5 mus musculu
18	32	88.9	193	12	Q99FU7	Q99FU7 human echov
19	32	88.9	195	5	Q18653	Q18653 caenorhabdi
20	32	88.9	230	10	Q945X8	Q945X8 theobroma c
21	32	88.9	244	10	Q945Y3	Q945Y3 theobroma c
22	32	88.9	248	4	Q96J10	Q96J10 homo sapien
23	32	88.9	250	10	Q945X9	Q945X9 theobroma c
24	32	88.9	251	16	Q9K8S3	Q9K8S3 bacillus ha
25	32	88.9	255	10	Q945Y4	Q945Y4 theobroma c
26	32	88.9	255	10	Q945Z3	Q945Z3 theobroma c
27	32	88.9	255	10	Q945Y5	Q945Y5 theobroma c
28	32	88.9	259	16	Q8Z6N5	Q8Z6N5 salmonella
29	32	88.9	271	17	Q978V7	Q978V7 thermoplasma
30	32	88.9	278	6	Q9XTA8	Q9XTA8 oryctolagus
31	32	88.9	302	16	Q8X8Q1	Q8X8Q1 escherichia
32	32	88.9	312	10	Q9AYF3	Q9AYF3 oryza sativ
33	32	88.9	315	13	Q9I838	Q9I838 coturnix co
34	32	88.9	349	5	Q17692	Q17692 caenorhabdi
35	32	88.9	379	16	Q8Z935	Q8Z935 salmonella
36	32	88.9	382	2	O68661	O68661 actinobacil
37	32	88.9	382	10	Q8H2C3	Q8H2C3 persea amer
38	32	88.9	383	16	Q8FKN0	Q8FKN0 escherichia
39	32	88.9	386	16	O84474	O84474 chlamydia t
40	32	88.9	391	16	P95247	P95247 mycobacteri
41	32	88.9	407	2	Q55047	Q55047 shigella so
42	32	88.9	414	2	Q9S0Y1	Q9S0Y1 plesiomonas
43	32	88.9	414	2	Q9F738	Q9F738 shigella so
44	32	88.9	414	11	Q9CXT6	Q9CXT6 mus musculu
45	32	88.9	415	16	Q8VJK7	Q8VJK7 mycobacteri

ALIGNMENTS

RESULT 1

Q98D63 PRELIMINARY; PRT; 241 AA.
ID Q98D63
AC Q98D63
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative hydrolase, ripening-related protein-like.
GN MLR4841.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003005; BAB51408.1; -
DR InterPro; IPR006402; HAD-SF-IA-v3.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR01509; HAD-SF-IA-v3; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 241 AA; 27332 MW; 6AB5B55907CCC27A CRC64;

Query Match 94.4%; Score 34; DB 16; Length 241;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
:|||||

Db 90 LDYSWL 95

RESULT 2

Q8NVL6 PRELIMINARY; PRT; 281 AA.
 ID Q8NVL6
 AC Q8NVL6
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein MW1944.
 GN MW1944.
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22040717; PubMed=12044378;
 RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Ikawa N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827 (2002).
 DR EMBL; AF004828; BAB95809.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 281 AA; 33223 MW; 82483760C6698B42 CRC64;

Query Match 94.4%; Score 34; DB 16; Length 281;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 132 LDYSWI 137

RESULT 3

Q932C8 PRELIMINARY; PRT; 282 AA.
 ID Q932C8
 AC Q932C8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein SAV0804.
 GN SAV0804.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240 (2001).
 DR EMBL; AF003360; BAB5966.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 282 AA; 33281 MW; 3529EEF88F1B1A6 CRC64;

Query Match 94.4%; Score 34; DB 16; Length 282;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 132 LDYSWI 137

RESULT 4

O06551 PRELIMINARY; PRT; 282 AA.
 ID O06551
 AC O06551
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 30.9 kDa protein (O-methyltransferase, putative).
 GN OMT OR RV1153C OR MTC165.20C OR MT1187.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekaiia F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.B.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z95584; CAB09012.1; -.
 DR EMBL; AE006996; AAK45444.1; -.
 DR TIGR; MT1187; -.
 DR Tuberculist; RV1153C; -.
 DR InterPro; IPR003455; DUF142.
 DR Pfam; PF02409; OmtN; 1.
 KW Hypothetical protein; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 282 AA; 30887 MW; 41760C508774154A CRC64;

Query Match 94.4%; Score 34; DB 16; Length 282;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 142 LDYSWM 147

RESULT 5

Q8BRE0 PRELIMINARY; PRT; 195 AA.
 ID Q8BRE0
 AC Q8BRE0
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RW EMBL; AK045045; BAC32196.1; -.
KM Hypothetical protein.
SQ SEQUENCE 195 AA; 22669 MW; 6C33550846800762 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 195;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 58 VDYSWL 63

RESULT 6
Q9JMF2 PRELIMINARY; PRT; 237 AA.
ID Q9JMF2 AC Q9JMF2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown protein (Fragment).
GN 3322402L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20145471; PubMed=10679242;
RA Inoue S., Sano H., Ohta M.;
RA "Growth suppression of Escherichia coli by induction of expression of
RT mammalian genes with transmembrane or ATPase domains.";
RL Biochem. Biophys. Res. Commun. 268:553-561(2000).
DR EMBL; AB030195; BAA92758.1; -.
DR MGD; MGI:1921273; 3322402L07RIK.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 237 AA; 26633 MW; B0928A9C7A41D377 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 237;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 167 VDYSWL 172

RESULT 7
Q9CRS3 PRELIMINARY; PRT; 263 AA.
ID Q9CRS3 AC Q9CRS3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 17 days embryo head cDNA, RIKEN full-length enriched library,
DE clone:3322402L07 product:hypothetical protein, full insert sequence
DE (Fragment).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Ikegami T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Hazama M., Nishine T., Harada A.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK014383; BAB29312.2; -.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 263 AA; 30215 MW; 692304F88AD341AF CRC64;

Query Match 91.7%; Score 33; DB 11; Length 263;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 126 VDYSWL 131

RESULT 8

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Q99KP5 PRELIMINARY; PRT; 392 AA.
 AC Q99KP5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to cyclin I.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004071; AH04071.1; -;
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 3.
 DR SMART; SM00320; WD40; 2.
 DR PROSITE; PS0294; WD REPEATS_REGION; 1.
 KW Cyclin; Repeat; WD repeat.
 SQ SEQUENCE 392 AA; 44527 MW; 4B2E5CBA3A22075A CRC64;
 Query Match 91.7%; Score 33; DB 11; Length 392;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 384 VDYSWL 389
 RESULT 9
 Q8CKQ2 PRELIMINARY; PRT; 66 AA.
 AC Q8CKQ2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical.
 GN Y3132.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AE013914; AM86682.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 66 AA; 7780 MW; EF5586E890246D88 CRC64;
 Query Match 88.9%; Score 32; DB 16; Length 66;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DYSSL 6
 Db 46 DYSSL 50
 RESULT 10
 O70791 PRELIMINARY; PRT; 93 AA.
 ID O70791
 AC O70791;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 GN 6.
 OS Rice yellow stunt virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Nucleorhabdovirus.
 OX NCBI_TaxID=59380;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fang R., Luo Z., Zhao H.;
 RL "Novel structure of the rice yellow stunt virus genome: a plant
 RT rhabdovirus encodes seven genes.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB011257; BAA25159.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 93 AA; 10543 MW; A10CC3BD41F88305 CRC64;
 Query Match 88.9%; Score 32; DB 12; Length 93;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 63 IDYSWL 68
 RESULT 11
 O68455 PRELIMINARY; PRT; 107 AA.
 AC O68455;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Haloacid dehalogenase (Fragment).
 OS Ancylobacter aquaticus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Hyphomicrobiaceae; Ancylobacter.
 OX NCBI_TaxID=100;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CN13;
 RA Fortin N., Fulthorpe R.R., Allen D.G., Greer C.W.;
 RT "Molecular analysis of bacterial isolates and total community DNA from
 RT kraft pulp mill effluent treatment systems.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF043240; AAC08952.1; -;
 DR HSP; O60099; 1A06.
 DR InterPro; IPR005833; Hlgnase/hydrlase.
 DR InterPro; IPR005834; Hydrolase.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00413; HALOALOGNASE.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 12177 MW; 2BF77D4354B5D0C8 CRC64;
 Query Match 88.9%; Score 32; DB 2; Length 107;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDYSWL 6
 Db 6 LEYSWL 11
 RESULT 12
 Q8GBK5 PRELIMINARY; PRT; 138 AA.
 ID Q8GBK5
 AC Q8GBK5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchesi J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenic pool in activated
RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511306; CAD54096.1; -.
FT NON_TER 138 138
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15508 MW; A10B803019693F53 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 6 LEYSWL 11

RESULT 13
Q8GBK0 PRELIMINARY; PRT; 138 AA.
AC Q8GBK0; 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchesi J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenic pool in activated
RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511311; CAD54101.1; -.
FT NON_TER 138 138
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15643 MW; 3F31CE5C83979082 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 6 LEYSWL 11

RESULT 14
Q8GBJ4 PRELIMINARY; PRT; 138 AA.
AC Q8GBJ4; 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchesi J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenic pool in activated

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RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511319; CAD54109.1; -.
FT NON_TER 138 138
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15525 MW; 9C48CD30E1C42F40 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 6 LEYSWL 11

RESULT 15
Q8XBY6 PRELIMINARY; PRT; 153 AA.
AC Q8XBY6; 20 (Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein 20706.
GN Z0706 OR ECS0606.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=1206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner P.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Omishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005236; AAG54901.1; -.
DR EMBL; AF002552; BAB34029.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 17334 MW; 1AD056E0EAA29C65 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
Db 83 LDYSW 87

Search completed: February 18, 2004, 14:35:52
Job time : 19.3684 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-12
Perfect score: 36
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: .127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	91.7	404	ADMR_HUMAN	015218 homo sapien
2	32	88.9	94	VLYS_BPAPS	09t1c7 bacterioph
3	32	88.9	229	HAD2_PSEPU	P24070 pseudomonas
4	32	88.9	253	HAD_XANAU	O60099 xanthobacte
5	32	88.9	259	SSAT_SALTY	P96068 salmonella
6	32	88.9	302	ABGR_ECOLI	P77744 escherichia
7	32	88.9	313	IRFI_CHICK	Q90876 gallus gall
8	32	88.9	400	AAT_RHILP	O86459 rhizobium l
9	32	88.9	524	VGLG_RABVV	O80899 rabies viru
10	32	88.9	684	XYNA_CALSR	P40944 caldicellul
11	32	88.9	735	FCT_ERMCH	O47162 erwinia chr
12	32	88.9	1039	GUNE_CALSA	P10474 c endogluc
13	31	86.1	200	YE15_HAEIN	P44187 haemophilus
14	31	86.1	431	UL78_HCMVA	P16751 human cytom
15	31	86.1	745	IKKA_HUMAN	O15111 h inhibitor
16	31	86.1	745	IKKA_MOUSE	O60680 m inhibitor
17	31	86.1	756	IKKB_HUMAN	O14920 homo sapien
18	31	86.1	757	IKKB_MOUSE	O88351 mus musculu
19	31	86.1	757	IKKB_RAT	Q9qy78 rattus norv
20	30	83.3	225	YMBB_BACSU	P39585 bacillus su
21	30	83.3	394	MPGS_AERPE	Q9ydm5 aeropyrum p
22	30	83.3	460	GUNC_CLOJO	P37701 clostridium
23	30	83.3	460	GUNC_CLOCE	P37699 clostridium
24	30	83.3	566	GOIM_COXBU	P45650 coxiella bu
25	30	83.3	670	ACLI_NEUCR	O8x097 neurospora
26	30	83.3	674	ACLI_SORMA	Q93988 sordaria ma
27	30	83.3	728	UVRC_STRCO	O92512 streptomyce
28	30	83.3	868	NI80_YEAST	P33420 saccharomyc
29	30	83.3	1029	YEC5_YEAST	P43571 saccharomyc
30	30	83.3	1091	ACLY_MOUSE	Q91v92 mus musculu
31	30	83.3	1100	ACLY_RAT	P16638 rattus norv
32	30	83.3	1101	ACLY_HUMAN	P53396 homo sapien
33	29	80.6	167	YMH6_CABEL	P34473 caenorhabdi

RESULT 1
ADMR_HUMAN
ID ADMR_HUMAN STANDARD; PRT; 404 AA.
AC 015218;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adrenomedullin receptor (AM-R).
GN ADMR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98042541; PubMed=9367907;
RA Haenze J., Dittrich K., Dotsch J., Rascher W.;
RT "Molecular cloning of a novel human receptor gene with homology to the
RT rat adrenomedullin receptor and high expression in heart and immune
RT system";
RL Biochem. Biophys. Res. Commun. 240:183-188(1997).
CC -!- FUNCTION: RECEPTOR FOR ADRENOMEDULLIN. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
IMMUNE SYSTEM, ADRENAL GLAND AND LIVER.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHEST RESEMBLANCE WITH THE RDC1 ORPHAN RECEPTOR.

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or send an email to license@isb-sib.ch).

CC EMBL: Y13583; CAA73910.1; --
CC PIR: JC5784; JC5784
CC Genew; HGNC:13708; ADMR.
CC MIM: 605307; --
CC GO: GO:0016021; C: integral to membrane; TAS.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1.1.
CC PRINTS: PR00237; GPCR_RHODPSN.
CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
CC G-PROTEIN COUPLED RECEPTOR; Transmembrane; Glycoprotein.
DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 58 79 1 (POTENTIAL).
FT DOMAIN 80 90 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 91 113 2 (POTENTIAL).
FT DOMAIN 114 127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149 3 (POTENTIAL).
FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).

P37904 escherichia
P32437 bacillus su
Q01399 moraxella s
Q59728 pseudomonas
Q52087 pseudomonas
Q59866 pseudomonas
Q53464 pseudomonas
O52423 neisseria m
O74558 archaetocch
Q28355 archaetoglob
P45543 escherichia
P80036 flavobacter

ALIGNMENTS

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FT TRANSMEM 171 193 4 (POTENTIAL).
FT DOMAIN 194 217 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 218 239 5 (POTENTIAL).
FT DOMAIN 240 258 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 259 280 6 (POTENTIAL).
FT DOMAIN 281 299 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 300 320 7 (POTENTIAL).
FT DOMAIN 321 404 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 202 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 404 AA; 45323 MW; EF187ECDFD2DC6C1 CRC64;

Query Match 91.7%; Score 33; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 115 LDYTWL 120

RESULT 2
VLXS BPAPS STANDARD; PRT; 94 AA.
AC Q9T17;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative lysis protein S (P11).
GN 11.
OS Bacteriophage APSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=106199;
RN [1]
RP MEDLINE=99420383; PubMed=10489345;
RA van der Wilk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
RT the secondary endosymbiont of acyrthosiphon pisum.";
RL Virology 262:104-113(1999).
CC -1- FUNCTION: ESSENTIAL FOR LYSIS OF THE BACTERIAL CELL WALL BY
CC DISRUPTING THE CELL MEMBRANE, THEREBY GIVING HYDROLYTIC ENZYMES
CC ACCESS TO THE CELL WALL (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LAMEDA PHAGE S PROTEIN FAMILY.
CC
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CC
CC EMBL; AF157835; AAF03954.1;
CC InterPro; IPR006481; Holin_lambda.
CC Pfam; PF05106; Phage_holin_3; 1.
CC TIGRFAMs; TIGR01594; holin_lambda; 1.
KW Phage lysis protein.
SQ SEQUENCE 94 AA; 10589 MW; C3EE1A3181150120 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYXSWL 6
Db 66 DYXSWL 70

RESULT 3
HAD2_PSESP STANDARD; PRT; 229 AA.
ID HAD2_PSESP

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AC P24070;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 2-haloalkanoic acid dehalogenase II [EC 3.8.1.2] (L-2-haloacid
DE dehalogenase II) (Halocarboxylic acid halohydrolyase II) (DBHCII).
OS Pseudomonas sp. (strain CBS3).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139597; PubMed=1995594;
RA Schneider B., Mueller R., Frank R., Lingens F.;
RT "Complete nucleotide sequences and comparison of the structural genes
RT of two 2-haloalkanoic acid dehalogenases from Pseudomonas sp. strain
RT CBS3.";
RL J. Bacteriol. 173:1530-1535(1991).
CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
CC halide.
CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
CC FAMILY.
CC
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CC
CC EMBL; M62909; AAA25833.1;
CC PIR; B38452; B38452.
CC HSP; Q53464; IZRN.
CC InterPro; IPR006328; HAD II.
CC InterPro; IPR006388; HAD_SF_IA_V2.
CC InterPro; IPR005833; Hlg_nase/hydrolase.
CC Pfam; PF00702; Hydrolase; 1.
CC PRINTS; PR00413; HADHALOGENASE.
CC TIGRFAMs; TIGR01493; HAD-SF-IA-V2; 1.
CC TIGRFAMs; TIGR01428; HAD_type_II; 1.
KW Hydrolase.
FT ACT SITE 10 10 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25712 MW; A77AA63C97DD40AB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 229;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
Db 45 LEYSWL 50

RESULT 4
HAD_XANAU STANDARD; PRT; 253 AA.
AC Q60099; Q56757;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid
DE dehalogenase) (Halocarboxylic acid halohydrolyase).
GN DHLB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
RX STRAIN=GJ10;
RX MEDLINE=92078101; PubMed=1744048;
RA van der Ploeg J., van Hall G., Janssen D.B.;

```

RT "Characterization of the haloacid dehalogenase from Xanthobacter
 RL autotrophicus GJ10 and sequencing of the dhlB gene."; [2]
 RN J. Bacteriol. 173:7925-7933(1991).
 RP

RC SEQUENCE OF 1-122 FROM N.A.
 RX STRAIN=GJ10;

RY MEDLINE=96086306; PubMed=7580000;
 RA van der Ploeg J., Janssen D.B.;

RT "Sequence analysis of the upstream region of dhlB, the gene encoding
 RL haloalkanoic acid dehalogenase of Xanthobacter autotrophicus GJ10."; [3]
 RN Biodegradation 6:257-263(1995).
 RP

RC X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) AND REVISION TO 84.
 RX STRAIN=GJ10;

RY MEDLINE=98070500; PubMed=9407083;
 RA Ridder I.S., Rozeboom H.J., Kalk K.H., Janssen D.B., Dijkstra B.W.;

RT "Three-dimensional structure of L-2-haloacid dehalogenase from
 RL Xanthobacter autotrophicus GJ10 complexed with the substrate-analogue
 formate."; [3]
 RN J. Biol. Chem. 272:33015-33022(1997).
 RP

CC -1- FUNCTION: CATALYZES THE HYDROLYTIC DEHALOGENATION OF SMALL L-2-
 CC HALOALKANOIC ACIDS TO YIELD THE CORRESPONDING D-2-HYDROXYALKANOIC
 CC ACIDS. ACTIVE WITH 2-HALOGENATED CARBOXYLIC ACIDS AND CONVERTS
 CC ONLY THE L-ISOMER OF 2-CHLOROPROPIONIC ACID WITH INVERSION OF
 CC CONFIGURATION TO PRODUCE D-LACTATE. OPTIMAL ACTIVITY IS BETWEEN PH
 CC 9-10, AND MAXIMAL ACTIVITY SEEN AT PH 9.5.
 CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
 CC halide.

CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
 CC FAMILY.

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 CC -----

DR ENBL; M81691; AAA27590.1; -;
 DR ENBL; X86084; CAA60039.1; -;
 DR PIR; S52840; S52840.

DR PDB; 1AQ6; 28-JAN-98.

DR PDB; 1QQ5; 29-NOV-99.

DR PDB; 1QQ6; 20-DEC-00.

DR PDB; 1QQ7; 20-DEC-00.

DR InterPro; IPR006328; HAD_II.

DR InterPro; IPR006388; HAD_SF_IA_v2.

DR InterPro; IPR005833; Hlgase/hydrase.

DR InterPro; IPR005834; Hydrolase.

DR Pfam; PF00702; Hydrolase; 1.

DR PRINTS; PR00413; HADHALOGENASE.

DR TIGRFAMS; TIGR01493; HAD-SF-IA-v2; 1.

DR TIGRFAMS; TIGR01428; HAD_type_II; 1.

KW Hydrolase; 3D-structure.

FT ACT SITE 8 8 NUCLEOPHILE.

FT CONFLICT 84 84 D -> G (IN REF. 1 AND 2).

FT STRAND 4 7

FT STRAND 10 10

FT TURN 11 13

FT TURN 14 14

FT STRAND 16 19

FT HELIX 20 26

FT TURN 28 29

FT HELIX 31 52

FT TURN 53 53

FT HELIX 58 72

FT TURN 73 74

FT HELIX 79 86

FT HELIX 87 91

FT STRAND 94 94

FT TURN 96 97

FT HELIX 98 105
 FT TURN 106 107
 FT STRAND 109 114
 FT HELIX 118 127
 FT TURN 128 129
 FT HELIX 131 133
 FT STRAND 136 139
 FT HELIX 140 143
 FT TURN 144 144
 FT TURN 147 148
 FT HELIX 150 160
 FT HELIX 164 186
 FT STRAND 167 171
 FT HELIX 174 183
 FT TURN 184 184
 FT STRAND 186 190
 FT HELIX 195 203
 FT HELIX 209 217
 FT TURN 222 223
 FT STRAND 229 231
 FT HELIX 234 236
 FT HELIX 237 243
 SQ SEQUENCE 253 AA; 27469 MW; E2AB8DEED37A5716 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 253;
 Best Local Similarity 83.3%; Pred. No. 34;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSLW 6

DB 43 LEYSWL 48

SSAT_SALT

ID SSAT_SALT STANDARD; PRT; 259 AA.

AC P96088;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Secretion system apparatus protein ssaf.

GN SSAT OR STM1421.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2;

RX MEDLINE=97285756; PubMed=9140973;

RA Hensel M., Shea J.E., Raupach B., Monack D., Falkow S., Gleeson C.,

RA Kubo T., Holden D.W.;

RT "Functional analysis of ssaf and the ssak/U operon, 13 genes encoding

RT components of the type III secretion apparatus of Salmonella

RT pathogenicity island 2.";

RL Mol. Microbiol. 24:155-167(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2.";

RL Nature 413:852-856(2001).

CC -1- FUNCTION: PART OF A TYPE III SECRETION SYSTEM.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.

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DR EMBL; X99944; CAA68201.1; -;
 DR EMBL; AE008761; AAL20345.1; -;
 DR SyGene; SG10717; ssat.
 DR InterPro; IPR002010; Bac_export_1.
 DR InterPro; IPR006304; Spar_YscT.
 DR Pfam; PF01311; Bac_export_1; 1.
 DR PRINTS; PR00953; TYPE1MBPROT.
 DR TIGRfams; TIGR01401; flir_like_III; 1.
 KW Transport; Protein transport; Transmembrane; Complete proteome.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 35 55 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT TRANSMEM 127 147 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 214 234 POTENTIAL.
 FT TRANSMEM 259 AA; 29218 MW; 8E5F0734991373DD CRC64;

Query Match 88.9%; Score 32; DB 1; Length 259;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
 |||||
 Db 67 DYSWL 71

RESULT 6
 ABGR_ECOLI
 ID ABGR_ECOLI STANDARD; PRT; 302 AA.
 AC P77744;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative transcriptional regulator abgr.
 GN ABGR OR B1339.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1685;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12.";
 RT Science 277:1453-1474 (1997).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251357; PubMed=9097039;
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sampa G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377 (1996).
 RN [3]
 RC CHARACTERIZATION.
 RP STRAIN=BN101;
 RX MEDLINE=99047572; PubMed=9829935;

RA Hussein M.J., Green J.M., Nichols B.P.;
 RT "Characterization of mutations that allow p-aminobenzoyl-glutamate
 RT utilization by Escherichia coli.";
 RL J. Bacteriol. 180:6260-6268 (1998).
 CC -!- FUNCTION: COULD BE THE REGULATOR OF THE ABG OPERON.
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----

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 CC -----

DR EMBL; AE000232; AAC74421.1; -;
 DR EMBL; D90772; BAA14941.1; -;
 DR EMBL; D90773; BAA14944.1; -;
 DR PIR; F64883; F64883.
 DR EcGene; EGI3353; abgr.
 DR InterPro; IPR000847; HTH_LysR.
 DR InterPro; IPR005119; LysR_subst.
 DR Pfam; PF00126; HTH 1; 1.
 DR Pfam; PF03466; LysR_substrate; 1.
 DR PRINTS; PR00039; HTHLYSR.
 DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
 KW Transcription regulation; DNA-binding; Complete proteome.
 FT DNA_BIND 22 41 H-T-H MOTIF (POTENTIAL).
 FT SEQUENCE 302 AA; 34058 MW; 57C83FA6DF8ABA66 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 302;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
 |||||
 Db 191 LDYSW 195

RESULT 7
 IRFL_CHICK
 ID IRFL_CHICK STANDARD; PRT; 313 AA.
 AC Q90876;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interferon regulatory factor 1 (IRF-1).
 GN IRF1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC MEDLINE=95241453; PubMed=7536924;
 RA Jungwirth C., Rebert M., Ozato K., Degen H.J., Schultz U.,
 RA David I.B.;
 RA "Chicken interferon consensus sequence-binding protein (ICSBP) and
 RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
 RT conservation in the IRF gene family";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109 (1995).
 CC -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
 CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
 CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the IRF family.
 CC -----
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CC -----

DR EMBL; L39766; AAA62160.1; -;
DR HSSP; P15314; 1IF1.
DR InterPro; IPR001346; IRF.
DR Pfam; PF00605; IRF; 1.
DR PRINTS; PR00267; INTERNREGCT.
DR ProDom; PD002355; IRF; 1.
DR SMART; SM00348; IRF; 1.
DR PROSITE; PS00601; IRF; 1.
DR Transcription regulation; DNA-binding; Activator; Nuclear protein.
KW DNA BIND 7 109 TRYPTOPHAN PENTAD REPEAT.
FT SEQUENCE 313 AA; 36009 MW; 0895FA3736FA7463 CRC64;
SQ

Query Match 88.9%; Score 32; DB 1; Length 313;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 295 LDFS WL 300
|||||

RESULT 8

ID_AAT_RHILP STANDARD; PRT; 400 AA.
AC O86459;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPAT).
GN ASFC OR AATA.
OS Rhizobium leguminosarum (biovar phaseoli).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OX Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OC NCBI_TaxID=385;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8002;
RA Allaway D.;
RT "Sequence of an aspartate aminotransferase from Rhizobium leguminosarum";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate + L-glutamate.
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SIMILARITY: BELONGS TO CLASS-1 OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

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CC -----

DR EMBL; AJ006709; CAA07198.1; -;
DR HSSP; Q56232; 1BKQ.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR004839; Aminotransf1/2.
DR InterPro; IPR004838; NHtransf 1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER CLASS 1; 1.
KW Transferase; Aminotransferase; Pyridoxal phosphate.
FT BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 400 AA; 43752 MW; 1375BE0A72934304 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 400;

Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDYSW 5
DB 87 LDYSW 91
|||||

RESULT 9

VGLG_RABVV STANDARD; PRT; 524 AA.
AC Q08089;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Spike glycoprotein precursor.
GN G.
OS Rabies virus (strain Vnukovo-32).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=45418;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95070778; PubMed=7979981;
RA Fodor I., Grabko V.I., Khozinski V.V., Selimov M.A.;
RT "Nucleotide and deduced amino acid sequences of the glycoprotein gene
of rabies virus vaccine strain Vnukovo-32";
RL Arch. Virol. 135:451-459(1994).
CC -1- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.
CC IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE
CC HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL.
CC THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND
CC THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND VIRUS
CC BUDDING.
CC

CC -1- SUBUNIT: Homotrimer.
CC -----
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CC -----

DR EMBL; X71879; CAA50713.1; -;
DR PIR; S33419; S33419.
DR InterPro; IPR001903; Rhabd glycop.
DR Pfam; PF00974; Rhabdo glycop; 1.
KW Transmembrane; Envelope protein; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 524 SPIKE GLYCOPROTEIN.
FT TRANSMEM 460 476 BY SIMILARITY.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 524 AA; 58692 MW; 6DB36ES0406CC16D CRC64;

Query Match 88.9%; Score 32; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6
DB 137 DYSWL 141
|||||

RESULT 10

XYNA_CALSR STANDARD; PRT; 684 AA.
ID XYNA_CALSR
AC P40944;
DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update).
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
 DE (1,4-beta-D-xylan xylanohydrolase A).
 GN XYNA.
 OS Caldicellulosiruptor sp. (strain Rt8B.4).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosiruptor.
 OX NCBI_TaxID=28238;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97077616; PubMed=8920183;
 RA Divedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
 RT "Cloning, sequencing and overexpression in *Escherichia coli* of a
 RT xylanase gene, xynA from the thermophilic bacterium Rt8B.4 genus
 RT Caldicellulosiruptor.";
 RL Appl. Microbiol. Biotechnol. 45:86-93(1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylonic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC -----
 CC EMBL: L18965; AAB42044.1; --
 DR PIR: S41788; S41788.
 DR HSP: P10478; IXY2.
 DR InterPro: IPR003305; CBM_CenC.
 DR InterPro: IPR001000; Glyco_hydro_10.
 DR Pfam: PF02018; CBM 4.9; 2.
 DR Pfam: PF00331; Glyco_hydro_10; 1.
 DR SMART: SM00633; Glyco_10; 1.
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 684 ENDO-1,4-BETA-XYLANASE A.
 FT ACT_SITE 490 490 PROTON DONOR (BY SIMILARITY).
 FT ACT_SITE 598 598 NUCLEOPHILE (BY SIMILARITY).
 SQ SEQUENCE 684 AA; 78353 MW; 0A575F4FB4B5E6 CRC64;
 Query Match 88.9%; Score 32; DB 1; Length 684;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DYSWL 6
 Db 650 DYSWL 654
 RESULT 11
 FCT_ERWCH STANDARD; PRT; 735 AA.
 AC Q47162;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ferrichrysoactin receptor precursor.
 GN FCT.
 OS *Erwinia chrysanthemi*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3937;
 RX MEDLINE=96165286; PubMed=8576065;

RA Sauvage C., Franza T., Expert D.;
 RT "Analysis of the *Erwinia chrysanthemi* ferrichrysoactin receptor
 RT gene: resemblance to the *Escherichia coli* fepA-fes bidirectional
 RT promoter region and homology with hydroxamate receptors.";
 RL J. Bacteriol. 178:1227-1231(1996).
 CC -1- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING
 CC CHRYSOACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE
 CC BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
 CC -----
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 CC -----
 CC EMBL: X87967; CAA61205.1; --
 DR PIR: S57486; S57486.
 DR HSP: P06971; 2FCF.
 DR InterPro: IPR000531; TonB_boxC.
 DR Pfam: PF00593; TonB_dep_Rec; 1.
 DR PROSITE: PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; 1.
 KW Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
 KW Transport; TonB box.
 FT SIGNAL 1 38
 FT CHAIN 39 735
 FT SITE 45 52
 FT SITE 718 735
 FT DOMAIN 39 45
 FT TRANSMEM 46 54
 FT DOMAIN 55 82
 FT TRANSMEM 83 91
 FT DOMAIN 92 107
 FT TRANSMEM 108 116
 FT DOMAIN 117 124
 FT TRANSMEM 125 133
 FT DOMAIN 134 169
 FT TRANSMEM 170 178
 FT DOMAIN 179 179
 FT TRANSMEM 180 188
 FT DOMAIN 189 194
 FT TRANSMEM 195 203
 FT DOMAIN 204 222
 FT TRANSMEM 223 231
 FT DOMAIN 232 261
 FT TRANSMEM 262 270
 FT DOMAIN 271 286
 FT TRANSMEM 287 295
 FT DOMAIN 296 312
 FT TRANSMEM 313 321
 FT DOMAIN 322 328
 FT TRANSMEM 329 337
 FT DOMAIN 338 343
 FT TRANSMEM 344 352
 FT DOMAIN 353 378
 FT TRANSMEM 379 387
 FT DOMAIN 388 392
 FT TRANSMEM 393 401
 FT DOMAIN 402 403
 FT TRANSMEM 404 412
 FT DOMAIN 413 424
 FT TRANSMEM 425 433
 FT DOMAIN 434 448
 FT TRANSMEM 449 457
 FT DOMAIN 458 461
 FT TRANSMEM 462 470
 FT DOMAIN 471 495
 FT TRANSMEM 496 504
 FT DOMAIN 505 509

FT TRANSMEM 510 POTENTIAL.
 FT DOMAIN 519 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 538 POTENTIAL.
 FT DOMAIN 539 POTENTIAL.
 FT TRANSMEM 547 PERIPLASMIC (POTENTIAL).
 FT DOMAIN 548 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 553 POTENTIAL.
 FT DOMAIN 561 POTENTIAL.
 FT TRANSMEM 562 POTENTIAL.
 FT TRANSMEM 569 POTENTIAL.
 FT TRANSMEM 578 POTENTIAL.
 FT TRANSMEM 600 POTENTIAL.
 FT TRANSMEM 608 POTENTIAL.
 FT TRANSMEM 609 POTENTIAL.
 FT TRANSMEM 649 POTENTIAL.
 FT TRANSMEM 650 POTENTIAL.
 FT TRANSMEM 658 POTENTIAL.
 FT TRANSMEM 674 POTENTIAL.
 FT TRANSMEM 675 POTENTIAL.
 FT TRANSMEM 683 POTENTIAL.
 FT TRANSMEM 684 POTENTIAL.
 FT TRANSMEM 696 POTENTIAL.
 FT TRANSMEM 704 POTENTIAL.
 FT TRANSMEM 705 POTENTIAL.
 FT TRANSMEM 706 POTENTIAL.
 FT TRANSMEM 707 POTENTIAL.
 FT TRANSMEM 715 POTENTIAL.
 FT TRANSMEM 716 POTENTIAL.
 FT TRANSMEM 727 POTENTIAL.
 FT TRANSMEM 735 POTENTIAL.
 SQ SEQUENCE 735 AA; 81055 MW; 3C37073E4538DC3C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 735;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDYSWL 6
 |||||
 Db 399 LDYKWL 404

RESULT 12
 GUNB CALSA
 ID GUNB CALSA STANDARD; PRT; 1039 AA.
 AC P10474;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase/exoglucanase B precursor (Inclucides: Endoglucanase
 (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 (Cellulohydrolase); Exoglucanase (EC 3.2.1.91) (Exocellulohydrolase)
 (1,4-beta-cellobiohydrolase)).
 DE (1,4-beta-cellobiohydrolase)).
 GN CBLB.
 OS Caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus).
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosiruptor.
 OX NCBI_TaxID=44001;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89098399; PubMed=2789517;
 RA Saul D.J., Williams L.C., Love D.R., Chamley I.W., Bergquist P.I.;
 RT "Nucleotide sequence of a gene from Caldocellum saccharolyticum
 encoding for exocellulase and endocellulase activity."
 RL Nucleic Acids Res. 17:439-439 (1989).
 CC -1- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL
 CC DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS
 CC AN ENDOGLUCANASE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 CC in cellulose and cellotetraose, releasing cellobiose from the non-
 CC reducing ends of the chains.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULOSE FAMILY
 CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULOSE FAMILY
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).
 CC
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CC EMBL; X13602; CAA31936.1; --
 DR PIR; S02711; S02711.
 DR HSSP; Q06851; INBC.
 DR InterPro; IPR001956; CBD_3.
 DR InterPro; IPR001000; Glyco_hydro_10.
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR Pfam; PF00942; CBM_3; 1.
 DR Pfam; PF00150; cellulase; 1.
 DR PRINTS; PR00134; Glyco_hydro_10; 1.
 DR ProDom; PD001947; CBD_3; 1.
 DR SMART; SM00633; Glyco_10; 1.
 DR PROSITE; PS00591; GLYCOSYL_HYDROL_F5; 1.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Repeat;
 KW Multifunctional enzyme; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 1039 ENDOGLUCANASE/EXOGLUCANASE B.
 FT DOMAIN 376 416 THR/PRO-RICH, TANDEM REPEATS OF T-P.
 FT DOMAIN 417 570 CELLULOSE-BINDING (BY SIMILARITY).
 FT DOMAIN 571 618 THR/PRO-RICH, TANDEM REPEATS OF T-P.
 FT ACT_SITE 177 177 PROTON DONOR (POTENTIAL).
 FT ACT_SITE 285 285 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 792 792 BY SIMILARITY.
 SQ SEQUENCE 1039 AA; 117641 MW; 0E0378171594DDAE CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1039;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
 |||||
 Db 339 DYSWL 343

RESULT 13
 YE15 HAEIN
 ID YE15 HAEIN STANDARD; PRT; 200 AA.
 AC P44187;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein H11415.
 GN H11415.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512 (1995).
 CC -1- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.
 CC
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CC EMBL; U32821; AAC23066.1; --
DR PIR; H64028; H64028.
DR HSP; P23951; 2BAA.
DR TIGR; H1415; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 200 AA; 22895 MW; 42199FDDA4859FBB CRC64;

Query Match 86.1%; Score 31; DB 1; Length 200;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6

Db 61 LNYISWL 66

RESULT 14

ID UL78 HCMVA STANDARD; PRT; 431 AA.
AC P16751;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein UL78.
GN UL78.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90289039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A. III, Kouzarides T., Martignetti J.A.,
RA Reddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169";
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17403; CAA35351.1; --
DR PIR; S09841; S09841.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; UNKNOWN_1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 111 131 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 279 299 POTENTIAL.
FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 431 AA; 47357 MW; 34668FE7F908C857 CRC64;

Query Match 86.1%; Score 31; DB 1; Length 431;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDYSWL 6

Db 180 LDYRWL 185

RESULT 15

ID IKKA HUMAN STANDARD; PRT; 745 AA.
AC O15111; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK- α) (IKK- α) (IkappaB kinase)
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1A).
GN CHUK OR IKK- α .
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=97386461; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkappaB kinase";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
RT factor NF-kappaB";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RX TISSUE=Cervical carcinoma;
RA MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Heart;
RA MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.
RX TISSUE=Cervical carcinoma;
RA MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain";
RL Cell. Mol. Biol. Res. 41:537-549(1995).
RN [6]
RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
RP AND SER-180.
RX MEDLINE=98188283; PubMed=9520446;
RA Ling L., Cao Z., Goeddel D.V.;
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
RT Ser-176";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
RN [7]
RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE=99413720; PubMed=10485710;
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,
RA Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt
RT serine-threonine kinase";

RL Nature 401:82-85(1999).
RN [8]
RP IKK- α -IKK β BINDING.
RX MEDLINE=99038238; Pubmed=9819420;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
RT IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [9]
RP IKK PHOSPHORYLATION
RX MEDLINE=99038238; Pubmed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [10]
RP REVIEW.
RX MEDLINE=20178139; Pubmed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
RN [11]
RP SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKK α AND IKK β .
RX MEDLINE=21968797; Pubmed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -/- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -/- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC when dephosphorylated.
CC -/- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-p65-P50
CC complex. A weak interaction with TRAF3 cannot be excluded. Part of
CC a complex composed of NCOA2, NCOA3, IKK α , IKK β and CREBBP.
CC -/- SUBCELLULAR LOCATION: Cytoplasmic.
CC -/- TISSUE SPECIFICITY: Widely expressed.
CC -/- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; AF012890; AAC51662.1; -
DR EMBL; AF009225; AAC51671.1; -
DR EMBL; AF080157; AAC08996.1; -
DR EMBL; U22512; AAC50713.1; -
DR HSP; Q63450; 1A06.
DR Genew; HGNC:1974; CHUK.
DR MTM; 600664; -
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0008384; F:IkappaB kinase activity; TAS.
DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; I.

DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC_1
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 302 PROTEIN KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 738 743 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
FT MUTAGEN 176 176 K->M: LOSS OF AUTOPHOSPHORYLATION.
FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
FT ACTIVITY.
FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
FT CONFLICT 543 543 E -> G (IN REF. 2).
FT CONFLICT 604 604 L -> R (IN REF. 5).
FT CONFLICT 679 680 TS -> AY (IN REF. 5).
FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
FT CONFLICT 686 687 TS -> DL (IN REF. 5).
SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
Query Match 86.1%; Score 31; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDYSWL 6
||:|
Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:28:10

Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-12
Perfect score: 36
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.76:
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.4	282	2 B70555	probable omt prote
2	33	91.7	404	2 JC5784	adrenomedullin rec
3	32	88.9	122	2 S52840	haloalkanoic acid
4	32	88.9	153	2 F90704	hypothetical prote
5	32	88.9	153	2 A85555	hypothetical prote
6	32	88.9	168	2 A83390	probable sigma-70
7	32	88.9	195	2 T29815	hypothetical prote
8	32	88.9	229	2 B38452	2-haloacid dehalog
9	32	88.9	251	2 B84016	hypothetical prote
10	32	88.9	259	2 AG0696	probable type III
11	32	88.9	302	2 C90869	probable transcrip
12	32	88.9	302	2 F85749	probable transcrip
13	32	88.9	302	2 F64883	probable transcrip
14	32	88.9	349	2 T15422	hypothetical prote
15	32	88.9	379	2 AH0542	conserved hypotet
16	32	88.9	386	2 H71511	probable 2-compone
17	32	88.9	391	2 A70663	probable PPE prote
18	32	88.9	414	2 T44513	hypothetical prote
19	32	88.9	440	2 T32190	hypothetical prote
20	32	88.9	524	2 S33419	glycoprotein G - r
21	32	88.9	684	2 S41788	endo-1,4-beta-xyla
22	32	88.9	694	2 A95251	antigen, cell wall
23	32	88.9	694	2 F98115	conserved hypotet
24	32	88.9	700	2 T30910	xylanase (EC 3.2.1
25	32	88.9	705	2 T34531	hypothetical prote
26	32	88.9	735	2 S57486	ferrichrysoabactin
27	32	88.9	872	2 B75073	ATP-dependent RNA
28	32	88.9	915	2 A43802	cellulase (EC 3.2.
29	32	88.9	1039	2 S02711	cellulase (EC 3.2.

30	32	88.9	1209	2 T16663	hypothetical prote
31	32	88.9	1232	2 D64413	cobalamin biosynth
32	32	88.9	1319	2 S75705	hypothetical prote
33	32	88.9	1779	2 T31085	xylanase - Caldice
34	31	86.1	200	2 H64028	hypothetical prote
35	31	86.1	234	2 AF3543	phosphoglycolate p
36	31	86.1	262	2 T20203	hypothetical prote
37	31	86.1	431	2 S09841	hypothetical prote
38	31	86.1	618	2 D71055	probable indolepyr
39	31	86.1	745	1 I49101	conserved helix-lo
40	31	86.1	837	2 H82970	hypothetical prote
41	31	86.1	1010	2 D72203	hypothetical prote
42	30	83.3	61	2 D82732	hypothetical prote
43	30	83.3	144	2 AI0698	probable pathogeni
44	30	83.3	154	2 F90195	conserved hypotet
45	30	83.3	225	2 S39672	ywbB protein - Bac

ALIGNMENTS

RESULT 1

B70555
probable omt protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70555
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Scares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70555
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-282 <COL>
A;Cross-references: GB:295584; GB:AL123456; NID:g3261774; PIDN:CAB09012.1; PID:e317129;
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: omt

Query Match 94.4%; Score 34; DB 2; Length 282;
Best Local Similarity 83.3%; Pred.No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||||
DB 142 LDYSWM 147

RESULT 2

JC5784
adrenomedullin receptor - human
C;Species: Homo sapiens (man)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: JC5784
R;Haenze, J.; Dittlich, K.; Doetsch, J.; Raecher, W.
Biochem. Biophys. Res. Commun. 240, 183-188, 1997
A;Title: Molecular cloning of a novel human receptor
A;Reference number: JC5784; MUID:98042541; PMID:9367907
A;Accession: JC5784
A;Molecule type: mRNA
A;Residues: 1-404 <HAE>
A;Cross-references: GB:Y13583; NID:g2652933; PIDN:CAA73910.1; PID:g2652934
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; receptor; transmembrane protein
F;58-79/Domain: transmembrane #status predicted <TM1>
F;91-113/Domain: transmembrane #status predicted <TM2>
F;128-149/Domain: transmembrane #status predicted <TM3>
F;171-193/Domain: transmembrane #status predicted <TM4>
F;218-239/Domain: transmembrane #status predicted <TM5>

F:260-280/Domain: transmembrane #status predicted <TW6>
 F:301-320/Domain: transmembrane #status predicted <TW7>
 F:28,37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.7%; Score 33; DB 2; Length 404;
 Best Local Similarity 83.3%; Pred. No. 82;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 115 LDYTWL 120

RESULT 3

S52840

haloalkanoic acid dehalogenase - Xanthobacter autotrophicus (fragment)

C:Species: Xanthobacter autotrophicus

C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jan-2000

C:Accession: S52840

R:van der Ploeg, J.; Janssen, D.B.

submitted to the EMBL Data Library, April 1995

A:Description: Sequence analysis of the upstream region of dh1B, the gene encoding haloal

A:Reference number: S52838

A:Accession: S52840

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-122 <VAN>

A:Cross-references: EMBL:X86084; NID:g763396; PIDN:CAA60039.1; PID:g763399

C:Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase

Query Match 88.9%; Score 32; DB 2; Length 122;
 Best Local Similarity 83.3%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
 |||||
 Db 43 LEYSWL 48

RESULT 4

F90704

hypothetical protein ECs0606 [imported] - Escherichia coli (strain O157:H7, substrain RI

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: F90704

R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F90704

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-153 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA034029.1; PID:g13360064; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:
 A:Gene: ECs0606

Query Match 88.9%; Score 32; DB 2; Length 153;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 5
 |||||
 Db 83 LDYSWL 87

RESULT 5

A85555

hypothetical protein 20706 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A85555
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85555
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-153 <STO>
 A:Cross-references: GB:AEQ05174; NID:g12513450; PIDN:AAGS4901.1; GSPDB:GN00145; UWGP:20.
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 20706

Query Match 88.9%; Score 32; DB 2; Length 153;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 5
 |||||
 Db 83 LDYSWL 87

RESULT 6

A83390

probable sigma-70 factor, ECF subfamily PA2050 [imported] - Pseudomonas aeruginosa (str

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83390

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: A83390

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-168 <STO>

A:Cross-references: GB:AE004631; GB:AE004091; NID:g9948050; PIDN:AAG05438.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2050

Query Match 88.9%; Score 32; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSSL 6
 |||||
 Db 18 DYSSL 22

RESULT 7

T29815

hypothetical protein C46A5.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29815

R:Johnson, D.; Stellyes, L.

submitted to the EMBL Data Library, June 1996

A:Description: The sequence of C. elegans cosmid C46A5.

A:Reference number: Z20690

A:Accession: T29815

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-195 <JOH>

A:Cross-references: EMBL:U61948; PIDN:AAB03148.1; GSPDB:GN00022; CESP:C46A5.8

A:Experimental source: strain Bristol N2; clone C46A5

C:Genetics:

A:Gene: CESP:C46A5.8

A:Map position: 4

A; Introns: 93/3; 122/3

Query Match 88.9%; Score 32; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DY5WL 6
| | | | |
Db 74 DY5WL 78

RESULT 8

B38452
2-haloacid dehalogenase (EC 3.8.1.2) II; Pseudomonas sp.

C; Species: Pseudomonas sp.
C; Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 24-Nov-1999

C; Accession: B38452

R; Schneider, B.; Mueller, R.; Frank, R.; Lingens, F.

J. Bacteriol. 173, 1530-1535, 1991

A; Title: Complete nucleotide sequences and comparison of the structural genes of two 2-haloacid dehalogenases from *Pseudomonas* sp.

A; Reference number: A38452; MUID: 91139597; PMID: 1995594

A; Accession: B38452

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-229; <SCH>

A; Cross-references: GB:M62909; GB:M37619; NID: g151249; PIDN: AAA25833.1; PID: g151250

C; Superfamily: Alkaligenes eutrophus phosphoglycolate phosphatase

C; Keywords: hydrolase

Query Match 88.9%; Score 32; DB 2; Length 229;

Best Local Similarity 83.3%; Pred. No. 70;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY5WL 6
| | | | |
Db 45 LEY5WL 50

RESULT 9

B84016
hypothetical protein BH2930 [imported] - Bacillus halodurans (strain C-125)

C; Species: Bacillus halodurans

C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C; Accession: B84016

R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and its relationship to other members of the family Halobacteriaceae

A; Reference number: A83650; MUID: 20512582; PMID: 11058132

A; Accession: B84016

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-251; <STO>

A; Cross-references: GB:AP001517; GB:BA000004; NID: g10175500; PIDN: BAB06649.1; GSPDB: GN000145; UMGP: ZP222222.1

A; Experimental source: strain C-125

C; Genetics:

A; Gene: BH2930

Query Match 88.9%; Score 32; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY5WL 5
| | | | |
Db 153 LDY5WL 157

RESULT 10

AG0696

probable type III secretion protein ssat [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C; Species: Salmonella enterica subsp. enterica serovar Typhi

A; Note: this species has also been called Salmonella typhi

C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C; Accession: AG0696

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium

A; Reference number: AB0502; MUID: 21534947; PMID: 11677608

A; Accession: AG0696

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-259; <PAR>

A; Cross-references: GB:AL513382; PIDN: CAD01944.1; PID: g16502786; GSPDB: GN00176

C; Genetics:

A; Gene: ssat

Query Match 88.9%; Score 32; DB 2; Length 259;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DY5WL 6
| | | | |
Db 67 DY5WL 71

RESULT 11

C90869

probable transcription regulator LYSR-type [imported] - Escherichia coli (strain O157:H7)

C; Species: Escherichia coli

C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001

C; Accession: C90869

R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasaara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genotyping of enterohemorrhagic Escherichia coli O157:H7

A; Reference number: A99629; MUID: 21156231; PMID: 11258796

A; Accession: C90869

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-302; <HAY>

A; Cross-references: GB:BA000007; PIDN: BAB35346.1; PID: g13361388; GSPDB: GN00154

A; Experimental source: strain O157:H7, substrain RMD 0509952

C; Genetics:

A; Gene: ECs1923

C; Superfamily: regulatory protein ilvY

Query Match 88.9%; Score 32; DB 2; Length 302;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDY5WL 5
| | | | |
Db 191 LDY5WL 195

RESULT 12

F85749

probable transcription regulator LYSR-type ydaK [imported] - Escherichia coli (strain O157:H7)

C; Species: Escherichia coli

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C; Accession: F85749

R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.;

Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.C.

Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID: 21074935; PMID: 11206551

A; Accession: F85749

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-302; <STO>

A; Cross-references: GB:AE005174; NID: g12515416; PIDN: AAG56458.1; GSPDB: GN00145; UMGP: ZP222222.1

A; Experimental source: strain O157:H7, substrain EDL933

C; Genetics:

A; Gene: ydaK

C;Superfamily: regulatory protein ilvY

Query Match 88.9%; Score 32; DB 2; Length 302;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5

|||||

Db 191 LDYSW 195

RESULT 13

F64883

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C;Accession: F64883

A;: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: F64883

A;Status: preliminary;

A;Molecule type: DNA

A;Residues: 1-302 <BLAT>

A;Cross-references: GB:AE000232; GB:U00096; NID:gl787600; PIDN:AACT4421.1; PID:gl787601;

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: ydaK

C;Superfamily: regulatory protein ilvY

C;Keywords: DNA binding; transcription regulation

F;21-51/Region: regulatory protein lysR motif

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 302;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5

|||||

Db 191 LDYSW 195

RESULT 14

T15422

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000

C;Accession: T15422

R;Leinbach, D.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid C06A8.

A;Reference number: Z18348

A;Accession: T15422

A;Status: preliminary;

A;Molecule type: DNA

A;Residues: 1-349 <LEI>

A;Cross-references: EMBL:U39849; NID:gl055041; PID:gl055044; PIDN:AAA81047.1; CESP:C06A8

C;Genetics:

A;Gene: CESP:C06A8.6

A;Introns: 29/3; 202/3; 263/3; 316/3

C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 349;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6

|||||

Db 49 DYSWL 53

RESULT 15

AH0542

conserved hypothetical protein STY0359 [imported] - Salmonella enterica subsp. enterica

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AH0542

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AH0542

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-379 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD08784.1; PID:gi6501600; GSPDB:GN00176

C;Genetics:

A;Gene: STY0359

C;Superfamily: Streptomyces coelicolor hypothetical protein SCE15.16c

Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 379;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6

|||||

Db 275 DYSWL 279

Search completed: February 18, 2004, 14:38:48

Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-12
Perfect score: 36
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfileai.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	91.7	404	1	US-08-696-770-2
2	33	91.7	404	2	US-09-015-557-2
3	32	88.9	217	4	US-09-107-532A-4133
4	32	88.9	228	4	US-09-252-391A-24998
5	32	88.9	230	2	US-08-637-759B-457
6	32	88.9	230	3	US-08-871-355A-457
7	32	88.9	230	4	US-09-201-945-457
8	32	88.9	351	3	US-08-591-685-7
9	32	88.9	375	3	US-08-591-685-11
10	32	88.9	404	2	US-08-282-197C-62
11	32	88.9	438	2	US-08-282-197C-59
12	32	88.9	1426	3	US-09-136-574A-43
13	31	86.1	745	2	US-08-887-518-3
14	31	86.1	745	2	US-09-023-321-3
15	31	86.1	745	2	US-08-890-851-4
16	31	86.1	745	2	US-09-032-475-3
17	31	86.1	745	2	US-09-099-125A-4
18	31	86.1	745	2	US-09-099-124A-4
19	31	86.1	745	3	US-09-032-476-4
20	31	86.1	745	3	US-08-890-854-4
21	31	86.1	745	3	US-09-023-324-4
22	31	86.1	745	3	US-09-168-629-2
23	31	86.1	745	3	US-08-910-820-10
24	31	86.1	745	3	US-08-810-131A-2
25	31	86.1	745	4	US-09-109-986-4
26	31	86.1	745	4	US-09-844-908-10
27	31	86.1	745	4	US-09-868-758-3

28	31	86.1	756	2	US-08-887-518-4	Sequence 4, Appl1
29	31	86.1	756	2	US-09-023-321-4	Sequence 4, Appl1
30	31	86.1	756	2	US-08-890-853-2	Sequence 2, Appl1
31	31	86.1	756	2	US-09-032-475-4	Sequence 4, Appl1
32	31	86.1	756	2	US-09-099-125A-2	Sequence 2, Appl1
33	31	86.1	756	2	US-09-099-124A-2	Sequence 2, Appl1
34	31	86.1	756	3	US-09-032-476-2	Sequence 2, Appl1
35	31	86.1	756	3	US-08-890-854-2	Sequence 2, Appl1
36	31	86.1	756	3	US-09-023-324-2	Sequence 2, Appl1
37	31	86.1	756	3	US-09-168-629-15	Sequence 15, Appl1
38	31	86.1	756	3	US-08-910-820-9	Sequence 9, Appl1
39	31	86.1	756	4	US-09-109-986-2	Sequence 9, Appl1
40	31	86.1	756	4	US-09-844-908-9	Sequence 9, Appl1
41	31	86.1	756	4	US-09-868-758-4	Sequence 4, Appl1
42	31	86.1	996	4	US-09-417-197-123	Sequence 123, App
43	31	86.1	997	4	US-09-417-197-121	Sequence 121, App
44	31	86.1	1709	4	US-09-392-812A-6	Sequence 6, Appl1
45	30	83.3	112	4	US-09-328-352-7614	Sequence 7614, Ap

ALIGNMENTS

RESULT 1
US-08-696-770-2
; Sequence 2, Application US/08696770
; Patent No. 5763218
; GENERAL INFORMATION:
; APPLICANT: Fujii, Ryo
; APPLICANT: Hinuma, Shuji
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAKS0001-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

US-08-696-770-2

Query Match 91.7%; Score 33; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||:|
Db 115 LDYTWL 120

RESULT 2

US-09-015-557-2
; Sequence 2, Application US/09015557
; Patent No. 5932702
; GENERAL INFORMATION:
; APPLICANT: Fujii, Ryo
; APPLICANT: Hiruma, Shuji
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,557
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/696,770
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAK50001-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

US-09-015-557-2

Query Match 91.7%; Score 33; DB 2; Length 404;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
|||:|
Db 115 LDYTWL 120

RESULT 3

US-09-107-532A-4133

; Sequence 4133, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4133:

SEQUENCE CHARACTERISTICS:

LENGTH: 217 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...217

SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

US-09-107-532A-4133

Query Match 88.9%; Score 32; DB 4; Length 217;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5

|||:|

Db 89 LDYSW 93

RESULT 4

US-09-252-991A-24998
; Sequence 24998, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 24998
;; LENGTH: 228
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24998

Query Match 88.9%; Score 32; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
|||
Db 78 DYSWL 82

RESULT 5
US-08-637-759B-457
; Sequence 457, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-457

Query Match 88.9%; Score 32; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
|||
Db 67 DYSWL 71

RESULT 6

US-08-871-355A-457
; Sequence 457, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-457

Query Match 88.9%; Score 32; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6
|||
Db 67 DYSWL 71

RESULT 7
US-09-201-945-457
; Sequence 457, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-457

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```

Query Match      88.9%; Score 32; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      2 DYSWL 6
        |||||
DB      67 DYSWL 71

```

```

RESULT 8
US-08-591-685-7
; Sequence 7, Application US/08591685
; Patent No. 6083733
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Thermostable xylanases
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,685
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-685-7

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Query Match      88.9%; Score 32; DB 3; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      2 DYSWL 6
        |||||
DB      317 DYSWL 321

```

```

RESULT 9
US-08-591-685-11
; Sequence 11, Application US/08591685

```

```

; Patent No. 6083733
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Thermostable xylanases
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,685
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-685-11

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Query Match      88.9%; Score 32; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 DYSWL 6
        |||||
DB      328 DYSWL 332

```

```

RESULT 10
US-08-282-197C-62
; Sequence 62, Application US/08282197C
; Patent No. 5871730
; GENERAL INFORMATION:
; APPLICANT: Brzezinski, Ryszard
; APPLICANT: Dery, Claude V
; APPLICANT: Beaulieu, Carole
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,197C
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0410000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-282-197C-62

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```

Query Match      88.9%; Score 32; DB 2; Length 404;

```

Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 2 DYSWL 6
Db 328 DYSWL 332

RESULT 11
US-08-282-197C-59
; Sequence 59, Application US/08282197C
; Patent No. 5871730
; GENERAL INFORMATION:
; APPLICANT: Brzezinski, Ryszard
; APPLICANT: Dery, Claude V
; APPLICANT: Beaulieu, Carole
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCE ADDRESSES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,197C
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0410000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-282-197C-59

Query Match 88.9%; Score 32; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 2 DYSWL 6
Db 339 DYSWL 343

RESULT 12
US-09-136-574A-43
; Sequence 43, Application US/09136574A
; Patent No. 6294366
; GENERAL INFORMATION:
; APPLICANT: Farrington, Graham K.
; APPLICANT: Anderson, Paige
; APPLICANT: Gibbs, Moreland
; APPLICANT: Bergquist, Peter
; APPLICANT: Daniels, Roy
; APPLICANT: Morgan, Hugh W.
; APPLICANT: Williams, Diane P.
; TITLE OF INVENTION: Compositions and Methods for
; Treating Cellulose Containing Fabrics Using Truncated
; Cellulase Enzyme Compositions

NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSES: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 8294366e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-136-574A-43

Query Match 88.9%; Score 32; DB 3; Length 1426;
Best Local Similarity 100.0%; Pred. No. 9.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 2 DYSWL 6
Db 339 DYSWL 343

RESULT 13
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||:||||
Db 738 LDWSWL 743

RESULT 14
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||:||||

Db 738 LDWSWL 743
RESULT 15
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
||:||||
Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:49
Job time : 7.06579 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-11
Perfect score: 35
Sequence: 1 LDFSML 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/1/iaa/PCUS COMB.pcp.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	91.4	452	4	US-09-252-991A-31360 Sequence 31360, A
2	31	88.6	21	1	US-08-798-897-13 Sequence 13, Appl
3	31	88.6	21	2	US-08-978-523-13 Sequence 13, Appl
4	31	88.6	23	2	US-08-337-646A-23 Sequence 23, Appl
5	31	88.6	23	2	US-08-927-326-23 Sequence 23, Appl
6	31	88.6	25	2	US-08-337-646A-29 Sequence 29, Appl
7	31	88.6	25	3	US-08-927-326-29 Sequence 29, Appl
8	31	88.6	154	1	US-08-077-848A-3 Sequence 3, Appl
9	31	88.6	154	3	US-09-211-640-3 Sequence 3, Appl
10	31	88.6	154	3	US-09-378-536-3 Sequence 3, Appl
11	31	88.6	154	4	US-09-687-260-3 Sequence 3, Appl
12	31	88.6	229	2	US-08-408-095-19 Sequence 19, Appl
13	31	88.6	232	2	US-08-408-095-17 Sequence 17, Appl
14	31	88.6	232	1	US-08-408-095-18 Sequence 18, Appl
15	31	88.6	236	1	US-08-112-208C-11 Sequence 11, Appl
16	31	88.6	236	1	US-08-248-819A-11 Sequence 11, Appl
17	31	88.6	236	1	US-08-607-269-21 Sequence 21, Appl
18	31	88.6	236	1	US-08-607-269-22 Sequence 22, Appl
19	31	88.6	236	2	US-08-337-646A-11 Sequence 11, Appl
20	31	88.6	236	2	US-08-856-531-11 Sequence 11, Appl
21	31	88.6	236	2	US-08-856-034-11 Sequence 11, Appl
22	31	88.6	236	3	US-09-127-048-9 Sequence 9, Appl
23	31	88.6	236	3	US-08-927-326-11 Sequence 11, Appl
24	31	88.6	236	4	US-09-379-820A-11 Sequence 11, Appl
25	31	88.6	236	5	PCT-US95-04600-21 Sequence 21, Appl
26	31	88.6	236	5	PCT-US95-04600-22 Sequence 22, Appl
27	31	88.6	239	1	US-08-333-565-51 Sequence 51, Appl

28	31	88.6	239	1	US-08-112-208C-10 Sequence 10, Appl
29	31	88.6	239	1	US-08-248-819A-10 Sequence 10, Appl
30	31	88.6	239	1	US-08-248-819A-12 Sequence 12, Appl
31	31	88.6	239	1	US-08-607-269-20 Sequence 20, Appl
32	31	88.6	239	1	US-08-471-058-12 Sequence 12, Appl
33	31	88.6	239	1	US-08-405-702A-12 Sequence 12, Appl
34	31	88.6	239	1	US-08-690-095-4 Sequence 4, Appl
35	31	88.6	239	2	US-08-465-485A-21 Sequence 21, Appl
36	31	88.6	239	2	US-08-661-479-51 Sequence 51, Appl
37	31	88.6	239	2	US-08-365-486A-15 Sequence 15, Appl
38	31	88.6	239	2	US-08-365-486A-17 Sequence 17, Appl
39	31	88.6	239	2	US-08-337-646A-10 Sequence 10, Appl
40	31	88.6	239	2	US-08-337-646A-12 Sequence 12, Appl
41	31	88.6	239	2	US-08-408-095-16 Sequence 16, Appl
42	31	88.6	239	2	US-08-856-531-10 Sequence 10, Appl
43	31	88.6	239	2	US-08-856-034-10 Sequence 10, Appl
44	31	88.6	239	3	US-08-471-057-12 Sequence 12, Appl
45	31	88.6	239	3	US-09-113-789-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-252-991A-31360
; Sequence 31360, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31360
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31360

Query Match 91.4%; Score 32; DB 4; Length 452;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSML 6
Db 410 LDFAWL 415

RESULT 2
US-08-798-897-13
; Sequence 13, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-798-897-13

Query Match      88.6%; Score 31; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
DB      7 DFSWL 11

RESULT 3
US-08-978-523-13
; Sequence 13, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; US-08-978-523-13

Query Match      88.6%; Score 31; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
DB      7 DFSWL 11

RESULT 3
US-08-978-523-13
; Sequence 13, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; US-08-978-523-13

Query Match      88.6%; Score 31; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
DB      7 DFSWL 11

RESULT 4
US-08-337-646A-23
; Sequence 23, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-337-646A-23

Query Match      88.6%; Score 31; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
DB      16 DFSWL 20

RESULT 5
US-08-927-326-23
; Sequence 23, Application US/08927326
; Patent No. 6184202
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
```

;; TITLE OF INVENTION: CELL DEATH REGULATORS
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Khourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,326
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/337,646
;; FILING DATE: 10-NOV-1994
;; APPLICATION NUMBER: US 08/248,819
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/112,208
;; FILING DATE: 26-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 15726A-000620
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-927-326-23

Query Match 88.6%; Score 31; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
DB 16 DFSWL 20

RESULT 6
US-08-337-646A-29
;; Sequence 29, Application US/08337646A
;; Patent No. 5856171
;; GENERAL INFORMATION:
;; APPLICANT: KORSMEYER, Stanley J.
;; TITLE OF INVENTION: CELL DEATH REGULATORS
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Khourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/337,646A

;; FILING DATE: 10-NOV-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/248,819
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/112,208
;; FILING DATE: 26-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 15726A-000620
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 25 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-337-646A-29

Query Match 88.6%; Score 31; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
DB 16 DFSWL 20

RESULT 7
US-08-927-326-29
;; Sequence 29, Application US/08927326
;; Patent No. 6184202
;; GENERAL INFORMATION:
;; APPLICANT: KORSMEYER, Stanley J.
;; TITLE OF INVENTION: CELL DEATH REGULATORS
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Khourie and Crew
;; STREET: 379 Lytton Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: US
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,326
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/337,646
;; FILING DATE: 10-NOV-1994
;; APPLICATION NUMBER: US 08/248,819
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/112,208
;; FILING DATE: 26-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 15726A-000620
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-326-29

Query Match 88.6%; Score 31; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
|||||
Db 16 DFSWL 20

RESULT 8

US-08-077-848A-3
Sequence 3, Application US/08077848A
Patent No. 5470955
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848A
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154

Query Match 88.6%; Score 31; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
|||||
Db 126 DFSWL 130

RESULT 9

US-09-211-640-3
Sequence 3, Application US/09211640
Patent No. 6020466
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,640
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,375
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154

Query Match 88.6%; Score 31; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
|||||
Db 126 DFSWL 130

RESULT 10

US-09-378-536-3
Sequence 3, Application US/09378536
Patent No. 620763
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,536
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154
US-09-378-536-3

Query Match 88.6%; Score 31; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 126 DFSWL 130

RESULT 11
US-09-687-260-3
Sequence 3, Application US/09687260
Patent No. 6528263
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/687,260
FILING DATE: 12-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,536
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
FEATURE:
NAME/KEY: Protein
LOCATION: 1..154
US-09-687-260-3

Query Match 88.6%; Score 31; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 126 DFSWL 130

RESULT 12
US-08-408-095-19
Sequence 19, Application US/08408095
Patent No. 5858678
GENERAL INFORMATION:
APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: protein
MOLECULE TYPE: protein
US-08-408-095-19

Query Match 88.6%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6
Db 126 DFSWL 130

```
Db      201 DFSWL 205

RESULT 13
US-08-408-095-17
; Sequence 17, Application US/08408095
; Patent No. 5858678
; GENERAL INFORMATION:
; APPLICANT: Chinnadurai, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-408-095-17

Query Match      88.6%; Score 31; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
Db      204 DFSWL 208

RESULT 14
US-08-095-18
; Sequence 18, Application US/08408095
; Patent No. 5858678
; GENERAL INFORMATION:
; APPLICANT: Chinnadurai, Govindaswamy
; TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-408-095-18

Query Match      88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
Db      208 DFSWL 212

RESULT 15
US-08-112-208C-11
; Sequence 11, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-112-208C-11

Query Match      88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
Db      208 DFSWL 212

RESULT 15
US-08-112-208C-11
; Sequence 11, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-112-208C-11

Query Match      88.6%; Score 31; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DFSWL 6
Db      208 DFSWL 212
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Search completed: February 18, 2004, 14:41:49
Job time : 8.06579 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	90.9	290	BLAL_XANMA	P52700 xanthomonas
2	30	90.9	648	1 Y084 HUMAN	Q14699 homo sapien
3	30	90.9	918	1 CAPP CORGL	P12880 corynebacte
4	30	90.9	919	1 CAPP CORCT	Q93mh3 corynebacte
5	29	87.9	177	1 CYCI_PARDE	P29899 paracoccus
6	29	87.9	245	1 HIS1_SHEON	Q8etb5 shewanella
7	29	87.9	277	1 THTI_CAEEL	P91247 caenorhabdi
8	29	87.9	286	1 YDBC ECOLI	P25906 escherichia
9	29	87.9	289	1 THTR CHICK	P25324 gallus gall
10	29	87.9	295	1 THTR RAT	P24329 rattus norv
11	29	87.9	296	1 RECO_ANASP	Q8vpl9 anabaena sp
12	29	87.9	296	1 THTM_HUMAN	P25325 homo sapien
13	29	87.9	296	1 THTR RAT	P97532 rattus norv
14	29	87.9	296	1 THTR BOVIN	P00586 bos taurus
15	29	87.9	296	1 THTR CRIGR	P46635 cricetus
16	29	87.9	296	1 THTR HUMAN	Q16762 homo sapien
17	29	87.9	296	1 THTR MOUSE	P52196 mus musculu
18	29	87.9	359	1 RFPG_SALTY	P26397 salmonella
19	29	87.9	360	1 WNT2_CAEEL	P26397 salmonella
20	29	87.9	424	1 Y826 METTH	O26914 methanobact
21	29	87.9	430	1 PUCK_BACSU	Q32140 bacillus su
22	29	87.9	459	1 NU4M_MOUSE	P03911 mus musculu
23	29	87.9	454	1 VT13_CAEEL	Q10917 caenorhabdi
24	29	87.9	477	1 RP54_ECOLI	P24455 escherichia
25	29	87.9	477	1 RP54_KLEPN	P06223 klebsiella
26	29	87.9	477	1 RP54_SALTY	P26979 salmonella
27	29	87.9	481	1 CBF5_EMENI	O43100 emericella
28	29	87.9	491	1 XYLE_ECOLI	P09098 escherichia
29	29	87.9	509	1 TDT_HUMAN	P04053 homo sapien
30	29	87.9	510	1 G6PD_ASPNG	P48826 aspergillus
31	29	87.9	511	1 G6PD_EMENI	P41764 emericella
32	29	87.9	514	1 DKC1_HUMAN	O60832 homo sapien
33	29	87.9	520	1 TDT_BOVIN	P06526 bos taurus

ALIGNMENTS

RESULT 1

ID	BLAL_XANMA	STANDARD;	PRT;	290 AA.
AC	P52700;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Metallo-beta-lactamase L1 precursor (Beta-lactamase, type II)			
DE	(EC 3.5.2.6) (Penicillinase).			
OS	Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC	Xanthomonadaceae; Stenotrophomonas.			
OX	NCBI_TaxID=40324;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=IID 1275;			
RX	MEDLINE=94289479; PubMed=8018721;			
RA	Walsh T.R., Hall L., Assinder S.J., Nichols W.W., Cartwright S.J.,			
RA	Macgowan A.P., Bennett P.M.;			
RT	"Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophilia."			
RT	maltophilia."			
RL	Biochim. Biophys. Acta 1218:199-201(1994).			
RN	[2]			
RP	SEQUENCE OF 34-65.			
RC	STRAIN=IID 1275;			
RX	MEDLINE=86025393; PubMed=3931629;			
RA	Bicknell R., Emanuel E.L., Gagnon J., Waley S.G.;			
RT	"The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275."			
RL	Biochem. J. 229:791-797(1985).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=99030465; PubMed=9811546;			
RA	Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S.,			
RA	Gambin S.J., Spencer J.;			
RT	"The crystal structure of the L1 metallo-beta-lactamase from Stenotrophomonas maltophilia at 1.7 A resolution."			
RL	J. Mol. Biol. 284:125-136(1998).			
CC	- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMPENEM. UNSTABLE BELOW PH			
CC	8, UNLESS ZINC IS PRESENT.			
CC	- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.			
CC	- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.			
CC	- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced			
CC	enzymatic activity in presence of Co(2+), Ni(2+), Cd(2+), and Mn(2+).			
CC	- SUBUNIT: Homotetramer.			
CC	- SUBCELLULAR LOCATION: Periplasmic (Potential).			
CC	- SIMILARITY: Belongs to the class-B beta-lactamase family.			
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Q9nr15 homo sapien
O52847 bacillus me
Q91mm4 nodamura vi
P27742 emericella
P00885 pseudomonas
Q8k9n1 buchnera ap
P10914 homo sapien
P74592 synchocyst
Q9np87 homo sapien
Q9muq6 mesostigma
P36195 gallus gall
O44081 drosophila

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DR EMBL; X75074; CAAS2968.1; -.
CC PIR; S45349; S45349.
DR PDB; 1SML; 20-SEP-99.
DR InterPro; IPR001018; Beta lactamase B.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase_B; 1
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
DR PROSITE; PS00744; BETA_LACTAMASE_B_2; FALSE NEG.
KW Hydrolase; Zinc; Antibiotic resistance; Periplasmic; Signal;
KW 3D-structure.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 33
FT CHAIN 34 290 METALLO-BETA-LACTAMASE L1.
FT DISULFID 239 267
FT METAL 105 105 ZINC 1.
FT METAL 107 107 ZINC 1.
FT METAL 109 109 ZINC 2.
FT METAL 181 181 ZINC 1.
FT METAL 205 205 ZINC 2.
FT METAL 217 217 ZINC 2.
FT CONFLICT 36 37 AS -> QR (IN REF. 2).
FT CONFLICT 40 40 Q -> A (IN REF. 2).
FT CONFLICT 56 58 TED -> ROH (IN REF. 2).
FT CONFLICT 63 63 L -> H (IN REF. 2).
FT HELIX 36 39
FT STRAND 41 41
FT STRAND 45 48
FT TURN 49 50
FT STRAND 51 53
FT STRAND 56 56
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 66
FT TURN 67 68
FT STRAND 69 73
FT STRAND 76 76
FT HELIX 78 80
FT HELIX 81 90
FT TURN 91 92
FT HELIX 95 97
FT STRAND 98 102
FT HELIX 108 111
FT TURN 112 113
FT HELIX 114 120
FT STRAND 124 127
FT TURN 137 139
FT STRAND 142 142
FT TURN 143 145
FT STRAND 146 146
FT TURN 147 147
FT STRAND 158 159
FT TURN 162 163
FT STRAND 165 168
FT TURN 169 170
FT STRAND 171 177
FT TURN 183 184
FT STRAND 186 194
FT TURN 195 196
FT STRAND 197 203
FT TURN 210 211
FT TURN 218 219
FT TURN 221 222
FT HELIX 223 235
FT TURN 236 236
FT STRAND 241 243
FT HELIX 247 250
FT TURN 251 251
FT HELIX 254 259
FT TURN 260 263
```

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FT HELIX 267 287
SQ SEQUENCE 290 AA; 30801 MW; 0B34CAB54518BC1E CRC64;

Query Match 90.9%; Score 30; DB 1; Length 290;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
   :|||||
Db 34 VDASWL 39

RESULT 2
Y084_HUMAN
ID Y084_HUMAN STANDARD; PRT; 648 AA.
AC Q14659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein KIAA0084 (HA2022) (Fragment).
GN KIAA0084
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Suzuki T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. III.
RT The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 2:37-43 (1995).
CC -----
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CC or send an email to license@isb-sib.ch).

-----
DR EMBL; D42043; BAA07644.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 648 AA; 70463 MW; 88F68A62D6C1CDA1 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 648;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
   :|||||
Db 384 LDANWL 389

RESULT 3
CAPP_CORGL
ID CAPP_CORGL STANDARD; PRT; 918 AA.
AC P12880;
DT 01-OCT-1989 (Rel. 12, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
GN PPC OR CGL1585.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]_
RP SEQUENCE FROM N.A.


```

```

RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=89384460; PubMed=2779518;
RA Birkmann B.J., Follett M.T., Griot M.U., Sinskey A.J.;
RT "The phosphoenolpyruvate carboxylase gene of Corynebacterium
RL glutamicum: molecular cloning, nucleotide sequence, and expression.";
RN Mol. Gen. Genet. 218:330-339(1989).
[2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=89326141; PubMed=2666264;
RA O'Regan M., Thierbach G., Bachmann B., Villevall D., Lepage P.,
RA Viret J.F., Lemoine Y.;
RT "Cloning and nucleotide sequence of the phosphoenolpyruvate
RL carboxylase-coding gene of Corynebacterium glutamicum ATCC13032.";
RN Gene 77:237-251(1989).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
CC the tricarboxylic acid cycle.
CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -!- ENZYME REGULATION: ACTIVITY NOT STIMULATED BY ACETYL-COA IN THE
CC ABSENCE OF ANY ALLOSTERIC INHIBITOR, WHILE THE CORRESPONDING
CC PROTEIN FROM E. COLI IS STRONGLY STIMULATED.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
CC
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CC
CC -----
CC EMBL; X14234; CAA32450.1; -.
CC EMBL; M25819; AAA83537.1; -.
CC EMBL; A09073; CAA00827.1; -.
CC EMBL; AP05279; BAB98978.1; -.
CC PIR; S05512; QYFKG.
CC HSP; P00864; IFYI.
CC HAMAP; MF_00595; -.
CC InterPro; IPR001449; PEPcase.
CC Pfam; PF00311; PEPcase; 1.
CC PRINTS; PR00150; PEPCARBXLASE.
CC PROSITE; PS00393; PEPcase; 2; 1.
CC PROSITE; PS00781; PEPcase; 1; 1.
CC Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
CC Complete proteome.
CC INIT MET 0
CC FT ACT_SITE 137 137 BY SIMILARITY.
CC FT ACT_SITE 578 578 BY SIMILARITY.
CC FT CONFLICT 606 607 KL -> NV (IN REF. 1).
CC FT CONFLICT 799 800 FT -> LP (IN REF. 1).
CC FT CONFLICT 914 914 L -> V (IN REF. 1).
CC SQ SEQUENCE 918 AA; 103066 MW; A56C2703169D0698 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 918;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 104 LDATWL 109
|||||
RESULT 4
CAPP_CORCT

RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=89384460; PubMed=2779518;
RA Birkmann B.J., Follett M.T., Griot M.U., Sinskey A.J.;
RT "The phosphoenolpyruvate carboxylase gene of Corynebacterium
RL glutamicum: molecular cloning, nucleotide sequence, and expression.";
RN Mol. Gen. Genet. 218:330-339(1989).
[2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=89326141; PubMed=2666264;
RA O'Regan M., Thierbach G., Bachmann B., Villevall D., Lepage P.,
RA Viret J.F., Lemoine Y.;
RT "Cloning and nucleotide sequence of the phosphoenolpyruvate
RL carboxylase-coding gene of Corynebacterium glutamicum ATCC13032.";
RN Gene 77:237-251(1989).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
CC the tricarboxylic acid cycle.
CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -!- ENZYME REGULATION: ACTIVITY NOT STIMULATED BY ACETYL-COA IN THE
CC ABSENCE OF ANY ALLOSTERIC INHIBITOR, WHILE THE CORRESPONDING
CC PROTEIN FROM E. COLI IS STRONGLY STIMULATED.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
CC
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CC -----
CC EMBL; X14234; CAA32450.1; -.
CC EMBL; M25819; AAA83537.1; -.
CC EMBL; A09073; CAA00827.1; -.
CC EMBL; AP05279; BAB98978.1; -.
CC PIR; S05512; QYFKG.
CC HSP; P00864; IFYI.
CC HAMAP; MF_00595; -.
CC InterPro; IPR001449; PEPcase.
CC Pfam; PF00311; PEPcase; 1.
CC PRINTS; PR00150; PEPCARBXLASE.
CC PROSITE; PS00393; PEPcase; 2; 1.
CC PROSITE; PS00781; PEPcase; 1; 1.
CC Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
CC Complete proteome.
CC INIT MET 0
CC FT ACT_SITE 137 137 BY SIMILARITY.
CC FT ACT_SITE 578 578 BY SIMILARITY.
CC FT CONFLICT 606 607 KL -> NV (IN REF. 1).
CC FT CONFLICT 799 800 FT -> LP (IN REF. 1).
CC FT CONFLICT 914 914 L -> V (IN REF. 1).
CC SQ SEQUENCE 918 AA; 103066 MW; A56C2703169D0698 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 918;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 104 LDATWL 109
|||||
RESULT 4
CAPP_CORCT

ID CAPP CORCT STANDARD; PRT; 919 AA.
AC Q93WH3.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
GN PPC.
OS Corynebacterium crenatum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=169810;
[1]
RP SEQUENCE FROM N.A.
RA Liu Y., Ding J., Wang Y.;
RT "Cloning and expression of phosphoenolpyruvate carboxylase-coding gene
RL in Corynebacterium crenatum CD945.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
CC the tricarboxylic acid cycle.
CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
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CC -----
CC EMBL; AF406314; AAK92540.1; -.
CC HAMAP; MF_00595; -.
CC InterPro; IPR001449; PEPcase.
CC Pfam; PF00311; PEPcase; 1.
CC PRINTS; PR00150; PEPCARBXLASE.
CC PROSITE; PS00781; PEPcase; 1; 1.
CC PROSITE; PS00393; PEPcase; 2; 1.
CC Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle.
CC FT ACT_SITE 138 138 BY SIMILARITY.
CC FT ACT_SITE 579 579 BY SIMILARITY.
CC SQ SEQUENCE 919 AA; 103331 MW; 10AF3F464AF6E604 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 919;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 105 LDATWL 110
|||||
RESULT 5
CYCL_PARDE
ID CYCL_PARDE STANDARD; PRT; 177 AA.
AC P29899;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c-L precursor (Cytochrome C55II) (C552).
GN MOXG.
OS Paracoccus denitrificans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=266;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=Fd 1222;
RX MEDLINE=92041581; PubMed=1657871;
RA van Spanning R.J.M., Wansell C.W., de Boer T., Hazelaar M.J.,

```

RA Anazawa H., Harms N., Oltmann L.F., Stouthamer A.H.;
 RT "Isolation and characterization of the moxJ, moxG, moxI, and moxR
 RT genes of Paracoccus denitrificans: inactivation of moxJ, moxG, and
 RT moxR and the resultant effect on methylothrophic growth.";
 RL J. Bacteriol. 173:6948-6961(1991).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=94188715; PubMed=8140419;
 RA Chen L., Darley R., Mathews F.S., Davidson V.L.;
 RA "Structure of an electron transfer complex: methylamine
 RT dehydrogenase, amicyanin, and cytochrome c551i.";
 RL Science 264:86-90(1994).
 CC -!- FUNCTION: ELECTRON ACCEPTOR FOR MDH. ACTS IN METHANOL OXIDATION.
 CC THIS CYTOCHROME HAS A REDOX POTENTIAL OF ABOUT +190 MV.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 CC -!- INDUCTION: DURING GROWTH ON METHANOL.
 CC -----
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 CC -----
 DR EMBL; M57684; AAA25583.1; --
 DR PIR; B41377; B41377.
 DR PDB; 2MFA; 31-JAN-94.
 DR INTERPRO; IPR000345; CytC heme bind.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 KW Electron transport; Heme; Signal; Methanol utilization; Periplasmic;
 KW 3D-structure.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 177 CYTOCHROME C-L.
 FT BINDING 79 79 HEME (COVALENT) (BY SIMILARITY).
 FT BINDING 82 82 HEME (COVALENT) (BY SIMILARITY).
 FT METAL 83 83 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT STRAND 27 27
 FT STRAND 34 34
 FT HELIX 37 39
 FT HELIX 42 44
 FT HELIX 48 56
 FT TURN 60 63
 FT TURN 65 67
 FT TURN 68 78
 FT TURN 79 79
 FT HELIX 80 83
 FT TURN 85 86
 FT HELIX 103 106
 FT HELIX 108 117
 FT TURN 121 122
 FT TURN 127 129
 FT HELIX 132 144
 FT TURN 145 145
 FT TURN 150 151
 FT TURN 154 155
 FT HELIX 158 162
 FT TURN 163 163
 SQ SEQUENCE 177 AA; 19396 MW; 6949FBD8B2C0566 CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 177;
 Best Local Similarity 100.0%; Pred.No.69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DASWL 6
 Db 152 DASWL 156
 RESULT 6
 HIS4 SHEON
 ID HIS4 SHEON PRT; 245 AA.
 AC Q8EF55;

DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
 DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)
 DE (Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
 DE isomerase).
 GN HISA OR SO2069.
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Shewanella.
 OX NCBI TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MR-1;
 RX MEDLINE=22297686; PubMed=12368813;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
 RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA DeJoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
 RA Mueller T.V., Smith H.O., Gill J., Utterback T.R., McDonald L.A.,
 RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis".
 RT Nat. Biotechnol. 20:1118-1123(2002).
 RL Nat. Catalytic ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-
 CC phosphoribosylamino)methylideneamino]imidazole-4-carboxamide = 5-
 CC [(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-
 CC phosphoribosyl)imidazole-4-carboxamide.
 CC -!- PATHWAY: Histidine biosynthesis; fourth step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE015648; AAN55116.1; --
 DR TIGR; SO2069; --
 DR HAMAP; MF_01014; --; 1.
 DR InterPro; IPR006063; His4.
 DR InterPro; IPR006062; His biosynth.
 DR Pfam; PF00977; His biosynth; 1.
 DR TIGRFAMs; TIGR00007; TIGR00007; 1.
 KW Isomerase; Histidine biosynthesis; Complete proteome.
 SQ SEQUENCE 245 AA; 26017 MW; 6D40B1B3604527DA CRC64;
 Query Match 87.9%; Score 29; DB 1; Length 245;
 Best Local Similarity 100.0%; Pred.No.96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DASWL 6
 Db 42 DASWL 46
 RESULT 7
 TH11 CAEEL
 ID TH11 CAEEL STANDARD; PRT; 277 AA.
 AC P91247;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative thiosulfate sulfurtransferase Flig11.9 (EC 2.8.1.1).
 GN Flig11.9.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;


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OC Rhabdittidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Latreille P., Deadman R.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
CC -1- SIMILARITY: Contains 2 rhodanese domains.
CC -----
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CC -----
CC EMBL; U80451; AAB37840.1; -.
CC FIRM; T29979; T29979.
CC HSSP; P00586; 1RHS.
CC WormPep; FL1G11.9; CE09351.
CC InterPro; IPR001763; Rhodanese-like.
CC InterPro; IPR001307; Rhodanese.
CC PFam; PF00581; Rhodanese; 1.
CC SMART; SM00450; RHOD; 1.
CC PROSITE; PS00683; RHODANASE 2; FALSE_NEG.
CC PROSITE; PS0206; RHODANASE 3; 2.
CC Hypothetical protein; Transferase; Repeat.
FT DOMAIN 15 153 RHODANASE 1.
FT DOMAIN 155 243 RHODANASE 2.
FT ACT_SITE 258 258 BY SIMILARITY.
SQ SEQUENCE 277 AA; 30699 MW; 25EDF66CE12824C CRC64;

Query Match 87.9%; Score 29; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
Db 22 LDASW 26

RESULT 8
YDBC_ECOLI STANDARD; PRT; 286 AA.
AC P25906;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase ydbc (EC 1.-.-.-).
GN YDBC OR B1406.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaeser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12."
RL Biochimie 73:1361-1374(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glaeser J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Ohtomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA Oshima T., Saito N., Sempel G., Seki Y., Sivasubram S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [4]
RP SEQUENCE OF 1-69 FROM N.A.
RC STRAIN=W / ATCC 11105;
RX MEDLINE=98421522; PubMed=9748275;
RA Fernandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,
RA Garcia J.L., Diaz E.;
RT "Catabolism of phenylacetic acid in Escherichia coli. Characterization
RT of a new aerobic hybrid pathway.";
RL J. Biol. Chem. 273:25974-25986(1998).
CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
CC -----
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CC -----
CC EMBL; X62680; CAA44553.1; -.
CC EMBL; AE000238; AAC74488.1; -.
CC EMBL; D90779; BAA15021.1; -.
CC EMBL; X97452; CAA66103.1; -.
CC FIRM; A48399; A48399.
CC HSSP; P06632; 1HW6.
CC Ecogene; EG11309; ydbc.
CC InterPro; IPR001395; Aldo/ket red.
CC PFam; PF00248; aldo ket red; 1.
CC PRINTS; PR00069; ALDKETREDTASE.
CC ProDom; PD000288; Aldo/ket red; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 286 AA; 30706 MW; 82B587AE9115EF9 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6
Db 92 DASWL 96

RESULT 9
THTR_CHICK STANDARD; PRT; 289 AA.
AC P25324;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thiosulfate sulfotransferase (EC 2.8.1.1) (Rhodanese).
GN TST.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.

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RC TISSUE=Liver;
RX MEDLINE=91113289; PubMed=2275748;
RA Kohanski R.A., Heinrikson R.L.;
RT "Primary structure of avian hepatic rhodanese.";
RL J. Protein Chem. 9:369-377(1990).
CC -!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
CC DETOXIFICATION.
CC -!- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
CC -!- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
CC -!- SIMILARITY: Contains 2 rhodanese domains.
DR PIR; A37209; A37209.
DR HSP; P00586; 1RHS.
DR InterPro; IPR001763; Rhodanese-like.
DR Pfam; PF00581; Rhodanese; 2.
DR SMART; SM00450; RHOD; 2.
DR PROSITE; PS00380; RHODANES1; 1.
DR PROSITE; PS00683; RHODANES2; 1.
DR PROSITE; PS0206; RHODANES3; 2.
KW Transferase; Mitochondrion; Repeat.
FT DOMAIN 24 142 RHODANES1.
FT DOMAIN 143 158 HINGE.
FT DOMAIN 172 284
FT ACT_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
FT ACT_SITE 186 186 SIMILARITY).
FT ACT_SITE 244 244 BY SIMILARITY.
FT ACT_SITE 245 245 SUBSTRATE (THIOSULFATE) BINDING
FT ACT_SITE 246 246 (BY SIMILARITY).
FT ACT_SITE 246 246 SUBSTRATE (THIOSULFATE) BINDING
FT ACT_SITE 246 246 (BY SIMILARITY).
SQ SEQUENCE 289 AA; 32286 MW; 8BFCF71DE0B2BA4 CRC64;
Query Match 87.9%; Score 29; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDASW 5
Db 31 LDASW 35
RESULT 10
THTR RAT
ID THTR RAT STANDARD; PRT; 295 AA.
AC P24329;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese) (Fragment).
GN TST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=91207296; PubMed=2018478;
RA Weiland K.L., Dooley T.P.;
RT "Molecular cloning, sequencing and characterization of cDNA to rat
RL liver rhodanese, a thiosulphate sulphurtransferase.";
RL Biochem. J. 275:227-231(1991).
RN [2]
RP MUTAGENESIS.
RC TISSUE=Liver;
RX MEDLINE=95332330; PubMed=7608189;
RA Nagahara N., Okazaki T., Nishino T.;
RT "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily

RT related to mitochondrial rhodanese. Striking similarity in active site
RT amino acid sequence and the increase in the mercaptopyruvate
RT sulfurtransferase activity of rhodanese by site-directed
RT mutagenesis.";
RL J. Biol. Chem. 270:16230-16235(1995).
CC -!- FUNCTION: INVOLVED IN THE FORMATION OF IRON-SULFUR COMPLEXES,
CC CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING
CC ENZYMES. OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR
CC ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE
CC (MST) ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
CC -!- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
CC -!- SIMILARITY: Contains 2 rhodanese domains.
CC -----
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CC -----
DR EMBL; X56228; CAA39677.1; -.
DR PIR; S15081; S15081.
DR HSP; P00586; 1RHS.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR001307; Rhodanese.
DR Pfam; PF00581; Rhodanese; 2.
DR SMART; SM00450; RHOD; 2.
DR PROSITE; PS00380; RHODANES1; 1.
DR PROSITE; PS00683; RHODANES2; 1.
DR PROSITE; PS0206; RHODANES3; 2.
KW Transferase; Mitochondrion; Repeat.
FT NON_TER 1 1
FT DOMAIN 23 141 RHODANES1.
FT DOMAIN 142 157 HINGE.
FT DOMAIN 171 286 RHODANES2.
FT ACT_SITE 185 185 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
FT ACT_SITE 185 185 SIMILARITY).
FT ACT_SITE 246 246 BY SIMILARITY.
FT ACT_SITE 247 247 SUBSTRATE (THIOSULFATE) BINDING.
FT ACT_SITE 248 248 SUBSTRATE (THIOSULFATE) BINDING.
FT MUTAGEN 247 247 R->G: UNALTERED RHODANES ACTIVITY;
FT MUTAGEN 248 248 INCREASED MST ACTIVITY.
FT MUTAGEN 248 248 K->S: DECREASED RHODANES ACTIVITY;
FT SEQUENCE 295 AA; 33176 MW; 24C55B35690934E1 CRC64;
Query Match 87.9%; Score 29; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDASW 5
Db 30 LDASW 34
RESULT 11
RECO ANASP
ID RECO ANASP STANDARD; PRT; 296 AA.
AC Q8VPL9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA repair protein reco (Recombination protein O).
GN RECO OR ALR4175.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

NCBI_TaxID=103690;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=21595285; PubMed=11759840;
 RA Kato T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 CC -!- FUNCTION: Involved in DNA repair and recF pathway recombination
 CC (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE RECO FAMILY.
 CC -----
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 CC -----
 CC EMBL; AP003595; BAB75874.1; -;
 DR PIR; AH2327; AH2327.
 DR HAMAP; MF 00201; -; 1.
 DR InterPro; IPR003717; RecO.
 DR Pfam; PF02565; RecO; 1.
 KW DNA repair; DNA recombination; Complete proteome.
 SQ SEQUENCE 296 AA; 32728 MW; A5B3D540F162BE72 CRC64;

 Query Match 87.9%; Score 29; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 DASWL 6
 Db 256 DASWL 260

 RESULT 12
 ID THYM_HUMAN STANDARD; PRT; 296 AA.
 AC P25375; O75750;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 3-mercaptopyruvate sulfoxyltransferase (EC 2.8.1.2) (MST).
 GN MST OR TST2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=92062122; PubMed=1953758;
 RA Pallini R., Guazzi G.C., Cannella C., Cacace M.G.;
 RT "Cloning and sequence analysis of the human liver
 RT 3-mercaptopyruvate sulfoxyltransferase (EC 2.8.1.2) rhodanese:
 RT comparison with the bovine and chicken enzymes.";
 RL Biochem. Biophys. Res. Commun. 180:887-893(1991).
 CC [2]
 CC SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.D., Langford C.F., Levensha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Rameay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton P., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dunanski J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Franeson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow, Muscle, and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Udwin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Villalón D.K., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: TRANSFER OF A SULFUR ION TO CYANIDE OR TO OTHER THIOL
 CC COMPOUNDS. ALSO HAS WEAK RHODANESE ACTIVITY. MAY HAVE A ROLE IN
 CC CYANIDE DEGRADATION OR IN THIOSULFATE BIOSYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: 3-mercaptopyruvate + cyanide = pyruvate +
 CC thiocyanate.
 CC -!- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -!- SIMILARITY: Contains 2 rhodanese domains.
 CC -!- CAUTION: Was originally (Ref.1) thought to be rhodanese.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X59434; CAA42060.1; --
 DR EMBL; Z73420; CAA97763.1; --
 DR EMBL; BC003508; AAH03508.1; --
 DR EMBL; BC016737; AAH16737.1; --
 DR EMBL; BC018717; AAH18717.1; --
 DR PIR; JH0461; ROHU.
 DR HSSP; P00586; LRHS.
 DR Genew; HGNC:7223; MPST.
 DR MIM; 602496; --
 DR GO; GO:0004792; F:thiosulfate sulfurtransferase activity; TAS.
 DR GO; GO:0009440; P:cyanate catabolism; TAS.
 DR GO; GO:0009636; P:response to toxin; TAS.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANESE_1; 1.
 DR PROSITE; PS00683; RHODANESE_2; 1.
 DR PROSITE; PS50206; RHODANESE_3; 2.
 KW Transferase; Repeat.
 FT INIT_MET 0 BY SIMILARITY.
 FT DOMAIN 24 143 RHODANESE 1.
 FT DOMAIN 144 159 HINGE.
 FT DOMAIN 173 287 RHODANESE 2.
 FT ACT_SITE 187 187 SUBSTRATE (MERCAPTOPYRUVATE) BINDING
 FT ACT_SITE 187 187 (BY SIMILARITY).
 FT ACT_SITE 196 196 SUBSTRATE (MERCAPTOPYRUVATE) BINDING
 FT ACT_SITE 247 247 (BY SIMILARITY).
 FT ACT_SITE 247 247 BY SIMILARITY.
 FT CONFLICT 45 47 RRE -> TO (IN REF. 1).
 SQ SEQUENCE 296 AA; 33047 MW; 1991F0F1CAE8CB1 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 DB 31 LDASW 35

RESULT 13
 THTM RAT STANDARD; PRT; 296 AA.
 AC P97532;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2) (MST).
 GN MPST.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=97066916; PubMed=8910318;
 RA Nagahara N., Nishino T.;
 RT "Role of amino acid residues in the active site of rat liver
 RT mercaptopyruvate sulfurtransferase. CDNA cloning, overexpression, and
 RT site-directed mutagenesis.";
 RL J. Biol. Chem. 271:27395-27401 (1996).
 RN [2]
 RP SEQUENCE OF 8-76 AND 146-284, AND CHARACTERIZATION.
 RC STRAIN=Wistar; TISSUE=Liver;

RX MEDLINE=95332330; PubMed=7608189;
 RA Nagahara N., Okazaki T., Nishino T.;
 RT "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily
 RT related to mitochondrial rhodanese. Striking similarity in active site
 RT amino acid sequence and the increase in the mercaptopyruvate
 RT sulfurtransferase activity of rhodanese by site-directed
 RT mutagenesis.";
 RL J. Biol. Chem. 270:16230-16235 (1995).
 CC -!- FUNCTION: TRANSFERS A SULFUR ION TO CYANIDE OR TO OTHER THIOL
 CC COMPOUNDS. ALSO HAS WEAK RHODANESE ACTIVITY. MAY HAVE A ROLE IN
 CC CYANIDE DEGRADATION OR IN THIOSULFATE BIOSYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: 3-mercaptopyruvate + cyanide = pyruvate +
 CC thiocyanate.
 CC -!- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER.
 CC -!- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -!- PTM: THE N-TERMINAL IS BLOCKED.
 CC -!- SIMILARITY: Contains 2 rhodanese domains.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

EMBL; D50564; BAA09127.1; --
 HSSP; P00586; LRHS.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANESE_1; 1.
 DR PROSITE; PS00683; RHODANESE_2; 1.
 DR PROSITE; PS50206; RHODANESE_3; 2.
 KW Transferase; Mitochondrion; Repeat.
 FT INIT_MET 0
 FT DOMAIN 24 143 RHODANESE 1.
 FT DOMAIN 144 159 HINGE.
 FT DOMAIN 173 287 RHODANESE 2.
 FT ACT_SITE 187 187 SUBSTRATE (MERCAPTOPYRUVATE) BINDING.
 FT ACT_SITE 196 196 SUBSTRATE (MERCAPTOPYRUVATE) BINDING.
 FT ACT_SITE 247 247
 FT MUTAGEN 187 187 R->G: LARGE DECREASE IN MST ACTIVITY;
 FT MUTAGEN 196 196 SOME DECREASE IN RHODANESE ACTIVITY.
 FT MUTAGEN 247 247 R->G: DECREASED MST ACTIVITY; INCREASED
 FT MUTAGEN 247 247 RHODANESE ACTIVITY.
 FT MUTAGEN 247 247 C->S: LOSS OF BOTH MST AND RHODANESE
 FT MUTAGEN 247 247 ACTIVITIES.
 FT MUTAGEN 248 248 G->R: DECREASED MST ACTIVITY; INCREASED
 FT MUTAGEN 249 249 RHODANESE ACTIVITY.
 FT MUTAGEN 249 249 S->K: SLIGHT DECREASE IN MST ACTIVITY;
 FT MUTAGEN 249 249 INCREASED RHODANESE ACTIVITY.
 FT MUTAGEN 249 249 S->A: SLIGHT DECREASE IN MST ACTIVITY.
 SQ SEQUENCE 296 AA; 32809 MW; 08CC176AC14C717C CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 DB 31 LDASW 35

RESULT 14
 THTM BOVIN STANDARD; PRT; 296 AA.
 ID THTM BOVIN
 AC P00586;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Thiosulfate sulfoxyltransferase (EC 2.8.1.1) (Rhodanese).
 GN TST.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91161544; PubMed=2002017;
 RA Miller D.M., Delgado R., Chirgwin J.M., Hardies S.C., Horowitz P.M.;
 RT "Expression of cloned bovine adrenal rhodanese.";
 RL J. Biol. Chem. 266:4686-4691(1991).
 RN [2]
 RP SEQUENCE OF 1-294.
 RC TISSUE=Liver;
 RX MEDLINE=79048424; PubMed=711737;
 RA Russell J., Weng L., Keim P.S., Heinrikson R.L.;
 RT "The covalent structure of bovine liver rhodanese. Isolation and
 RT partial structural analysis of cyanogen bromide fragments and the
 RT complete sequence of the enzyme.";
 RL J. Biol. Chem. 253:8102-8108(1978).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=79007483; PubMed=691057;
 RA Ploegman J.H., Drent G., Kalk K.H., Hol W.G.J.;
 RT "Structure of bovine liver rhodanese. I. Structure determination at
 RT 2.5-A resolution and a comparison of the conformation and sequence of
 RT its two domains.";
 RL J. Mol. Biol. 123:557-594(1978).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.36 ANGSTROMS).
 RX MEDLINE=98437562; PubMed=9761843;
 RA Gliubich F., Berni R., Colapietro M., Barba L., Zanotti G.;
 RT "Structure of sulfur-substituted rhodanese at 1.36-A resolution.";
 RL Acta Crystallogr. D 54:481-486(1998).
 RN [5]
 RP ACTIVE SITE.
 RX MEDLINE=79048425; PubMed=711738;
 RA Weng L., Heinrikson R.L., Westley J.;
 RT "Active site cysteinyl and arginyl residues of rhodanese. A novel
 RT formation of disulfide bonds in the active site promoted by
 RT phenylglyoxal.";
 RL J. Biol. Chem. 253:8109-8119(1978).
 RN [6]
 RP MUTAGENESIS OF ARG-186 AND LYS-249.
 RX MEDLINE=94179198; PubMed=8132546;
 RA Luo G.-X., Horowitz P.M.;
 RT "The sulfoxyltransferase activity and structure of rhodanese are
 RT affected by site-directed replacement of Arg-186 or Lys-249.";
 RL J. Biol. Chem. 269:8220-8225(1994).
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
 CC DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -1- SIMILARITY: Contains 2 rhodanese domains.
 CC -----
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 CC -----
 CC EMBL; M58561; AAA30753.1; -.

DR PIR; A23704; ROBO.
 DR PDB; 1RHD; 27-JAN-84.
 DR PDB; 1RHS; 21-JAN-98.
 DR PDB; 2ORA; 01-AUG-96.
 DR PDB; 1ORB; 15-OCT-95.
 DR PDB; 1BOH; 27-APR-99.
 DR PDB; 1BOI; 27-APR-99.
 DR PDB; 1DP2; 13-DEC-00.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANESE_1; 1.
 DR PROSITE; PS00683; RHODANESE_2; 1.
 DR PROSITE; PS0306; RHODANESE_3; 2.
 KW Transferase; Mitochondrion; 3D-structure; Repeat.
 FT INIT MET 0 0
 FT DOMAIN 24 142 RHODANESE 1.
 FT DOMAIN 143 158 HINGE.
 FT DOMAIN 172 287 RHODANESE 2.
 FT ACT_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING.
 FT ACT_SITE 247 247
 FT ACT_SITE 248 248
 FT ACT_SITE 249 249
 FT ACT_SITE 249 249
 FT VARIANT 1 2
 FT MUTAGEN 186 186
 FT MUTAGEN 249 249
 FT CONFLICT 99 99
 FT CONFLICT 214 214
 FT CONFLICT 219 219
 FT STRAND 9 10
 FT HELIX 12 20
 FT TURN 21 22
 FT STRAND 25 25
 FT TURN 26 27
 FT STRAND 28 32
 FT TURN 38 39
 FT HELIX 43 49
 FT STRAND 51 51
 FT TURN 53 54
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 FT HELIX 77 86
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 FT STRAND 94 98
 FT HELIX 108 117
 FT TURN 118 119
 FT STRAND 123 126
 FT TURN 127 128
 FT HELIX 129 135
 FT TURN 136 137
 FT STRAND 141 141
 FT HELIX 158 160
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FT STRAND 243 246
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 FT STRAND 269 271
 FT HELIX 274 281
 FT HELIX 284 286
 FT STRAND 287 289
 FT TURN 290 291
 FT STRAND 292 292
 SQ SEQUENCE 296 AA; C8769696FA6AC111 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 |||||
 Db 31 LDASW 35

RESULT 15

THTR_CRIGR STANDARD; PRT; 296 AA.
 AC P46635;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
 GN TST.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_Taxid=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=96106946; PubMed=8535164;
 RA Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;
 RT "Chinese hamster rhodanese cDNA: activity of the expressed protein is
 not blocked by a C-terminal extension.";
 RL Protein Expr. Purif. 6:693-699(1995).
 CC -!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
 DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
 CC -!- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
 CC -!- SIMILARITY: Contains 2 rhodanese domains.
 CC -----
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 use by non-profit institutions as long as its content is in no way
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U23943; AAB84305.1; -.
 DR HSSP; P00586; 1RHS.
 DR InterPro; IPR001763; Rhodanese-like.
 DR InterPro; IPR001307; Rhodanese.
 DR Pfam; PF00581; Rhodanese; 2.
 DR SMART; SM00450; RHOD; 2.
 DR PROSITE; PS00380; RHODANESE_1; 1.
 DR PROSITE; PS00683; RHODANESE_2; 1.
 DR PROSITE; PS50206; RHODANESE_3; 2.
 KW Transferase; Mitochondrion; Repeat.
 FT INIT MET 0 0 BY SIMILARITY.
 FT DOMAIN 24 142 RHODANESE 1.

FT DOMAIN 143 158
 FT DOMAIN 172 287
 FT ACT_SITE 186 186
 FT 247
 FT ACT_SITE 247 247
 FT ACT_SITE 248 248
 FT ACT_SITE 249 249
 FT SEQUENCE 296 AA; 33205 MW; 8811022BF9BAD666 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 |||||
 Db 31 LDASW 35

Search completed: February 18, 2004, 14:28:08

Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-10
Perfect score: 33
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	90.9	919	3	US-08-985-916-16
2	30	90.9	935	4	US-09-271-438A-3
3	30	90.9	935	4	US-09-271-438A-8
4	29	87.9	118	4	US-09-634-238-354
5	29	87.9	136	4	US-09-370-838-123
6	29	87.9	194	4	US-09-252-991A-22578
7	29	87.9	277	4	US-09-252-991A-26048
8	29	87.9	438	4	US-09-252-991A-16758
9	29	87.9	661	4	US-09-252-991A-18225
10	29	87.9	834	4	US-09-252-991A-17616
11	28	84.8	128	4	US-09-205-258-254
12	28	84.8	210	3	US-08-611-587-4
13	28	84.8	219	3	US-09-247-373B-52
14	28	84.8	323	3	US-09-029-213B-25
15	28	84.8	342	4	US-09-328-352-5861
16	28	84.8	402	4	US-09-252-991A-26529
17	28	84.8	511	4	US-09-252-991A-27306
18	28	84.8	523	4	US-09-323-195A-17
19	28	84.8	588	4	US-09-252-991A-18861
20	27	81.8	36	1	US-08-118-270-244
21	27	81.8	36	5	PCT-US93-08528-244
22	27	81.8	134	4	US-09-732-210-395
23	27	81.8	144	4	US-09-732-210-629
24	27	81.8	167	4	US-09-252-991A-27865
25	27	81.8	233	4	US-09-252-991A-27758
26	27	81.8	263	2	US-08-790-137-4
27	27	81.8	263	2	US-08-824-874-5

28	27	81.8	263	3	US-08-807-151-5	Sequence 5, Appl
29	27	81.8	263	3	US-09-210-084-5	Sequence 5, Appl
30	27	81.8	263	4	US-09-478-957-5	Sequence 5, Appl
31	27	81.8	263	4	US-09-764-762-5	Sequence 5, Appl
32	27	81.8	276	4	US-09-252-991A-22260	Sequence 22260, A
33	27	81.8	316	4	US-09-252-991A-18153	Sequence 2, Appl
34	27	81.8	385	2	US-08-694-915-2	Sequence 2, Appl
35	27	81.8	413	2	US-08-960-756-2	Sequence 2, Appl
36	27	81.8	416	2	US-08-694-915-4	Sequence 7, Appl
37	27	81.8	423	1	US-08-844-064-7	Sequence 7, Appl
38	27	81.8	423	3	US-09-008-433-7	Sequence 7, Appl
39	27	81.8	423	4	US-08-850-348A-2	Sequence 2, Appl
40	27	81.8	464	4	US-09-634-238-295	Sequence 295, App
41	27	81.8	479	4	US-09-634-238-248	Sequence 248, App
42	27	81.8	561	2	US-08-532-795-2	Sequence 2, Appl
43	27	81.8	562	4	US-08-851-567B-30	Sequence 30, Appl
44	27	81.8	569	2	US-08-532-795-23	Sequence 23, Appl
45	27	81.8	569	2	US-08-532-795-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-985-916-16
; Sequence 16, Application US/08985916
; Patent No. 6221636
; GENERAL INFORMATION:
; APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON SPIVAK, MCLELLAND, MATIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; COUNTRY: VA
; ZIP: 22152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,916
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-325658
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 919 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-916-16

Query Match 90.9%; Score 30; DB 3; Length 919;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6

Db 105 LDATWL 110

RESULT 2

US-09-271-438A-3
 ; Sequence 3, Application US/09271438A
 ; Patent No. 6331419
 ; GENERAL INFORMATION:
 ; APPLICANT: IZUI, Hiroshi
 ; APPLICANT: ONO, Ei-ji
 ; APPLICANT: MATSUI, Kazuhiko
 ; APPLICANT: MORIYA, Mika
 ; APPLICANT: ITO, Hisao
 ; APPLICANT: HARA, Yoshihiko
 ; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
 ; FILE REFERENCE: 0010-0989-0
 ; CURRENT APPLICATION NUMBER: US/09/271,438A
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR FILING DATE: 1998-03-18
 ; PRIOR APPLICATION NUMBER: JP10-297129
 ; PRIOR FILING DATE: 1998-10-19
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 935
 ; TYPE: PRT
 ; ORGANISM: Enterobacter agglomerans
 US-09-271-438A-3

Query Match 90.9%; Score 30; DB 4; Length 935;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 DB 10 LDSSWL 15

RESULT 3
 US-09-271-438A-8
 ; Sequence 8, Application US/09271438A
 ; Patent No. 6331419
 ; GENERAL INFORMATION:
 ; APPLICANT: IZUI, Hiroshi
 ; APPLICANT: ONO, Ei-ji
 ; APPLICANT: MATSUI, Kazuhiko
 ; APPLICANT: MORIYA, Mika
 ; APPLICANT: ITO, Hisao
 ; APPLICANT: HARA, Yoshihiko
 ; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
 ; FILE REFERENCE: 0010-0989-0
 ; CURRENT APPLICATION NUMBER: US/09/271,438A
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR FILING DATE: 1998-03-18
 ; PRIOR APPLICATION NUMBER: JP10-69068
 ; PRIOR FILING DATE: 1998-03-18
 ; PRIOR APPLICATION NUMBER: JP10-297129
 ; PRIOR FILING DATE: 1998-10-19
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 935
 ; TYPE: PRT
 ; ORGANISM: Enterobacter agglomerans
 US-09-271-438A-8

Query Match 90.9%; Score 30; DB 4; Length 935;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
 DB 10 LDSSWL 15

RESULT 4
 US-09-634-238-354
 ; Sequence 354, Application US/09634238
 ; Patent No. 6544772
 ; GENERAL INFORMATION:
 ; APPLICANT: Glenn, Matthew
 ; APPLICANT: Havukkala, Ilkka J.
 ; APPLICANT: Bloksberg, Leonard, N.
 ; APPLICANT: Lubbers, Mark W.
 ; APPLICANT: Dekker, James
 ; APPLICANT: Christensson, Anna C.
 ; APPLICANT: Holland, Ross
 ; APPLICANT: O'Toole, Paul W.
 ; APPLICANT: Reid, Julian R.
 ; APPLICANT: Coolbear, Timothy
 ; TITLE OF INVENTION: Polynucleotides, materials incorporating
 ; FILE REFERENCE: 11000.1043UI
 ; CURRENT APPLICATION NUMBER: US/09/634,238
 ; CURRENT FILING DATE: 2000-08-08
 ; NUMBER OF SEQ ID NOS: 422
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 354
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Lactobacillus rhamnosus
 US-09-634-238-354

Query Match 87.9%; Score 29; DB 4; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 DB 52 LDASW 56

RESULT 5
 US-09-370-838-123
 ; Sequence 123, Application US/09370838
 ; Patent No. 6444425
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Mohamath, Roadoh
 ; APPLICANT: Secrist, Heather
 ; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
 ; FILE REFERENCE: 210121.475C1
 ; CURRENT APPLICATION NUMBER: US/09/370,838
 ; CURRENT FILING DATE: 1999-08-09
 ; EARLIER APPLICATION NUMBER: US 09/285,323
 ; EARLIER FILING DATE: 1999-04-02
 ; NUMBER OF SEQ ID NOS: 289
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 123
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-370-838-123

Query Match 87.9%; Score 29; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
 DB 32 LDASW 36

RESULT 6
 US-09-252-991A-22578
 ; Sequence 22578, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22578
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22578

Query Match 87.9%; Score 29; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6
|||
Db 161 DASWL 165

RESULT 7
US-09-252-991A-26048
; Sequence 26048, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26048
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26048

Query Match 87.9%; Score 29; DB 4; Length 277;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
|||
Db 89 LDASWL 94

RESULT 8
US-09-252-991A-16758
; Sequence 16758, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16758
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16758

Query Match 87.9%; Score 29; DB 4; Length 438;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
|||
Db 142 LDASWL 147

RESULT 9
US-09-252-991A-18225
; Sequence 18225, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18225
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18225

Query Match 87.9%; Score 29; DB 4; Length 661;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
|||
Db 546 LDASWL 551

RESULT 10
US-09-252-991A-17616
; Sequence 17616, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17616
; LENGTH: 834
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17616

Query Match 87.9%; Score 29; DB 4; Length 834;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDASW 5
Db      474 LDASW 478

RESULT 11
US-09-205-258-254
; Sequence 254, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 254
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-254

Query Match      84.8%; Score 28; DB 4; Length 128;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDASWL 6
Db      14 LDISWL 19

RESULT 12
US-08-611-587-4
; Sequence 4, Application US/08611587
; Patent No. 6150091
; GENERAL INFORMATION:
; APPLICANT: PANDOLFO, MASSIMO
; APPLICANT: MONTERMINI, LAURA
; APPLICANT: MOLTO, MARIA D.
; APPLICANT: Koenig, Michael
; APPLICANT: Campuzano, Victoria
; APPLICANT: Cossee, Mireille
; TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77010
; COMPUTER READABLE FORM:
```

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/611,587
;; FILING DATE: 03-MAR-1996
;; CLASSIFICATION: 436
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brashers-Macatee, Sarah J.
;; REGISTRATION NUMBER: 38,087
;; REFERENCE/DOCKET NUMBER: D-5901
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713-651-5620
;; TELEFAX: 713-651-5246
;; TELEX: 76-2829
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 210 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; POSITION IN GENOME:
;; UNITS: bp
US-08-611-587-4

Query Match 84.8%; Score 28; DB 3; Length 210;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 198 LDLSWL 203

RESULT 13
US-09-247-373B-52
; Sequence 52, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; CURRENT FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 52
; LENGTH: 219
; TYPE: PRT
; ORGANISM: SOYBEAN
US-09-247-373B-52

Query Match 84.8%; Score 28; DB 3; Length 219;
Best Local Similarity 56.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 102 LDAAWI 107

RESULT 14
US-09-029-213B-25
; Sequence 25, Application US/09029213B
; Patent No. 6180098
; GENERAL INFORMATION:

;; APPLICANT: CHRISTIAN, Peter D.
;; TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES
;; TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McDermott, Will & Emery
;; STREET: 600 13th Street, NW
;; CITY: Washington
;; STATE: District of Columbia
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/029,213B
;; FILING DATE: 31-AUG-1998
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Joseph Hyosuk Kim
;; REGISTRATION NUMBER: 41,425
;; REFERENCE/DOCKET NUMBER: 50179-048
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-756-8000
;; TELEFAX: 202-756-8087
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 323 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-029-213B-25

Query Match 84.8%; Score 28; DB 3; Length 323;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 191 LDSSWI 196

RESULT 15
US-09-328-352-5861
; Sequence 5861, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5861
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5861

Query Match 84.8%; Score 28; DB 4; Length 342;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6
DB 307 LDAPWL 312

Search completed: February 18, 2004, 14:41:48
Job time : 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	95.0	526	8 Q9B964	Q9B964 ceratopsolen
2	38	95.0	3103	5 Q9GV77	Q9GV77 lytechinus
3	37	92.5	204	16 Q9KER2	Q9KER2 bacillus ha
4	37	92.5	311	16 Q92MU7	Q92MU7 rhizobium m
5	37	92.5	337	16 Q8UB44	Q8UB44 agrobacteri
6	37	92.5	464	12 Q9WRS0	Q9WRS0 macaca mula
7	36	90.0	207	16 Q8FIE3	Q8FIE3 leptospira
8	36	90.0	210	11 Q9EPG8	Q9EPG8 rattus norv
9	36	90.0	254	2 Q9LBY3	Q9LBY3 shewanella
10	36	90.0	330	16 Q8XYA4	Q8XYA4 ralestonia s
11	36	90.0	380	8 Q47545	Q47545 chlamydomon
12	36	90.0	442	10 Q9FED7	Q9FED7 oryza sativ
13	36	90.0	460	8 Q8HLG1	Q8HLG1 parazen pac
14	36	90.0	460	8 Q8HLJ32	Q8HLJ32 aptocyclius
15	36	90.0	460	16 Q8ZL24	Q8ZL24 salmonella
16	36	90.0	460	16 Q8Z2J8	Q8Z2J8 salmonella

Q8RCS4 thermoanaer
Q8FPI18 corynebacter
Q8GGP7 pantoea agg
Q9J1H1 mus musculu
Q99K28 mus musculu
Q9D758 mus musculu
Q9I496 pseudomonas
Q33087 mycobacteri
Q8G651 bifidobacte
Q73637 fugu rubrip
Q68039 rhodobacter
Q05744 mycobacteri
Q8I010 drosophila
Q8G964 vibrio vuln
Q22375 caenorhabdi
Q94515 drosophila
Q98134 rhizobium 1
Q47815 geomys pers
Q95KV1 bos taurus
Q8BCI2 gremmenieil
Q8CBT3 mus musculu
Q95KV0 bos taurus
Q9P491 trichoderma
Q59898 ampelomyces
Q9P8J3 coniothyriu
Q87032 vibrio chol
Q8GLU5 mus musculu
Q9K4K4 streptomyce
Q966EQ6 homo sapien

ALIGNMENTS

RESULT 1

Q9B964 PRELIMINARY; PRT; 526 AA.

ID Q9B964
AC Q9B964;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cytochrome oxidase subunit I (EC 1.9.3.1) (COI) (Cytochrome c oxidase polypeptide I) (Fragment).
OS Ceratopsolen nanus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
OC Agaonidae; Agaoninae; Ceratopsolen.
OX NCBI_TaxID=130016;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G077;
RA Weiblen G.D.;
RT "Phylogenetic analyses of dioecious fig pollinators based on mitochondrial DNA sequences and morphology."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.
CC -!- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY. EMBL; AF200382; AAK00073.1; -.
DR HSSP; Pf8401; 1FFT.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.

DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Electron transport; Heme; Inner membrane; Membrane;
 KW Oxidoreductase; Respiratory chain; Transmembrane; Transport;
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 526 AA; 59586 MW; 587FE82D8C4F2B62 CRC64;
 Query Match 95.0%; Score 38; DB 8; Length 526;
 Best Local Similarity 83.3%; Pred. NO. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db :|||||
 10 LNWSWL 15
 RESULT 2
 Q9GV77 PRELIMINARY; PRT; 3103 AA.
 AC Q9GV77;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Embryonic blastocoelar extracellular matrix protein precursor.
 GN ECM3
 OS Lytechinus variegatus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20340282; PubMed=10885756;
 RA Hodor P.G., Illies M.R., Broadley S., Ettensohn C.A.;
 RT "Cell-substrate interactions during sea urchin gastrulation: migrating
 RT primary mesenchyme cells interact with and align extracellular matrix
 RT fibers that contain ECM3, a molecule with NG2-like and multiple
 RT calcium-binding domains.";
 RL Dev. Biol. 222:181-194(2000).
 DR EMBL; AF287478; AAG00570.1; -.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR003644; Calx_beta.
 DR Pfam; PF03160; Calx-beta; 5.
 DR SMART; SM00112; CA; 1.
 DR SMART; SM00237; Calx_beta; 5.
 DR PROSITE; PS0268; CADHERIN_2; 1.
 KW Matrix protein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 SQ SEQUENCE 3103 AA; 343770 MW; 79D7EBDE1C54393 CRC64;
 Query Match 95.0%; Score 38; DB 5; Length 3103;
 Best Local Similarity 83.3%; Pred. NO. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 1724 LNWSWI 1729
 RESULT 3
 Q9KER2 PRELIMINARY; PRT; 204 AA.
 AC Q9KER2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein BH0787.
 GN BH0787.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001509; BAB04506.1; -.
 DR InterPro; IPR006938; DUF624.
 DR Pfam; PF04854; DUF624; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 204 AA; 23786 MW; 7C476B67E71015E2 CRC64;
 Query Match 92.5%; Score 37; DB 16; Length 204;
 Best Local Similarity 83.3%; Pred. NO. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 22 LNNAWL 27
 RESULT 4
 Q92MU7 PRELIMINARY; PRT; 311 AA.
 ID Q92MU7;
 AC Q92MU7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Putative sugar transport system permease ABC transporter protein.
 GN R02512 OR SMC01978.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
 RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Fournelle B., Ramsperger U.,
 RA Renard C., Trebault P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591790; CAC47091.1; -.
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; 1.
 KW Complete proteome.
 SQ SEQUENCE 311 AA; 34300 MW; 4BF3487341A2C198 CRC64;
 Query Match 92.5%; Score 37; DB 16; Length 311;
 Best Local Similarity 83.3%; Pred. NO. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 138 LNNAWL 143
 RESULT 5
 Q8UB44 PRELIMINARY; PRT; 337 AA.
 ID Q8UB44;
 AC Q8UB44;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ABC transporter, membrane spanning protein.

GN ATU3173 OR AGRL_3272.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Perry M.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldan B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmlel K., Gordon J., Vaudin M., Kartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL; AE009247; AAL43989.1; -;
 DR EMBL; AE009366; AAK90213.1; -;
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 DR PROSITE; PS00402; BPD_TRANS_INN_MEMBER; 1.
 KW Complete proteome.
 SQ SEQUENCE 337 AA; 37313 MW; 0F35E9A6E0D34813 CRC64;
 Query Match 92.5%; Score 37; DB 16; Length 337;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 164 LNWSWL 169
 RESULT 6
 Q9WRS0 PRELIMINARY; PRT; 464 AA.
 ID Q9WRS0
 AC Q9WRS0
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Hypothetical 52.0 kDa protein (ORF32).
 OS Macaca mulatta rhadinovirus 17577, and
 OS Macaca mulatta rhadinovirus 26-95.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=83534, 119193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Macaca mulatta rhadinovirus 17577;
 RX MEDLINE=99174001; PubMed=10074154;
 RA Searles R.P., Berquam E.P., Arthelm M.K., Wong S.W.;
 RT "Sequence and genomic analysis of a Rhesus macaque rhadinovirus with
 similarity to Kaposi's sarcoma-associated herpesvirus/human
 herpesvirus 8.";
 RL J. Virol. 73:3040-3053(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC SPECIES=Macaca mulatta rhadinovirus 26-95;
 RC STRAIN=MACACA MULATTA RHADINOVIRUS ISOLATE 26-95;
 RX MEDLINE=20173730; PubMed=10708456;
 RA Alexander L., Denekamp L., Knapp A., Auerbach M.R., Damania B.,
 RA Desrosiers R.C.;
 RT "The primary sequence of rhesus monkey rhadinovirus isolate 26-95;
 RT sequence similarities to Kaposi's sarcoma-associated herpesvirus and
 RT rhesus monkey rhadinovirus isolate 17577.";
 RL J. Virol. 74:3388-3398(2000).
 DR EMBL; AF083501; AAD21358.1; -;
 DR EMBL; AF210726; AAF60010.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51993 MW; ADB519AE96F511E5 CRC64;
 Query Match 92.5%; Score 37; DB 12; Length 464;
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 397 VNWSWL 402
 RESULT 7
 Q8F1E3 PRELIMINARY; PRT; 207 AA.
 ID Q8F1E3
 AC Q8F1E3
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fruiting body developmental protein S-like protein.
 GN DEVS OR LA3193
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE011481; AAN50391.1; -;
 KW Complete proteome.
 SQ SEQUENCE 207 AA; 23460 MW; 14775910CB7BB668 CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NWSWL 6
 Db 157 NWSWL 161
 RESULT 8
 Q9EPG8 PRELIMINARY; PRT; 210 AA.
 ID Q9EPG8
 AC Q9EPG8
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Brain Na+/Ca++ exchanger-associated protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Michaelis M.L., Hadwiger G.H., Islam S.I., Kumar K.N.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U53512; AAG38872.1; -;
 DR InterPro; IPR00456; Ribosomal_L17.
 DR Pfam; PF01196; Ribosomal_L17; 1.

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SQ SEQUENCE      210 AA;   24405 MW;    3C9170304235B02D CRC64;
Query Match          90.0%; Score 36; DB 11; Length 210;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches       5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSW 5
Db 126 LNWSW 130
|||||

RESULT 9
Q9LBY3 PRELIMINARY; PRT; 254 AA.
AC Q9LBY3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Quinol oxidase subunit III.
GN CYOA.
OS Shewanella violacea.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=60217;
RN [1]
RP SEQUENCE FROM N.A.
RA Oureshi M.H., Kato C., Nakasone K., Yamada M., Horikoshi K.;
RT "Pressure-regulation of a membrane-bound quinol oxidase in a deep-sea piezophilic bacterium, Shewanella violacea.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033827; BAA94864.1; -.
DR HSP; P18400; 1CYW.
DR InterPro; IPR001505; Copper_CUA.
DR InterPro; IPR006333; CyOA_II.
DR ProDom; PD000131; Copper_CUA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
SQ SEQUENCE      254 AA;   28657 MW;    F1870460580AACED CRC64;
Query Match          90.0%; Score 36; DB 2; Length 254;
Best Local Similarity 83.3%; Pred.No. 2.6e+02;
Matches       5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LNWSWL 6
Db 84 LNWKWL 89
|||||

RESULT 10
Q8XYA4 PRELIMINARY;; PRT; 330 AA.
AC Q8XYA4;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II) oxidoreductase protein (EC 1.10.3.-).
GN CYOA2 OR RSC1858 OR RS03418.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S., Arlat M., Ballault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisein N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiek T., Siguer P., Thebaud P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).
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AC Q9FED7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0001B06.11 protein (P0671B11.33 protein).
GN P0001B06.11 OR P0671B11.33.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0671B11.1";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002537; BAB16858.1; -;
DR EMBL; AF002746; BAB12717.1; -;
DR Gramineae; Q9FED7; -;
DR InterPro; IPR000048; IQ_region.
DR Pfam; PF00612; IQ; 3.
DR SMART; SM00015; IQ; 1.
SQ SEQUENCE 442 AA; 48947 MW; 2F783FBE3740632 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db 274 NWSWL 278
|||||

RESULT 13
Q8HLG1 PRELIMINARY; PRT; 460 AA.
AC Q8HLG1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 4.
GN ND4.
OS Parazen pacificus (parazen).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zeiformes; Parazenidae; Parazen.
OX NCBI_TaxID=181440;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Miya M., Takeshima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major Patterns of higher teleostean phylogenies: A new perspective
based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2002).
DR EMBL; AF004433; BAC23537.1; -;
KW Mitochondrion.
SQ SEQUENCE 460 AA; 51399 MW; 2CF21B48B7B6CD7A CRC64;

Query Match 90.0%; Score 36; DB 8; Length 460;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db 388 NWSWL 392
|||||

RESULT 14
Q8HL32 PRELIMINARY; PRT; 460 AA.
AC Q8HL32;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 4.
GN ND4.
OS Aptocylchus ventricosus (smooth lumpsucker).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidae; Cyclopteridae; Aptocycius.
OX NCBI_TaxID=181459;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Miya M., Takeshima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major Patterns of higher teleostean phylogenies: A new perspective
based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2002).
DR EMBL; AF004443; BAC23666.1; -;
KW Mitochondrion.
SQ SEQUENCE 460 AA; 51277 MW; 335D673853B97A26 CRC64;

Query Match 90.0%; Score 36; DB 8; Length 460;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5
Db 387 LNWSW 391
|||||

RESULT 15
Q8ZL24 PRELIMINARY; PRT; 460 AA.
AC Q8ZL24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative glycosyl hydrolase family.
GN STM3775.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL: AE008876; AAL22633.1; -.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 1.
DR PRINTS; PR00131; GLHYDRLASE1.
DR PRODOM; PD000650; Glyco_hydro_1; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
KW Hydrolase; Hypothetical protein; Complete proteome.
SQ SEQUENCE 460 AA; 53173 MW; 1FC5F45D6E96709 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 460;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db |||||
418 NWSWL 422

Search completed: February 18, 2004, 14:35:46
Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	204	YT16_CAEEL	Q10919 caenorhabdi
2	36	90.0	767	METE_BIFLO	Q8G651 bifidobacte
3	35	87.5	325	RIR2_MYCLE	Q9cbq2 mycobacteri
4	35	87.5	745	IKKA_HUMAN	O15111 h inhibitor
5	35	87.5	745	IKKA_MOUSE	O60680 m inhibitor
6	35	87.5	756	IKKB_HUMAN	O14920 homo sapien
7	35	87.5	757	IKKB_MOUSE	O88351 mus musculu
8	35	87.5	757	IKKB_RAT	Q9qv78 rattus norv
9	34	85.0	154	Y451_SYNY3	P74676 synchocyst
10	34	85.0	345	NUO8_PARDE	P29920 paracoccus
11	34	85.0	345	NUO8_RHOCA	P42032 rhodobacter
12	34	85.0	444	T1SD_ECOLI	P06991 escherichia
13	34	85.0	612	YAWD_SCHPO	Q10187 schizosacch
14	34	85.0	685	RORI_DROME	Q24488 drosophila
15	33	82.5	54	ATP8_ASTPE	Q33822 asterina pe
16	33	82.5	157	RNH_WIGBR	Q8d3d3 wigglewort
17	33	82.5	169	PKBS_BOVIN	P30535 bos taurus
18	33	82.5	169	PKBS_HUMAN	P30536 homo sapien
19	33	82.5	169	PKBS_MOUSE	P50637 mus musculu
20	33	82.5	169	PKBS_RAT	P16257 rattus norv
21	33	82.5	330	EMB_MOUSE	P21995 mus musculu
22	33	82.5	444	CYB_RHOSH	Q02761 streptobacter
23	33	82.5	455	PHR_STRGR	P12768 streptomyce
24	33	82.5	470	NRAM_IKIE	P31348 influenza a
25	33	82.5	470	NRAM_IALEN	P31349 influenza a
26	33	82.5	470	NRAM_IAUSS	P03469 influenza a
27	33	82.5	479	LMRB_BACSU	Q35018 bacillus su
28	33	82.5	514	T3RH_HAEIN	Q35018 bacillus su
29	33	82.5	529	YQPA_CAEEL	O09531 caenorhabdi
30	33	82.5	627	YHEO_YEAST	P38731 saccharomyc
31	33	82.5	735	DHR2_YEAST	P36009 saccharomyc
32	33	82.5	752	8511_TRYCR	P18269 trypanosoma
33	33	82.5	877	SULH_SCHPO	O74377 schizosacch

ALIGNMENTS

```

RESULT 1
YT16_CAEEL          STANDARD;          PRT;   204 AA.
ID   YT16_CAEEL
AC   Q10919;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Hypothetical 23.6 kDa protein B0252.6 in chromosome II.
GN   B0252.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Du Z., Waterston R.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
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CC   or send an email to license@isb-sib.ch).
-----
EMBL: U23453; AAC46760.1; -.
DR   FIR; T15295; T15295.
DR   WormPep; B0252.6; CE02422.
KW   Hypothetical protein.
SQ   SEQUENCE 204 AA; 23610 MW; 59FB15536CD22F43 CRC64;
      Query Match          90.0%; Score 36; DB 1; Length 204;
      Best Local Similarity 100.0%; Pred. No. 32;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NMSWL 6
      |||||
DB      96 NMSWL 100

RESULT 2
METE_BIFLO          STANDARD;          PRT;   767 AA.
ID   METE_BIFLO
AC   Q8G651;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   5-methyltetrahydropteroyltylglutamate--homocysteine methyltransferase
DE   (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
DE   (Cobalamin-independent methionine synthase).
DE   METE OR BL0798.
GN   Bifidobacterium longum.
OS   Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC   Bifidobacteriaceae; Bifidobacterium.

```

Q10283 schizosacch
Q9p7m8 schizosacch
P27920 avian infec
P34836 anopheles g
P33506 anopheles q
Q37707 artemia san
Q9m6p7 cochliomyia
P15997 paracentrot
P15997 strongyloce
Q9br46 homo sapien
P81329 methanococc
Q9kre2 vibrio chol

34 33 82.5 1053 1 HMDH_SCHPO
35 33 82.5 1564 1 N184_SCHPO
36 33 82.5 3951 1 VGP1_EBVB
37 32 80.0 53 1 ATP8_ANOGA
38 32 80.0 53 1 ATP8_ANOQU
39 32 80.0 53 1 ATP8_ARTSF
40 32 80.0 54 1 ATP8_COLHO
41 32 80.0 54 1 ATP8_PARLI
42 32 80.0 55 1 ATP8_STRPU
43 32 80.0 151 1 CT78_HUMAN
44 32 80.0 154 1 YB6A_METUA
45 32 80.0 181 1 ISPZ_VIBCH

OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RA "The genome sequence of *Bifidobacterium longum* reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -!- FUNCTION: Catalyzes the transfer of a methyl group from 5-
CC methyltetrahydrofolate to homocysteine resulting in methionine
CC formation (By similarity).
CC -!- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-
CC homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
CC -!- COFACTOR: Zinc; binds one ion per subunit (By similarity).
CC -!- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -!- SIMILARITY: Belongs to the vitamin-B12 independent methionine
CC synthase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB014702; AAN24613.1; -;
CC HAMAP; MF 00172; -; 1.
CC InterPro; IPR002629; Methionine synt.
CC InterPro; IPR006276; Met_syn_B12ind.
CC Pfam; PF01171; Methionine synt; 1.
CC ProDom; PD004692; Methionine synt; 2.
CC TIGRFAMs; TIGR01371; met_syn_B12ind; 1.
CC Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
CC Complete proteome.
CC METAL 652 652 ZINC (BY SIMILARITY).
CC METAL 654 654 ZINC (BY SIMILARITY).
CC METAL 737 737 ZINC (BY SIMILARITY).
CC SEQUENCE 767 AA; 85358 MW; 839AC629629F9D26 CRC64;
CC -----
CC Query Match 90.0%; Score 36; DB 1; Length 767;
CC Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
CC Matches 5; Conservative 0; Mismatches 0; Mismatches 0; Gaps 0;
CC -----
CC QY 1 LNWSW 5
CC Db 569 LNWSW 573
CC -----
CC RESULT 3
CC RIR2 MYCLE STANDARD; PRT; 325 AA.
CC AC Q9CBQ2:
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1)
CC DE (Ribonucleotide reductase small subunit).
CC GN NRDF OR ML1731.
CC OS Mycobacterium leprae.
CC OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CC NCBI_TaxID=1769;
CC RN [1]
CC SEQUENCE FROM N.A.
CC STRAIN=TN;
CC RX MEDLINE=21128732; PubMed=11234002;
CC Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
CC Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
CC Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: CATALYZES THE BIOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FROM
CC THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY
CC FOR DNA SYNTHESIS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized
CC thiorodexin + H(2)O = ribonucleoside diphosphate + reduced
CC thiorodexin.
CC -!- COFACTOR: BINDS 2 IRON IONS (BY SIMILARITY).
CC -!- PATHWAY: DNA replication pathway; first step.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
CC SMALL CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDF THAN TO
CC NRDF.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL583923; CAC30684.1; -;
CC PIR; B87125; B87125.
CC HSP; F17424; 2R2F.
CC Leproma; ML1731; -;
CC InterPro; IPR00358; Ribonucleotide synt.
CC Pfam; PF00268; ribonuc red sm; 1.
CC PROSITE; PS00368; RIBONUC RED SMALL; 1.
CC Oxidoreductase; DNA replication; Iron; Complete proteome.
CC METAL 73 73 IRON 1 (BY SIMILARITY).
CC METAL 104 104 IRON 1 AND 2 (BY SIMILARITY).
CC METAL 107 107 IRON 1 (BY SIMILARITY).
CC METAL 164 164 IRON 2 (BY SIMILARITY).
CC METAL 198 198 IRON 2 (BY SIMILARITY).
CC METAL 201 201 IRON 2 (BY SIMILARITY).
CC ACT_SITE 111 111 BY SIMILARITY.
CC SEQUENCE 325 AA; 37316 MW; A80D29751183358B CRC64;
CC -----
CC Query Match 87.5%; Score 35; DB 1; Length 325;
CC Best Local Similarity 66.7%; Pred. No. 71;
CC Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 LNWSW 6
CC Db 15 INWNW 20
CC -----
CC RESULT 4
CC IKKA HUMAN STANDARD; PRT; 745 AA.
CC ID IKKA_HUMAN Q13132; Q92467;
CC AC O1511; O14666; Q13132; Q92467;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
CC DE (I kappa-B kinase alpha) (IKK- α) (IKK- α) (IKK- α) (IKK- α) (IKK- α)
CC DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
CC kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
CC GN CHUK OR IKKA.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CC RN [1]

SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RA TISSUE=T-cell;
 RX MEDLINE=97386461; PubMed=9244310;
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
 RT "Identification and characterization of an IkappaB kinase.";
 RL Cell 90:373-383(1997).
 RN [2]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97394468; PubMed=9252186;
 RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RA "A cytokine-responsive IkappaB kinase that activates the transcription
 RT factor NF-kappaB.";
 RT Nature 388:548-554(1997).
 RL [3]
 RN SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [5]
 RN SEQUENCE OF 32-745 FROM N.A.
 RP TISSUE=Cervical carcinoma;
 RX MEDLINE=96258427; PubMed=877433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RN PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RT Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RN PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RN [8]
 RN IKKA-IKKB BINDING.
 RP MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RA "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [9]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RX

Jobin C., Sartor R.B.;
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11]
 RN SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKBK.
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RA "Regulation of SRC-3 (PCIP/ACTR/ATB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKB-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKBK and CREBBP.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF012890; AAC51662.1; -;
 DR EMBL; AF009225; AAC51671.1; -;
 DR EMBL; AF080157; AAD0896.1; -;
 DR EMBL; U22512; AAC50713.1; -;
 DR HSP; 063450; 1A06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0008384; P:IkappaB kinase activity; TAS.
 DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
 DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD0000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 FT DECREASE OF KINASE ACTIVITY.

FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 686 687 TS -> DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 87.5%; Score 35; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNWSWL 6
 Db 738 LDWSWL 743
 RESULT 5
 IKKA MOUSE STANDARD; PRT; 745 AA.
 ID IKKA MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.1-)
 DE (I kappa-B kinase alpha) (IKK α) (IKK-A) (Ikappab kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/C;
 RX MEDLINE=96044444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RT chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/C;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito C., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustingich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Geleziunas R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKK α and IKK-beta-P65-P50
 CC complex..A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKK α , IKK β and CREBBP (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
 CC -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.

CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC ENBL; U12473; AAC52589.1; --
CC EMBL; AK018671; BAB31335.1; --
CC PIR; I49101; I49101.
CC HSP; Q63450; I406.
CC MGD; MGI:199484; Chuk.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser Thr pkinase.
CC Pfam; PF00069; pkinase; 1
CC PRINTS; PR0109; TYRKINASE.
CC ProDom; PD000001; Prot kinase; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation; Alternative splicing.
CC DOMAIN 15 300
CC FT DOMAIN 455 476
CC FT DOMAIN 738 743
CC FT NP_BIND 21 29
CC FT BINDING 44 44
CC FT ACT_SITE 144 144
CC FT MOD_RES 23 23
CC FT MOD_RES 176 176
CC FT MOD_RES 452 471
CC FT VARSPLIC 472 745
CC FT VARSPLIC 577 584
CC FT VARSPLIC 585 745
CC FT CONFLICT 236 236
CC FT CONFLICT 400 400
CC FT SEQUENCE 745 AA; 84728 MW; 3FEF5582AFP92233 CRC64;
CC
CC Query Match 87.5%; Score 35; DB 1; Length 745;
CC Best Local Similarity 83.3%; Pred. No. 1.6e+02;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 LKWSWL 6
CC DB 738 LDWSWL 743
CC
CC RESULT 6
CC IKKB HUMAN
CC ID -IKKB_HUMAN STANDARD; PRT; 756 AA.
CC AC O14920; O75327;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
CC DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
CC DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
CC GN IKKB OR IKKB.
CC OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Roche M., Goeddel D.V.;
RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
RT 8p12-->p11 by in situ hybridization.";
RL Cytogenet. Cell Genet. 82:32-33(1998).
RN [5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [7]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
RN [8]

RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKBG.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
O'Malley B.W.;
RT "Regulation of SRC-3 (pCTP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (by similarity).
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
CC complex. Phosphorylated IKB-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF029684; AAC51860.1; -;
DR EMBL; AF080158; AAD08997.1; -;
DR EMBL; AF031416; AAC64675.1; -;
DR EMBL; BC062331; AAH06231.1; -;
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:5960; IKKBK.
DR MIM; 603258; -;
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0005524; F:ATP binding activity; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR00719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 PHOSPHORYLATION.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
FT EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT CONFLICT 231 255 WHSKVRQKSEVDIVVSEDINGTVKF -> CVRMMPDGTVAHS

FT CONFLICT 425 425 CNPSTLGRGRWI (IN REF. 5).
FT Q -> H (IN REF. 1).
SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
Query Match 87.5%; Score 35; DB 1; Length 756;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNWSWL 6
DB 737 LDWSWL 742
RESULT 7
IKKB_MOUSE
ID IKKB_MOUSE STANDARD; PRT; 757 AA.
AC 088351; Q9R1J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIBK).
GN IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of Ikb.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=99455228; PubMed=10523828;
RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
RT developmentally regulated protein kinase.";
RL Oncogene 18:5514-5524(1999).
RN [4]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [5]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RN JOBIN C., SARTOR R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can

also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50 complex. Phosphorylated IKK-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG and CREBBP (By similarity).

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.

-1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout the mouse embryo, at E9.5 day its expression begins to be localized to the brain, neural ganglia, neural tube, and in liver at E12.5 day. At E15.5 day, the expression is further restricted to specific tissues of the embryo.

-1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK. Weakly autophosphorylated.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.

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EMBL; AF026524; AAC23557.1; -.
 EMBL; AF088910; AAD52095.1; -.
 HSP; O63450; 1A06.
 MGI; 1338071; Ikbb.
 InterPro; IPR000719; Prot_kinase.
 InterPro; IPR002290; Ser_thr_pkinase.
 InterPro; IPR001245; Tyr_pkinase.
 Pfam; PF00069; pkinase; 1.
 PRINTS; PR00109; TYRKINASE.
 ProDom; PD000001; Prot_kinase; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.

KW Phosphorylation.

FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 K -> E (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDSWQLQMEDEERCSLEQACD -> VTA (IN REF. 2).

SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;

Query Match 87.5%; Score 35; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKWSWL 6
 |:|:|:|
 Db 737 LDWSWL 742

RESULT 8
 IKKB RAT
 ID -IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (SC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKBK) (IKK-beta) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKBK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 OX [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RA "IKK beta in megakaryocyte differentiation."; .
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
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 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection."; .
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC **-1- FUNCTION:** Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC **-1- SUBUNIT:** Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBBP (By similarity).
 CC **-1- SUBCELLULAR LOCATION:** Cytoplasmic.
 CC **-1- PTM:** Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC **-1- SIMILARITY:** BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.

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EMBL; AF115282; AAF21978.1; -.
 HSP; O63450; 1A06.
 InterPro; IPR000719; Prot_kinase.
 InterPro; IPR002290; Ser_thr_pkinase.
 InterPro; IPR001245; Tyr_pkinase.
 Pfam; PF00069; pkinase; 1.
 PRINTS; PR00109; TYRKINASE.
 ProDom; PD000001; Prot_kinase; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.

KW Phosphorylation.

FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 K -> E (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDSWQLQMEDEERCSLEQACD -> VTA (IN REF. 2).

SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;

Query Match 87.5%; Score 35; DB 1; Length 757;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKWSWL 6
 |:|:|:|
 Db 737 LDWSWL 742

RESULT 8
 IKKB RAT
 ID -IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

FT MOD RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 757 AA; 86866 MW; 3AF6A6A7DF91F9C CRC64;

Query Match 87.5%; Score 35; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. NO. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6
Db 737 LDWSWL 742

RESULT 9
Y451_SVNY3
ID Y451_SVNY3 STANDARD; PRT; 154 AA.
AC P/4676;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sl10451.
GN SL10451.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasaki S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- SIMILARITY: BELONGS TO THE UPF0039 (ELAA) FAMILY.
CC
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CC
CC EMBL; D90917; BAA18794.1; -.
CC PIR; S76882; S76882.
CC InterPro: IPR000182; GCN5acetyltransf.
CC Pfam; PF00583; Acetyltransf; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 154 AA; 17612 MW; C84777660627F9C2 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 154;
Best Local Similarity 80.0%; Pred. NO. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSW 5
Db 3 INWSW 7

RESULT 10
NQ08_PARDE
ID NQ08_PARDE STANDARD; PRT; 345 AA.
AC P29920;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NADH-quinone oxidoreductase chain 8 (EC 1.6.99.5) (NADH dehydrogenase
DE 1, chain 8) (NDH-1, chain 8).
GN NQ08.

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OS Paracoccus denitrificans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=266;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93136200; PubMed=8422400;
RA Xu X., Mateu-Yagi A., Yagi T.;
RT "DNA sequencing of the seven remaining structural genes of the gene
RT cluster encoding the energy-transducing NADH-quinone oxidoreductase
RT of Paracoccus denitrificans.";
RL Biochemistry 32:968-981(1993).
CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be ubiquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient.
CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNIT NQ07-14
CC CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC
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CC
CC EMBL; L02354; AAA25592.1; -.
CC PIR; C45456; C45456.
CC InterPro: IPR001694; Resp_NADH_dhl.
CC Pfam; PF00146; NADHdh; 1.
CC PROSITE; PS00667; COMPLEX1_ND1_1; 1.
CC PROSITE; PS00668; COMPLEX1_ND1_2; 1.
CC Oxidoreductase; NAD; Quinone; Ubiquinone; Transmembrane.
FT TRANSMEM 15 35 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT TRANSMEM 190 210 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
FT TRANSMEM 278 298 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
SQ SEQUENCE 345 AA; 38751 MW; E33B667E569506B4 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 345;
Best Local Similarity 83.3%; Pred. NO. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LNWSWL 6
Db 191 LNWSWL 196

RESULT 11
NUOH_RHOCA
ID NUCOH_RHOCA STANDARD; PRT; 345 AA.
AC P42032;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NADH-quinone oxidoreductase chain H (EC 1.6.99.5) (NADH dehydrogenase
DE 1, chain H) (NDH-1, chain H).
GN NUOH OR NDHA.
OS Rhodobacter capsulatus (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.

```

OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RX MEDLINE=92233948; PubMed=1568483;
RA Dupuis A.;
RT "Identification of two genes of Rhodobacter capsulatus coding for
RT proteins homologous to the ND1 and 23 kDa subunits of the
RT mitochondrial Complex I.";
RL FEBS Lett. 301:215-218(1992).
CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be ubiquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient.
CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC -----
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CC -----
DR EMBL; AF029365; AAC24997.1; -;
DR EMBL; Z11611; CAA77684.1; -;
DR PIR; S22368; S22368.
DR InterPro; IPR001694; Resp_NADH_dh1.
DR Pfam; PF00146; NADhdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Oxidoreductase; NAD; Quinone; Ubiquinone; Transmembrane.
FT TRANSMEM 14 34 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT TRANSMEM 190 210 POTENTIAL.
FT TRANSMEM 248 268 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
SQ SEQUENCE 345 AA; 37852 MW; 5F9E9D640D911854 CRC64;
Query Match 85.0%; Score 34; DB 1; Length 345;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LNWSWL 6
Db 191 LNWYWL 196
RESULT 12
ID T1SD_ECOLI STANDARD; PRT; 444 AA.
AC P06931;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Type I restriction enzyme EcodI specificity protein (S protein)
DE (S.EcodI).
GN HSDS OR HSS.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / E166;

RX MEDLINE=83216118; PubMed=6304321;
RA Gough J.A., Murray N.E.;
RT "Sequence diversity among related genes for recognition of specific
RT targets in DNA molecules.";
RL J. Mol. Biol. 166:11-19(1983).
CC -1- FUNCTION: THE M AND S SUBUNITS TOGETHER FORM A METHYLTRANSFERASE
CC (MTASE) THAT METHYLATES TWO ADENINE RESIDUES IN COMPLEMENTARY
CC STRANDS OF BIPARTITE DNA RECOGNITION SEQUENCE. IN THE PRESENCE OF
CC THE R SUBUNIT THE COMPLEX CAN ALSO ACT AS AN ENDONUCLEASE. BINDING
CC TO THE SAME TARGET SEQUENCE BUT CUTTING THE DNA SOME DISTANCE FROM
CC THIS SITE. WHETHER THE DNA IS CUT OR MODIFIED DEPENDS ON THE
CC METHYLATION STATE OF THE TARGET SEQUENCE. WHEN THE TARGET SITE IS
CC UNMODIFIED, THE DNA IS CUT. WHEN THE TARGET SITE IS
CC HEMIMETHYLATED, THE COMPLEX ACTS AS A MAINTENANCE MTASE MODIFYING
CC THE DNA SO THAT BOTH STRANDS BECOME METHYLATED. SUBUNIT S DICTATES
CC DNA SEQUENCES SPECIFICITY. THE ECODI ENZYME RECOGNIZES 5'-
CC TTA(N7)GTCC-3'.
CC -1- SUBUNIT: THE TYPE I RESTRICTION/MODIFICATION SYSTEM IS COMPOSED
CC OF THREE POLYPEPTIDES R,M AND S.
CC -1- DOMAIN: CONTAINS TWO DNA RECOGNITION DOMAINS, EACH SPECIFYING
CC RECOGNITION OF ONE OF THE TWO DEFINED COMPONENTS OF THE TARGET
CC SEQUENCE.
CC -1- SIMILARITY: BELONGS TO THE TYPE-I RESTRICTION SYSTEM S METHYLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; V00287; CAA23553.1; -;
DR REBASE; 3640; S.ECODI.
DR InterPro; IPR000055; Rest mod DNA.
DR Pfam; PF01420; Methylase S; 2.
KW Restriction system; DNA-Binding.
SQ SEQUENCE 444 AA; 49893 MW; 14BE17B5325294F0 CRC64;
Query Match 85.0%; Score 34; DB 1; Length 444;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 NWSWL 6
Db 215 NWSWM 219
RESULT 13
ID YAWD_SCHPO STANDARD; PRT; 612 AA.
AC Q10187;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein C3F10.13 in chromosome I.
GN SPAC3F10.13.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Muncall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Certutti L., Lowe T., McCombie W.R., Paulsen J., Forsberg S.L.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC -!- SIMILARITY: Contains 1 UBA domain.
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 CC -----
 DR EMBL; Z69369; CAA93311.1; -;
 DR PIR; T38714; T38714.
 DR GeneDB SPombe; SPAC3F10.13; -;
 DR InterPro; IPR000449; UBA_domain.
 DR Pfam; PF00627; UBA; 1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS0030; UBA; 1.
 KW Hypothetical protein; Glycoprotein; Transmembrane.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 437 457 POTENTIAL.
 FT DOMAIN 3 42 UBA.
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 612 AA; 68720 MW; 3FBFDF380BF554CD CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 612;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NWSWL 6
 Db 296 NWSWI 300
 ID ROR1 DROME STANDARD; PRT; 685 AA.
 AC Q24488;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor
 DE (EC 2.7.1.112) (dRor).
 GN ROR OR CG4926.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 STRAIN=Canton-S; TISSUE=Larval brain;
 MEDLINE=93348222; PubMed=8394009;
 RA Wilson C., Guberhan D.C.I., Steller H.;
 RT "Dror, a potential neurotrophic receptor gene, encodes a Drosophila
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
 RT kinases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
 RN [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Berkley;
 CC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [3]
 CC SEQUENCE OF 545-597 FROM N.A.
 CC MEDLINE=98401146; PubMed=9731193;
 RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT Polymerase chain reaction with genomic DNA.";
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -!- FUNCTION: Tyrosine-protein kinase receptor that functions during
 CC early stages of neuronal development.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
 CC system.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR
 CC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L20297; AAA28860.1; -;
DR EMBL; A5003628; AAF52885.1; -;
DR EMBL; AJ002908; CAA05743.1; -;
DR PIR; A48289; A48289.
DR HSP; P11362; IFGK.
DR FlyBase; FBgn010407; Ror.
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0004713; F: protein tyrosine kinase activity; NAS.
DR GO; GO:0007417; P: central nervous system development; IEP.
DR GO; GO:0006468; P: protein amino acid phosphorylation; NAS.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002011; RTK_kinaseII.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00239; RECEPTOR TYR_KIN_II; 1.
KW Transferase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KW Developmental protein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 685 TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT RECEPTOR ROR.
FT TRANSMEM 318 338 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 339 685 POTENTIAL.
FT DOMAIN 36 225 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 310 FZ.
FT DOMAIN 410 677 KRINGLE.
FT NP_BIND 416 424 PROTEIN KINASE.
FT BINDING 442 442 ATP (BY SIMILARITY).
FT ACT_SITE 539 539 BY SIMILARITY.
FT MOD_RES 565 565 PHOSPHORYLATION (AUTO-) (BY
SIMILARITY).
FT MOD_RES 569 569 PHOSPHORYLATION (AUTO-) (BY
SIMILARITY).
FT MOD_RES 570 570 PHOSPHORYLATION (AUTO-) (BY
SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 685 AA; 78142 MW; 526162D27D5FD7C7 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 685;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6
| | | | |
Db 259 LNWSWL 264

RESULT 15
ATP8_ASTPE

ID ATP8_ASTPE STANDARD; PRT; 54 AA.
AC Q33822;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DR ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN MTATP8 OR ATP8.
OS Asterina pectinifera (Starfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
RX NCBI_TaxID=7594;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95402598; PubMed=7672576;
RA Asakawa S., Himeno H., Miura K.-I., Watanabe K.;
RT "Nucleotide sequence and gene organization of the starfish Asterina
pectinifera mitochondrial genome.";
RL Genetics 140:1047-1060(1995).
CC -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC -!- (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPase COMPLEX.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: BELONGS TO THE ATPase PROTEIN 8 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

DR EMBL; D16387; BAA03883.1; -;
DR PIR; S70600; S70600.
DR InterPro; IPR001421; ATPase8_mit.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 8 28 POTENTIAL.
SQ SEQUENCE 54 AA; 6241 MW; 9EABDACEB9CDF5F1 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 54;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5
| | | | |
Db 49 LNWTW 53

Search completed: February 18, 2004, 14:28:07
Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	204	2 C83748	hypothetical prote
2	37	92.5	337	2 AG2946	hypothetical prote
3	37	92.5	337	2 C98336	probable integral
4	36	90.0	204	2 T15295	hypothetical prote
5	36	90.0	380	2 T11041	ubiquinol-cytochro
6	36	90.0	460	2 AG0965	probable glycosyl
7	36	90.0	590	2 C83491	hypothetical prote
8	36	90.0	744	2 T10035	hypothetical prote
9	35	87.5	116	2 T03472	conserved hypothet
10	35	87.5	321	2 T24773	hypothetical prote
11	35	87.5	325	2 B87125	ribonucleotide red
12	35	87.5	745	1 I49101	conserved helix-lo
13	35	87.5	777	2 T09056	glucan 1,3-beta-gl
14	34	85.0	154	2 S76882	hypothetical prote
15	34	85.0	345	2 C45456	NADH2 dehydrogenas
16	34	85.0	345	2 S22368	NADH2 dehydrogenas
17	34	85.0	355	2 F70983	probable serine pr
18	34	85.0	612	2 T38714	hypothetical prote
19	34	85.0	685	1 A48289	neurotrophic recep
20	34	85.0	903	2 E88221	protein TOH3.2 [i
21	34	85.0	919	2 T37062	probable transcrip
22	34	85.0	980	2 T24336	hypothetical prote
23	34	85.0	1147	2 T35781	hypothetical prote
24	33	82.5	52	2 D90532	HA-transporting tw
25	33	82.5	54	2 S70600	hypothetical prote
26	33	82.5	72	2 AD2464	hypothetical prote
27	33	82.5	169	2 T38724	mitochondrial benz
28	33	82.5	169	2 JC1393	benzodiazepine rec
29	33	82.5	169	2 I57953	peripheral-type be

30	33	82.5	169	2 A53405	peripheral-type be
31	33	82.5	169	2 S14257	benzodiazepine rec
32	33	82.5	169	2 A39473	peripheral-type be
33	33	82.5	169	2 JE0149	peripheral benzoda
34	33	82.5	275	2 AB2466	ABC transporter su
35	33	82.5	281	2 AF2161	cation-efflux syst
36	33	82.5	289	2 A82953	ATP synthase A cha
37	33	82.5	310	2 C84701	hypothetical prote
38	33	82.5	315	2 A86710	transposase of IS9
39	33	82.5	315	2 G85712	transposase of IS9
40	33	82.5	315	2 D86741	transposase of IS9
41	33	82.5	315	2 G86787	transposase of IS9
42	33	82.5	315	2 G86794	transposase of IS9
43	33	82.5	315	2 C86814	transposase of IS9
44	33	82.5	315	2 B86837	transposase of IS9
45	33	82.5	315	2 E86860	transposase of IS9

ALIGNMENTS

RESULT 1

C83748

hypothetical protein BH0787 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: C83748

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83748

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-204 <STO>

A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BA04506.1; GSPDB:GN01

A;Experimental source: strain C-125

C:Genetics:

A;Gene: BH0787

C;Superfamily: Bacillus subtilis conserved hypothetical protein yeeL

Query Match 92.5%; Score 37; DB 2; Length 204;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6

DB 22 LNMAWL 27

RESULT 2

AG2946

hypothetical protein Atu3173 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C:Accession: AG2946

R;Wood, D.W.; Stutbal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

star, E.W

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AG2946

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-337 <KUP>

A;Cross-references: GB:AE008689; PIDN:AAL43989.1; PID:g17741546; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)

C:Genetics:

A;Gene: Atu3173

A;Map position: linear chromosome

Qy	2	NWSWL	6
Db	96	NWSWL	100
RESULT 5			
T11041			

```

Query Match          90.0%; Score 36; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 NWSWL 6
      |||||
Db      418 NWSWL 422

RESULT 7
C83491
hypothetical protein PA1242 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83491
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey,

```



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adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83491
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <STO>
A:Cross-references: GB:AE004553; GB:AE004091; NID:g9947164; PIDN:AG04631.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1242

Query Match          90.0%; Score 36; DB 2; Length 590;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5
Db 360 LNWSW 364
|||||

RESULT 8
T10035
hypothetical protein MLCB628.16c - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C:Accession: T10035
R:Eiglmeyer, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A:Title: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A:Reference number: Z16917; MUID:93188700; PMID:8446027
A:Accession: T10035
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-744 <BIG>
A:Cross-references: EMBL:Y14967; NID:g2370268; PIDN:CAA75203.1; PID:g2370283
C:Genetics:
A:Note: MLCB628.16c

Query Match          90.0%; Score 36; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6
Db 265 NWSWL 269
|||||

RESULT 9
T03472
conserved hypothetical protein - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C:Accession: T03472
R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haseelkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A:Title: Sequence of a 189-Kb segment of the chromosome of Rhodobacter capsulatus SB1003
A:Reference number: Z14955; MUID:97404404; PMID:9256491
A:Accession: T03472
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-116 <VLC>
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16125.1; PID:g3128273
C:Genetics:
A:Map position: 1

Query Match          87.5%; Score 35; DB 2; Length 116;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6

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Db 63 LWSWL 68
|||||

RESULT 10
T24773
hypothetical protein T10B10.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T24773
R:Sims, M.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19934
A:Accession: T24773
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-321 <WIL>
A:Cross-references: EMBL:Z72514; PIDN:CAA96680.1; GSPDB:GN000028; CESP:T10B10.8
A:Experimental source: clone T10B10
C:Genetics:
A:Gene: CESP:T10B10.8
A:Map position: X
A:Introns: 40/3; 54/2; 64/3; 123/3; 229/2; 262/3

Query Match          87.5%; Score 35; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6
Db 221 LNWSWL 226
|||||

RESULT 11
E87125
ribonucleotide reductase small subunit [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: E87125
R:Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: E87125
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <STO>
A:Cross-references: GB:AL450380; NID:gl3093483; PIDN:CAC30684.1; GSPDB:GN00147
C:Genetics:
A:Gene: nrdf
C:Superfamily: ribonucleoside-diphosphate reductase beta

Query Match          87.5%; Score 35; DB 2; Length 325;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
Db 15 INWSWL 20
|||||

RESULT 12
I49101
conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I49101
R:Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

```

A;Reference number: I49101; MUID:96044444; PMID:7558004
 A;Accession: I49101
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-745 <RES>
 A;Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
 C;Genetics:

A;Gene: CHUK
 C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolog
 C;Keywords: ATP; phosphotransferase
 F;13-283/Domain: protein kinase homology <KIN>

Query Match 87.5%; Score 35; DB 1; Length 745;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 :|||
 Db 738 LQWSWL 743

RESULT 13

T09056
 glucan 1,3-beta-glucosidase (EC 3.2.1.58) - Ampelomyces quisqualis
 N;Alternate names: exo-beta-1,3-glucanase
 C;Species: Ampelomyces quisqualis
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: T09056

R;Rotem, Y.; Yarden, O.; Szejnberg, A.
 submitted to the EMBL Data Library, October 1997
 A;Reference number: Z16541

A;Accession: T09056

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-777 <ROT>

A;Cross-references: EMBL:AF029354; NID:g3004862; PID:g3004863

A;Experimental source: strain AQ10

C;Genetics:

A;Gene: exga

C;Function:

A;Description: catalyzes the hydrolysis of beta-D-glucose units from the non-reducing en

C;Keywords: glycosidase; hydrolase

Query Match 87.5%; Score 35; DB 2; Length 777;
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 :|||
 Db 266 MNWSWL 271

RESULT 14

S76882

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S76882

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76882

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-154 <KAN>

A;Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAAL8794.1; PID:g165388

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Start codon: GTG

C;Superfamily: hypothetical protein b2267

Query Match 85.0%; Score 34; DB 2; Length 154;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5
 :|||
 Db 3 INWSW 7

RESULT 15

C45456

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Paracoccus denitrificans
 N;Alternate names: NADH-quinone oxidoreductase chain 1
 C;Species: Paracoccus denitrificans

C;Date: 24-Feb-1994 #sequence_revision 15-Oct-1994 #text_change 03-Jun-2002

C;Accession: C45456

R;Xu, X.; Matsuno-Yagi, A.; Yagi, T.

Biochemistry 32, 968-981, 1993

A;Title: DNA sequencing of the seven remaining structural genes of the gene cluster enc

A;Reference number: A45456; MUID:93136200; PMID:8422400

A;Accession: C45456

A;Molecule type: DNA

A;Residues: 1-345 <XU1>

A;Cross-references: GB:L02354; NID:g150606; PIDN:AAA25592.1; PID:g150608

A;Note: sequence extracted from NCBI backbone (NCBIN:123409, NCBIPI:123413)

C;Genetics:

A;Gene: NQ08

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1

C;Keywords: membrane-associated complex; NAD; oxidative phosphorylation; oxidoreductase;

Query Match 85.0%; Score 34; DB 2; Length 345;
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 :|||
 Db 191 LNWTWL 196

Search completed: February 18, 2004, 14:38:43

Job time : 7.5921 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-9
Perfect score: 40
Sequence: 1 LNWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	117	4	US-09-149-476-360 Sequence 360, App
2	36	90.0	609	4	US-09-252-991A-20134 Sequence 20134, A
3	35	87.5	745	2	US-08-887-518-3 Sequence 3, Appli
4	35	87.5	745	2	US-09-023-321-3 Sequence 3, Appli
5	35	87.5	745	2	US-08-890-853-4 Sequence 4, Appli
6	35	87.5	745	2	US-09-032-475-3 Sequence 3, Appli
7	35	87.5	745	2	US-09-099-125A-4 Sequence 4, Appli
8	35	87.5	745	2	US-09-099-124A-4 Sequence 4, Appli
9	35	87.5	745	3	US-09-032-476-4 Sequence 4, Appli
10	35	87.5	745	3	US-08-890-854-4 Sequence 4, Appli
11	35	87.5	745	3	US-09-023-324-4 Sequence 4, Appli
12	35	87.5	745	3	US-09-168-629-2 Sequence 2, Appli
13	35	87.5	745	3	US-08-910-820-10 Sequence 10, Appl
14	35	87.5	745	3	US-08-810-131A-2 Sequence 2, Appli
15	35	87.5	745	4	US-09-109-986-4 Sequence 4, Appli
16	35	87.5	745	4	US-09-844-908-10 Sequence 10, Appl
17	35	87.5	745	4	US-09-868-758-3 Sequence 3, Appli
18	35	87.5	756	2	US-08-887-518-4 Sequence 4, Appli
19	35	87.5	756	2	US-09-023-321-4 Sequence 2, Appli
20	35	87.5	756	2	US-08-890-853-2 Sequence 2, Appli
21	35	87.5	756	2	US-09-032-475-4 Sequence 4, Appli
22	35	87.5	756	2	US-09-099-125A-2 Sequence 2, Appli
23	35	87.5	756	2	US-09-099-124A-2 Sequence 2, Appli
24	35	87.5	756	3	US-09-032-476-2 Sequence 2, Appli
25	35	87.5	756	3	US-08-890-854-2 Sequence 2, Appli
26	35	87.5	756	3	US-09-023-324-2 Sequence 2, Appli
27	35	87.5	756	3	US-09-168-629-15 Sequence 15, Appl

28	35	87.5	756	3	US-08-910-820-9 Sequence 9, Appli
29	35	87.5	756	4	US-09-109-986-2 Sequence 2, Appli
30	35	87.5	756	4	US-09-844-908-9 Sequence 9, Appli
31	35	87.5	756	4	US-09-868-758-4 Sequence 4, Appli
32	35	87.5	996	4	US-09-417-197-123 Sequence 123, App
33	35	87.5	997	4	US-09-417-197-121 Sequence 121, App
34	34	85.0	144	4	US-09-252-991A-21138 Sequence 21138, A
35	34	85.0	355	3	US-08-818-112-79 Sequence 79, Appl
36	34	85.0	355	4	US-08-818-111-80 Sequence 80, Appl
37	34	85.0	355	4	US-09-056-556-79 Sequence 79, Appl
38	34	85.0	355	4	US-09-072-596-80 Sequence 80, Appl
39	34	85.0	454	4	US-09-252-991A-28780 Sequence 28780, A
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41	33	82.5	303	4	US-09-253-991A-19160 Sequence 19160, A
42	33	82.5	396	4	US-09-134-001C-4443 Sequence 4443, Ap
43	33	82.5	455	2	US-08-272-255-14 Sequence 14, Appl
44	33	82.5	455	3	PCT-US95-08565-14 Sequence 14, Appl
45	33	82.5	471	4	US-08-311-731A-168 Sequence 168, App

ALIGNMENTS

RESULT 1
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; Sequence 360, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
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; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/040,626
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61	EARLIER FILING DATE: 1997-08-22
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63	EARLIER FILING DATE: 1997-08-22
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65	EARLIER FILING DATE: 1997-06-06
66	EARLIER APPLICATION NUMBER: 60/057,650
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69	EARLIER FILING DATE: 1997-08-22

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; EARLIER FILING DATE: 1937-09-05
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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1937-10-02

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Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels

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Db	30	LN	SW	34

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RESULT 2
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; Sequence 20134, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

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Query Match 90.0%; Score 36; DB 4; Length 609;
Best Local Similarity 100.0%; Pred.No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels

Qy 1 LNWSW 5
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US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
;   APPLICANT: Rothe, Mike
;   APPLICANT: Wu, Lin
;   TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;     STREET: 268 BUSH STREET, SUITE 3200
;     CITY: SAN FRANCISCO
;     STATE: CALIFORNIA
;     COUNTRY: USA
;     ZIP: 94104
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/887,518
;     FILING DATE:
;     CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:

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, NAME: OSMAN, RICHARD A
, REGISTRATION NUMBER: 36,627
, REFERENCE/DOCKET NUMBER: T97-008
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (415) 343-4341
, TELEFAX: (415) 343-4342
, INFORMATION FOR SEQ ID NO: 3:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 745 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
US-08-887-518-3

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Query Match      87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5: Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LNWSWL 6
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p6 738 LDWSWL 743

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RESULT 4
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

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Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5: Conservative 1; Mismatches 0; Indels

Qy 1 LNWSWL 6

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Db 738 LDWSWL 743
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: 08/887,518
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
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Db 738 LDWSWL 743

RESULT 7
US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/099,125A
; APPLICATION NUMBER: 08/890,853
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 87.5%; Score 35; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
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Db 738 LDWSWL 743

RESULT 6
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-125A-4

Query Match 87.5%; Score 35; DB 2; Length 745;
 Best Local Similarity 83.3%; Pred. No. 7.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
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 Db 738 LDWSWL 743

RESULT 8

US-09-099-124A-4
 ; Sequence 4, Application US/09099124A
 ; Patent No. 5939302
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Wotonicz, John
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104

COMPUTER READABLE FORM:
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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,124A
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA: US/08/890,853
 APPLICATION NUMBER: US/08/890,853
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-124A-4

Query Match 87.5%; Score 35; DB 2; Length 745;
 Best Local Similarity 83.3%; Pred. No. 7.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
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 Db 738 LDWSWL 743

RESULT 9

US-09-032-476-4
 ; Sequence 4, Application US/09032476
 ; Patent No. 6235492
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaodan
 APPLICANT: R gnier, Catherine
 TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/032,476
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA: 08/890,854
 APPLICATION NUMBER: 08/890,854
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-032-476-4

Query Match 87.5%; Score 35; DB 3; Length 745;
 Best Local Similarity 83.3%; Pred. No. 7.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6
 |:|||||
 Db 738 LDWSWL 743

RESULT 10

US-08-890-854-4
 ; Sequence 4, Application US/08890854
 ; Patent No. 6235512
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothe, Mike
 ; APPLICANT: Cao, Zhaodan
 ; APPLICANT: R gnier, Catherine
 ; TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,854
 FILING DATE:

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-910-820-10

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6

|:||||

Db 738 LQMSWL 743

RESULT 14

US-08-810-131A-2

Sequence 2, Application US/08810131A

Patent No. 6268194

GENERAL INFORMATION:

APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,131A

FILING DATE: 25-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2408

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-810-131A-2

Query Match 87.5%; Score 35; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6

|:||||

Db 738 LQMSWL 743

RESULT 15

US-09-109-986-4

Sequence 4, Application US/09109986

Patent No. 6479266

GENERAL INFORMATION:

APPLICANT: Roche, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R. Gnier, Catherine
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/109,986

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-109-986-4

Query Match 87.5%; Score 35; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNWSWL 6

|:||||

Db 738 LQMSWL 743

Search completed: February 18, 2004, 14:41.48
Job time: 8.06579 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-8
Sequence: 1 LEWSWL 6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTEMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	36	92.3	387 10 Q8LJE0
2	36	92.3	482 5 Q9VQ45
3	36	92.3	544 10 Q9FEE1
4	36	92.3	645 8 Q63620
5	36	92.3	740 6 Q95KV1
6	36	92.3	745 11 Q8CBT3
7	36	92.3	756 6 Q95KV0
8	35	89.7	48 16 Q8VKB2
9	35	89.7	110 16 Q8DY14
10	35	89.7	173 17 Q9HHP7
11	35	89.7	196 13 Q9VH31
12	35	89.7	276 2 Q47020
13	35	89.7	311 5 Q94380
14	35	89.7	371 5 Q25333
15	35	89.7	387 16 Q8YFW8
16	35	89.7	390 16 Q8G212

17	35	89.7	391 2 Q8KPK4
18	35	89.7	391 16 Q8YPT8
19	35	89.7	469 10 Q8RXB1
20	35	89.7	481 11 Q8VCV5
21	35	89.7	522 10 Q9SJ13
22	35	89.7	522 10 Q8LAH9
23	35	89.7	522 10 Q8H175
24	35	89.7	604 4 Q9V475
25	35	89.7	645 2 Q69315
26	35	89.7	645 2 Q8GEA9
27	35	89.7	683 4 Q96DU7
28	35	89.7	823 5 Q8SQQ0
29	35	89.7	1173 16 Q8ERJ0
30	35	89.7	1345 16 Q9L060
31	35	89.7	1367 16 Q9PPR8
32	35	89.7	1379 13 P79701
33	35	89.7	1591 3 Q9HFW1
34	35	89.7	2054 5 Q9GZ13
35	34	87.2	116 2 Q68039
36	34	87.2	135 2 Q05744
37	34	87.2	145 5 Q8I0L0
38	34	87.2	248 4 Q8WZ05
39	34	87.2	321 5 Q94515
40	34	87.2	355 16 Q07175
41	34	87.2	395 17 Q97V10
42	34	87.2	398 16 P74568
43	34	87.2	465 16 Q8P701
44	34	87.2	469 16 Q8FG82
45	34	87.2	471 16 Q8P4L6

ALIGNMENTS

RESULT 1

Q8LJE0 PRELIMINARY; PRT; 387 AA.
ID Q8LJE0
AC Q8LJE0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0496H05.7 protein.
GN P0496H05.7.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0496H05.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003267; BAC03279.1; -
DR Gramene; Q8LJE0; -
SQ SEQUENCE 387 AA; 41273 MW; C3D070BB59808ACB CRC64;

Query Match 92.3%; Score 36; DB 10; Length 387;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6

:|||||
242 VEWSWL 247

RESULT 2

Q9VQ45 PRELIMINARY; PRT; 482 AA.
ID Q9VQ45
AC Q9VQ45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE CG31664 protein.
 GN CG31933 OR CG15622.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
 RA Shue B.C., Sinden-Kiamos I., Simpson M., Skupski M.P., Shen T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Cocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorset V., Doup L.E., Doyle C., Drensek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., S.E.;
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003585; AAF51336.2; --
 DR FlyBase; FBgn0051664; CG31664.
 DR FlyBase; FBgn0051933; CG31933.
 DR InterPro; IPR004245; DUF229.
 DR Pfam; PF02995; DUF229; 1.
 SQ SEQUENCE 482 AA; 55495 MW; A91F2F2D2DFB5C5D CRC64;
 Query Match 92.3%; Score 36; DB 5; Length 482;
 Best Local Similarity 83.3%; Pred. NO. 5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 DB 57 VEWSWL 62
 ID Q9FEE1 PRELIMINARY; PRT; 544 AA.
 AC Q9FEE1;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Putative cytochrome P450.
 GN P0688A04.9 OR P0006C01.24.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; *Oryza*.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0688A04."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 clone: P0006C01."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AP002839; BAB19103.1; --
 DR EMBL; AP002744; BAB19082.1; --
 DR Gramene; Q9FEE1; --
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME P450; 1.
 KW Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 544 AA; 60867 MW; 273EAF5968D1A024 CRC64;
 Query Match 92.3%; Score 36; DB 10; Length 544;
 Best Local Similarity 83.3%; Pred. NO. 5.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LEWSWL 6
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Db 48 LEWAWL 53

RESULT 4
O63620 PRELIMINARY; PRT; 645 AA.
ID O63620;
AC O63620;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NADH dehydrogenase subunit 5.
OS Balanoglossus carnosus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychoderidae;
OC Balanoglossus.
OX NCBI_TaxID=35080;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99016090; PubMed=9799263;
RA Castresana J., Feldmaier-Fuchs G., Yokobori S., Satoh N., Paabo S.;
RT "The mitochondrial genome of the hemichordate Balanoglossus carnosus
and the evolution of deuterozoome mitochondria.";
RL Genetics 150:1115-1123(1998).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=98188267; PubMed=9520430;
RX Castresana J., Feldmaier-Fuchs G., Paabo S.;
RA Castresana J., Feldmaier-Fuchs G., Paabo S.;
RT "Codon reassignment and amino acid composition in hemichordate
mitochondria.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3703-3707(1998).
RN [3]
RN SEQUENCE FROM N.A.
RP Castresana J., Feldmaier-Fuchs G., Paabo S.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF051097; AAD11945.1; -.
DR InterPro; IPR003916; NADHub_oxred5.
DR InterPro; IPR001750; Oxidored_g1.
DR InterPro; IPR001516; Oxidored_g1_N.
DR Pfam; PF00361; oxidored_g1; 1.
DR Pfam; PF00662; oxidored_g1_N; 1.
DR PRINTS; PR01434; NADHHDGNASES.
KW NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
KX NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
SQ SEQUENCE 645 AA; 69455 MW; C8A498941B61F392 CRC64;

Query Match 92.3%; Score 36; DB 8; Length 645;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
    |||:|
Db 96 LEWTWL 101

RESULT 5
Q95KV1 PRELIMINARY; PRT; 740 AA.
ID Q95KV1;
AC Q95KV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RP Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKBs)
```

```
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ414555; CAC93686.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKG; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F4D176 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 740;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
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Db 733 LDWSWL 738

RESULT 6
Q8CBT3 PRELIMINARY; PRT; 745 AA.
ID Q8CBT3;
AC Q8CBT3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved helix-loop-helix ubiquitous kinase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354883; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RL EMBL; AK035326; BAC29034.1; -.
SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;

Query Match 92.3%; Score 36; DB 11; Length 745;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
    |||:|
Db 738 LDWSWL 743

RESULT 7
Q95KV0 PRELIMINARY; PRT; 756 AA.
ID Q95KV0;
AC Q95KV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-beta.
GN BIKKBETA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RP
```

RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
 RT "Identification and characterisation of the bovine Ikb kinases (IKKs)
 RL alpha, beta and gamma."; to the EMBL/GenBank/DBJ databases.
 CC Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ414556; CAC93687.1; -.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00669; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot kinase; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 756;
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 Db 737 LQMSWL 742

RESULT 8
 Q8VKB2 ID Q8VKB2 PRELIMINARY; PRT; 48 AA.
 AC Q8VKB2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein MT0946.
 GN MT0946.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."; to the EMBL/GenBank/DBJ databases.
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AS006980; AAK45193.1; -.
 DR TIGR; MT0946; -.
 KW Hypothetical protein.
 SQ SEQUENCE 48 AA; 5265 MW; C0BFA9D6AA2BF8DF CRC64;

Query Match 89.7%; Score 35; DB 16; Length 48;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
 Db 14 EWSWL 18

RESULT 9
 Q8DYI4 ID Q8DYI4 PRELIMINARY; PRT; 110 AA.
 AC Q8DYI4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SAG1496.

OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=22222988; PubMed=12200547;
 RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae."; to
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014260; AAN00363.1; -.
 DR TIGR; SAG1496; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 110 AA; 12689 MW; 243D6BE9029709A4 CRC64;

Query Match 89.7%; Score 35; DB 16; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSW 5
 Db 14 LEWSW 18

RESULT 10
 Q9HHP7 ID Q9HHP7 PRELIMINARY; PRT; 173 AA.
 AC Q9HHP7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Vng6292c.
 GN VNG6292c.
 OS Halobacterium sp. (strain NRC-1).
 OG Plasmid pNRC200.
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."; to
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE005159; AAG20929.1; -.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00665; rve; 1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 173 AA; 20267 MW; E8E02EDC76ED4371 CRC64;

Query Match 89.7%; Score 35; DB 17; Length 173;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
 Db 14 EWSWL 18

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Db          42 EMSWL 46

RESULT 11
Q9YH31      PRELIMINARY;      PRT;      196 AA.
AC Q9YH31;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative fibroblast growth factor-4.
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei Y.;
RT "Putative Newt Fibroblast Growth Factor-4.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76998; AAC98812.1; --
DR HSSP; P09039; 1BFF.
DR InterPro; IPR001084; Crystallin.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 196 AA; 22033 MW; AC4688CD989C6EAF CRC64;

Query Match      89.7%; Score 35; DB 13; Length 196;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEWSW 5
      |||||
Db      37 LEWSW 41

RESULT 12
Q47020
ID Q47020      PRELIMINARY;      PRT;      276 AA.
AC Q47020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA An G.; Bendak D.S.; Mamelak L.A.; Friesen J.D.;
RT "Organization and nucleotide sequence of a new ribosomal operon in
RT Escherichia coli containing the genes for ribosomal proteins S2 and
RT elongation factors Ts.";
RL Nucleic Acids Res. 9:4163-4172(1981).
RN [2]
RP SEQUENCE FROM N.A.
RA Stephens P.E.; Darlison M.G.; Guest J.R.;
RT "The pyruvate dehydrogenase complex of Escherichia coli K12.
RT Nucleotide sequence encoding the pyruvate dehydrogenase component.";
RL Eur. J. Biochem. 133:155-162(1983).
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=K-12;
RX MEDLINE=83234434; PubMed=6345153;
RA Stephens P.E.; Darlison M.G.; Lewis H.M.; Guest J.R.;
RT "The pyruvate dehydrogenase complex of Escherichia coli K12.
RT Nucleotide sequence encoding the dihydrolipoamide acetyltransferase
RT component.";
RL Eur. J. Biochem. 133:481-489(1983).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=84004369; PubMed=6352260;
RA Stephens P.E.; Lewis H.M.; Darlison M.G.; Guest J.R.;
RT "Nucleotide sequence of the lipoamide dehydrogenase gene of
RT Escherichia coli K12.";
RL Eur. J. Biochem. 135:519-527(1983).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=85054973; PubMed=6094577;
RA Richard C.; Richard F.; Martin C.; Haziza C.; Patte J.C.;
RT "Regulation of expression and nucleotide sequence of the Escherichia
RT coli ddp gene.";
RL J. Biol. Chem. 259:14824-14828(1984).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=85127060; PubMed=3882429;
RA Broome-Smith J.K.; Edelman A.; Yousif S.; Spratt B.G.;
RT "The nucleotide sequences of the ponA and ponB genes encoding
RT penicillin-binding proteins 1A and 1B of Escherichia coli K12.";
RL Eur. J. Biochem. 147:437-446(1985).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=86085668; PubMed=3079747;
RA Coulton J.W.; Mason P.; Cameron D.R.; Carmel G.; Jean R.; Rode H.N.;
RT "Protein fusions of beta-galactosidase to ferrichrome-iron receptor of
RT Escherichia coli K-12.";
RL J. Bacteriol. 165:181-192(1986).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=86278132; PubMed=3015933;
RA Breton R.; Sanfacon H.; Papayanopoulos I.; Biemann K.; Lapointe J.;
RT "Glutaryl-tRNA synthetase of Escherichia coli. Isolation and primary
RT structure of the gltX gene and homology with other aminoacyl-tRNA
RT synthetases.";
RL J. Biol. Chem. 261:10610-10617(1986).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=87014116; PubMed=3020380;
RA Koester W.; Braun V.;
RT "Iron hydroxamate transport of Escherichia coli: Nucleotide sequence
RT of the fhuB gene and identification of the protein.";
RL Mol. Gen. Genet. 204:435-442(1986).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=87083395; PubMed=3025182;
RA Chye M.L.; Pittard J.;
RT "Transcription control of the aroP gene in Escherichia coli K-12:
RT Analysis of operator mutants.";
RL J. Bacteriol. 169:386-393(1987).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=87109068; PubMed=3027045;
RA Ben-Basat A.; Bauer K.; Chang S.Y.; Myambo K.; Boosman A.; Chang S.;
RT "Processing of the initiation methionine from proteins: Properties of
RT the Escherichia coli methionine aminopeptidase and its gene
RT structure.";
RL J. Bacteriol. 169:751-757(1987).

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RN [12] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=87279948; PubMed=3301821;
RX Coulton J.W., Mason P., Allatt D.D.;
RA "fhuc and fhud genes for iron(III)-ferrichrome transport into
RT Escherichia coli K-12";
RL J. Bacteriol. 169:3844-3849(1987).
RN [13] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=88058963; PubMed=3316212;
RX Tabor C.W., Tabor H.;
RA "The speEsed operon of Escherichia coli: Formation and processing of
RT a proenzyme form of S-adenosylmethionine decarboxylase";
RL J. Biol. Chem. 262:16037-16040(1987).
RN [14] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=88152237; PubMed=2450046;
RX Gebhard W., Schreitmuller T., Hochstrasser K.;
RA "Complementary DNA and derived amino acid sequence of the precursor of
RT one of the three protein components of the inter-alpha-trypsin
RT inhibitor complex";
RL FEBS Lett. 229:63-67(1988).
RN [15] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=88227880; PubMed=3372485;
RX Mellano M.A., Cooksey D.A.;
RA "Nucleotide sequence and organization of copper resistance genes from
RT Pseudomonas syringae pv. tomato";
RL J. Bacteriol. 170:2879-2883(1988).
RN [16] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=89155419; PubMed=2537812;
RX Liu J., Parkinson J.S.;
RA "Genetics and sequence analysis of the pcnB locus, an Escherichia coli
RT gene involved in plasmid copy number control";
RL J. Bacteriol. 171:1254-1261(1988).
RN [17] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=89057448; PubMed=3057437;
RX Lipinska B., Sharma S., Georgopoulos C.;
RA "Sequence analysis and regulation of the htrA gene of Escherichia
RT coli: A sigma-32-independent mechanism of heat-inducible
RT transcription";
RL Nucleic Acids Res. 16:10053-10067(1988).
RN [20] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=90128278; PubMed=2693214;
RX Roncero M.I., Jepsen L.P., Stroman P., van Heeswijk R.;
RA "Characterization of a leuA gene and an ARS element from *Mucor*
RT *circinelloides*";
RL Gene 84:335-343(1989).

RN [21] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=89327165; PubMed=2666401;
RX Xie Q.W., Tabor C.W., Tabor H.;
RA "Spermidine biosynthesis in Escherichia coli the promoter and the
RT termination regions of the speED operon";
RL J. Bacteriol. 171:4457-4465(1989).
RN [22] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=90113890; PubMed=2691840;
RX Lindquist S., Galleni M., Lindberg F., Normark S.;
RA "Signalling proteins in enterobacterial ampC beta-lactamase
RT regulation";
RL Mol. Microbiol. 3:1091-1102(1989).
RN [23] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=90202727; PubMed=2180916;
RX Kang P.J., Craig E.A.;
RA "Identification and characterization of a new Escherichia coli gene
RT that is a dosage-dependent suppressor of a dnaK deletion mutation";
RL J. Bacteriol. 172:2055-2064(1990).
RN [24] SEQUENCE FROM N.A.
RP STRAIN=K-12;
RC MEDLINE=90202727; PubMed=2180916;
RX Kang P.J., Craig E.A.;
RA "Identification and characterization of a new Escherichia coli gene
RT that is a dosage-dependent suppressor of a dnaK deletion mutation";
RL J. Bacteriol. 172:2055-2064(1990).

Query Match 89.7%; Score 35; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
DB 9 EWSWL 13

RESULT 13
Q94380 PRELIMINARY; PRT; 311 AA.
ID Q94380;
AC Q94380;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ZC47.13 protein.
GN ZC47.13.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI TaxID=6239;
RN [1] SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBSJ databases.
RN [2] SEQUENCE FROM N.A.
RP MEDLINE=99069613; PubMed=9851916;
RX none;
RA "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
DR EMBL; Z81141; CAB03488.2; -.
DR WormPep; ZC47.13; CE25668.
DR InterPro; IPR002900; DUF38.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01827; FTH; 1.
SQ SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;

Query Match 89.7%; Score 35; DB 5; Length 311;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 1 LEWSWL 13

Db 295 LEWEWL 300

RESULT 14

Q25333 PRELIMINARY; PRT; 371 AA.
 ID Q25333
 AC Q25333; (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Surface antigen P2 (Fragment).
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V121;
 RX MEDLINE=92105105; PubMed=1761547;
 RA Murray P.J., Spithill T.W.;
 RT "Variants of a Leishmania Surface Antigen Derived from a Multigenic
 RT Family.";
 RL J. Biol. Chem. 266:24477-24484(1991).
 DR EMBL; X57134; CAA40413.1; -.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR Pfam; PF00560; LRR_2_rich_extensn.
 DR PRINTS; PR01217; PRICHEXTENS.
 DR PROSITE; PSS0502; LRR_PS; 1.
 FT NON_TER
 SQ SEQUENCE 371 AA; 39765 MW; 82D0A0BE163E247D CRC64;

Query Match 89.7%; Score 35; DB 5; Length 371;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
 Db 1 EWSWL 5

RESULT 15

Q8YFW8 PRELIMINARY; PRT; 387 AA.
 ID Q8YFW8
 AC Q8YFW8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Mannose-6-phosphate isomerase (EC 5.3.1.8).
 GN BMEI1394.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapratir V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009577; AAL52575.1; -.
 KW Isomerase; Complete proteome.
 SQ SEQUENCE 387 AA; 44267 MW; 4E1F33C6461663F CRC64;

Query Match 89.7%; Score 35; DB 16; Length 387;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
 Db 245 EWSWL 249

Search completed: February 18, 2004, 14:35:44
 Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-8
Perfect score: 39
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	92.3	745	1 IKKA HUMAN	O15111 h inhibitor
2	36	92.3	745	1 IKKA MOUSE	O60680 m inhibitor
3	36	92.3	756	1 IKKB HUMAN	O14920 homo sapien
4	36	92.3	757	1 IKKB MOUSE	O88351 mus musculus
5	36	92.3	757	1 IKKB RAT	O90778 rattus norv
6	35	89.7	400	1 HOPC-ECOLI	P36646 escherichia
7	34	87.2	334	1 GTR8 BOVIN	P58354 bos taurus
8	34	87.2	477	1 GTR8 HUMAN	O9ny64 homo sapien
9	34	87.2	477	1 GTR8 MOUSE	O9jif3 mus musculus
10	34	87.2	478	1 GTR8 RAT	O9jiz1 rattus norv
11	34	87.2	685	1 ROR1 DROME	O24488 drosophila
12	33	84.6	512	1 VG29 BPNU	O9tlw5 bacterioph
13	33	84.6	777	1 TDR1 MOUSE	O9bxt4 homo sapien
14	33	84.6	928	1 TDR1 MOUSE	O99mvl mus musculus
15	33	84.6	1698	1 Y076 HUMAN	O14999 homo sapien
16	32	82.1	83	1 VG41 BPML5	O05252 mycobacteri
17	32	82.1	94	1 VG41 BPMD2	O64231 mycobacteri
18	32	82.1	296	1 CYOA BUCAI	P57544 buchneira ap
19	32	82.1	307	1 QOX2 ACEAC	P50653 acetobacter
20	32	82.1	314	1 CYOA PSEPU	O9wwr1 pseudomonas
21	32	82.1	362	1 DCUP YEAST	P32347 saccharomyc
22	32	82.1	375	1 D12 CREAL	O81931 crepis alpi
23	32	82.1	387	1 MANA RHIME	P29954 rhizobium m
24	32	82.1	561	1 RK BOVIN	P28327 bos taurus
25	32	82.1	563	1 RK HUMAN	O15835 homo sapien
26	32	82.1	564	1 RK MOUSE	O9wvl4 mus musculus
27	32	82.1	564	1 RK RAT	O63651 rattus norv
28	32	82.1	576	1 GRK6 HUMAN	P43250 homo sapien
29	32	82.1	576	1 GRK6 MOUSE	O70293 mus musculus
30	32	82.1	576	1 GRK6 RAT	P97711 rattus norv
31	32	82.1	578	1 GRK4 HUMAN	P32298 homo sapien
32	32	82.1	590	1 GRK5 BOVIN	P43249 bos taurus
33	32	82.1	590	1 GRK5_HUMAN	P43947 homo sapien

RESULT 1

ID	IKKA HUMAN	STANDARD;	PRT;	745 AA.
AC	O15111: O14666; Q13132; Q92467;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.1.-)			
DE	(I kappa-B kinase alpha) (IKK α) (IKK-alpha) (IKK α -alpha) (IKK α -B kinase)			
DE	(I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous			
DE	kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).			
GN	CHUK OR IKKA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97386461; PubMed=9244310;			
RA	Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;			
RT	"Identification and characterization of an IkappaB kinase.";			
RL	Cell 90:373-383(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=97394468; PubMed=9252186;			
RA	DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;			
RT	"A cytokine-responsive IkappaB kinase that activates the transcription			
RT	factor NF-kappaB.";			
RL	Nature 388:548-554(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND			
RP	SER-176.			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=98008813; PubMed=9346484;			
RA	Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,			
RA	Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;			
RT	"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for			
RT	NF-kappaB activation.";			
RL	Science 278:860-866(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Heart;			
RX	MEDLINE=99012998; PubMed=9813230;			
RC	TISSUE=Heart;			
RA	Hu M.C.-T., Wang Y.-P.;			
RT	"IkappaB kinase-alpha and -beta genes are coexpressed in adult and			
RT	embryonic tissues but localized to different human chromosomes.";			
RL	Gene 222:31-40(1998).			
RN	[5]			
RP	SEQUENCE OF 32-745 FROM N.A.			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=96258427; PubMed=8777433;			
RA	Connelly M.A., Marcu K.B.;			
RT	"CHUK, a new member of the helix-loop-helix and leucine zipper			
RT	families of interacting proteins, contains a serine-threonine kinase			
RT	catalytic domain.";			

Q62833 rattus norv
Q09537 caenorhabdi
P32866 drosophila
Q9jmi0 mus musculu
Q9jhl3 rattus norv
Q99597 bacillus th
P37896 lactobacill
P29318 gallus gall
P29310 homo sapien
P29319 mus musculu
O08680 rattus norv
P10474 c endogluc

Cell. Mol. Biol. Res. 41:537-549(1995).
[6]
PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
AND SER-180.
RX MEDLINE=98188283; PubMed=9520446;
RA Ling L., Cao Z., Goeddel D.V.;
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
Ser-176.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
[7]
PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE=99413720; PubMed=10485710;
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,
RA Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt
serine-threonine kinase.";
RL Nature 401:82-85(1999).
[8]
IKK- α -IKK β BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
[9]
IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
[10]
REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
[11]
SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; IKKB AND IKK β .
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
the dissociation of the inhibitor/NF-kappa-B complex and
ultimately the degradation of the inhibitor. Also phosphorylates
NCOA3.
CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
when dephosphorylated.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
complex. A weak interaction with TRAF2 cannot be excluded. Part of
a complex composed of NCOA2, NCOA3, IKKB, IKK β and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
MEK1, and dephosphorylated by PP2A. Autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.

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or send an email to license@isb-sib.ch).

DR EMBL; AF012890; AAC51662.1; --
DR EMBL; AF009225; AAC51671.1; --
DR EMBL; AF080157; AAD08996.1; --
DR EMBL; U22512; AAC50713.1; --
DR HSSP; Q63450; 1A06.
DR Gnew; HGNC:1974; CHUK.
DR MIM; 600664; --
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0008384; E:IkappaB kinase activity; TAS.
DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 302 PROTEIN KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT NP_BIND 21 29 NEMO-BINDING.
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 ATP (BY SIMILARITY).
FT MOD_RES 23 23 BY SIMILARITY.
FT MOD_RES 176 176 PHOSPHORYLATION (BY PKB/AKT1).
FT MUTAGEN 23 23 PHOSPHORYLATION (BY MAP3K14).
FT MUTAGEN 44 44 T->A: LOSS OF PHOSPHORYLATION AND
DECREASE OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
FT MUTAGEN 176 176 K->M: LOSS OF AUTOPHOSPHORYLATION.
FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
ACTIVITY.
FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
FT CONFLICT 543 543 E -> G (IN REF. 2).
FT CONFLICT 604 604 L -> R (IN REF. 5).
FT CONFLICT 679 680 TS -> AY (IN REF. 5).
FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
FT CONFLICT 686 687 TS -> DL (IN REF. 5).
SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
Query Match 92.3%; Score 36; DB 1; Length 745;
Best Local Similarity 83.3%; Pred No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
Db 738 LDWSWL 743

RESULT 2
IKKA_MOUSE
ID IKKA_MOUSE STANDARD; PRT; 745 AA.
AC Q0680; Q9D2K3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
DE CHUK OR IKKA.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX

```

RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX STRAIN=BALB/c;
RX MEDLINE=9604444; PubMed=7558004;
RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
RL chromosome 10 and mouse chromosome 19."
RL Genomics 27:348-351(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX STRAIN=BALB/c;
RX MEDLINE=96258427; PubMed=8777433;
RA Connelly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain."
RL Cell. Mol. Biol. Res. 41:537-549(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Peole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=20198447; PubMed=10733566;
RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
RA Galezunas R., Marcu K.B.;
RA "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
RT IKKbeta have different activation requirements."
RL Mol. Cell. Biol. 20:2635-2649(2000).
RN [5]
RP PHOSPHORYLATION BY MAP3K14/NIK.
RX MEDLINE=998188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase-1."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [6]
RP IKK-1/IKK2 BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Dalhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
RT IKKbeta subunit phosphorylation."
RL Science 284:309-313(1999).
RN [7]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase."
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [8]
RP REVIEW.
RX MEDLINE=20171839; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection."
RL Am. J. Physiol. 278:C451-C462(2000).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC when dephosphorylated.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MAP3K14/NIK, MEK1, IKAP and IKB-alpha-P55-P50
CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q0680-1; Sequence=Displayed;
CC Name=2; Synonyms=Delta LH;
CC IsoId=Q0680-2; Sequence=VSP_004866, VSP_004867;
CC Name=3; Synonyms=Delta H;
CC IsoId=Q0680-3; Sequence=VSP_004868, VSP_004869;
CC -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
CC 3 are expressed predominantly in brain and T-lymphocytes.
CC -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
CC E11, E15 and E17 days. In the limb development, its expression
CC predominates in the limb buds at E12.5 day.
CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; U12473; AAC52589.1; -.
DR EMBL; AK018671; BAB31335.1; -.
DR PIR; I49101; I49101.
DR HSSP; Q63450; IAO6.
DR MGD; MGI:99484; Chuk.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 15 300 PROTEIN_KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT BINDING 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
FT (BY SIMILARITY).
FT (BY SIMILARITY).

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FT VARSPLIC 452 471 MSLRLRYNANLTKMNTLIS --> IFRKNVKSMERNRKGKH
FT SLF (in isoform 2).
FT /FTID=VSP 004866.
FT VARSPLIC 472 745 Missing (in isoform 2).
FT /FTID=VSP 004867.
FT VARSPLIC 577 584 DHLYSDST --> GKTLQSQY (in isoform 3).
FT /FTID=VSP 004868.
FT VARSPLIC 585 745 Missing (in isoform 3).
FT /FTID=VSP 004869.
FT CONFLICT 236 236 K --> E (IN REF. 3).
FT CONFLICT 400 400 S --> Y (IN REF. 3).
SQ SEQUENCE 745 AA; 84728 MW; 3FEF582AF9F2233 CRC64;

Query Match 92.3%; Score 36; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6
Db 738 LDWSWL 743

RESULT 3
IKKB_HUMAN
ID IKKB_HUMAN STANDARD; PRT; 756 AA.
AC O14920; O75327;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032398; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
RT 8p12-->p11 by in situ hybridization.";
RL Cytogenet. Cell Genet. 82:32-33(1998).
RN [5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [7]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
RN [8]
RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKBG.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (By similarity)
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
CC complex. Phosphorylated IKB-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF029684; AAC51860.1; -
DR EMBL; AF080158; AAD08997.1; -
DR EMBL; AF031416; AAC64675.1; -
DR EMBL; BC006231; AAH06231.1; -

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DR HSSP; Q63450; 1A06.
DR Genew; HGNC:5960; IKKB.
DR MIM; 603258; -.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0005224; P:protein serine/threonine kinase activity; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 K-A: LOSS OF KINASE ACTIVITY AND NO
FT MUTAGEN 44 44 EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S-A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S-B: FULL ACTIVATION.
FT MUTAGEN 181 181 S-A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S-B: FULL ACTIVATION.
FT CONFLICT 231 255 WHSKVRSKSDIVVSDLDGTVKF -> CVRWMPGCTVAHS
FT CONFLICT 425 425 CNSTLGGGRWV (IN REF. 5).
FT CONFLICT 425 425 Q -> H (IN REF. 1).
FT SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
SQ QUERY Match 92.3%; Score 36; DB 1; Length 756;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:|:|
Db 737 LDWSWL 742

RESULT 4
IKKB_MOUSE STANDARD; PRT; 757 AA.
AC Q88351; Q9RAJ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; Tissue=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542 (1998).
RN [2]

SEQUENCE FROM N.A.
Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
constitutively phosphorylates serine residues of IKB."
Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[3]
DEVELOPMENTAL STAGE.
MEDLINE=99455228; PubMed=10523828;
Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., stress response signaling
pathway activates IkkappaB kinases (IKK-alpha/beta) and IKK-beta is a
developmentally regulated protein kinase."
Oncogene 18:5514-5524 (1999).
[4]
IKK PHOSPHORYLATION.
MEDLINE=99038238; PubMed=9819420;
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein
kinase kinase 1 and NF-kappaB-inducing kinase."
Mol. Cell. Biol. 18:7336-7343 (1998).
[5]
REVIEW.
MEDLINE=20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
inflammation and protection."
Am. J. Physiol. 278:C451-C462 (2000).
-1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
the dissociation of the inhibitor/NF-kappa-B complex and
ultimately the degradation of the inhibitor. Also phosphorylates
NCOA3.
-1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
also as a homodimer. Directly interacts with IKK-gamma/NEMO.
Heterodimers form the active complex. The tripartite complex can
also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
complex. Phosphorylated IKK-alpha is further released from the
complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
and CREBBP (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
-1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
the mouse embryo, at E9.5 day its expression begins to be
localized to the brain, neural ganglia, neural tube, and in liver
at E12.5 day. At E15.5 day, the expression is further restricted
to specific tissues of the embryo.
-1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
Weakly autophosphorylated.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
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EMBL; AF026524; AAC23557.1; -.
EMBL; AF088910; AAD52095.1; -.
HSSP; Q63450; 1A06.
MGD; MGI:1338071; Ikbb.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_Thr_kinase.
InterPro; IPR001245; Tyr_kinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.

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FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 56 56 N -> D (IN REF. 2).
FT CONFLICT 343 343 N -> D (IN REF. 2).
FT CONFLICT 356 356 K -> E (IN REF. 2).
FT CONFLICT 390 390 L -> F (IN REF. 2).
FT CONFLICT 406 406 P -> Q (IN REF. 2).
FT CONFLICT 573 573 K -> R (IN REF. 2).
FT CONFLICT 736 736 TDWSLQWDEDEERCSLEQACD -> VTA (IN REF. 2).
SQ SEQUENCE 757 AA; 86690 MW; PED962F095449C5E CRC64;

Query Match 92.3%; Score 36; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. NO. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 737 LDWSWL 742

RESULT 5
IKKB RAT STANDARD; PRT; 757 AA.
AC Q9Q78;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Sun S., Ravid K.;
RT "IKK beta in megakaryocyte differentiation.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343 (1998).
RN [3]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462 (2000).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP (By similarity).
CC
```

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CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF115282; AAF21978.1; -.
CC HSP; O63450; IA06.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_Thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 757 AA; 86866 MW; 3AF6E46A7DF91F9C CRC64;

Query Match 92.3%; Score 36; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. NO. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 737 LDWSWL 742

RESULT 6
HOF_C ECOLI STANDARD; PRT; 400 AA.
ID HOF_C ECOLI STANDARD; PRT; 400 AA.
AC P36646; P75648;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein transport protein hofc.
DE HOF_C OR HOF_C OR B0106.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=95047556; PubMed=7959070;
RA Whitchurch C.B., Mattick J.S.;
RT "Escherichia coli contains a set of genes homologous to those
RT involved in protein secretion, DNA uptake and the assembly of type-4
RT fimbriae in other bacteria.";
RL Gene 150:9-15 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RX
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RA Fujita N., Mori H., Yura T., Ishihama A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 RL the 2.4-4.1 min (110,917-193,643 bp) region.";
 RN Nucleic Acids Res. 22:1637-1639(1994).
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE OF 165-400 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=89061679; PubMed=2904262;
 RA Andrews S.C., Guest J.R.;
 RT "Nucleotide sequence of the gene encoding the GMP reductase of
 RL Escherichia coli K12.";
 RL Biochem. J. 255:35-43(1988).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (probable).
 CC
 CC -1- SIMILARITY: BELONGS TO THE PULF/OUTF/EXEF/XPSF/XPCS FAMILY.
 CC -1- CAUTION: REF.2 AND REF.4 SEQUENCES DIFFER IN THE N- AND C-TERMINAL
 CC AS WELL AS IN THE CENTRAL PART DUE TO FRAMESHIFTS.
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 CC
 CC EMBL; L28105; AAC36925.1; -;
 DR EMBL; D26562; -; NOT ANNOTATED_CDS.
 DR EMBL; AE000119; AAC73217.1; -;
 DR EMBL; X07917; -; NOT ANNOTATED_CDS.
 DR EMBL; B64733; B64733.
 DR EcoGene; EG11798; hofC.
 DR InterPro; IPR003004; Bac_GSPF.
 DR InterPro; IPR001992; Bact_secr_systII.
 DR Pfam; PF00482; GSPII.F.1.
 DR PRINTS; PR00812; BCTERIALGSPF.
 DR PROSITE; PS00874; T2SP_F.1.
 DR Transport; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 165 185 POTENTIAL.
 FT TRANSMEM 209 229 POTENTIAL.
 FT TRANSMEM 370 390 POTENTIAL.
 FT CONFLICT 1 39 MASKQLRWGIGITGDGNAQDGMWASRTLLMALQQQM
 FT -> MAVSNGAGWAYAQVLT (IN REF. 1).
 SQ SEQUENCE 400 AA; 44450 MW; 9D37332B87AE07D5 CRC64;
 Query Match 89.7%; Score 35; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EWSWL 6
 Db 215 EWSWL 219
 RESULT 7
 GTR8_BOVIN STANDARD; PRT; 334 AA.
 ID GTR8_BOVIN
 AC P58354;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 DE (Glucose transporter type X1) (Fragment).
 GN SLIC2A8 OR GLUT8 OR GLUTX1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21482567; PubMed=11599048;
 RA Augustin R., Pocar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F.,
 RA Niemann H., Fischer B.;
 RT "Glucose transporter expression is developmentally regulated in in
 RT vitro derived bovine preimplantation embryos.";
 RL Mol. Reprod. Dev. 60:370-376(2001).
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be
 CC a dual-specific sugar transporter as it is inhibitable by
 CC fructose (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally
 CC intracellular. May move between intracellular vesicles and the
 CC plasma membrane. The dileucine internalization motif is critical
 CC for intracellular sequestration (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
 CC TRANSPORTERS SUBFAMILY.
 CC
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 CC
 CC EMBL; AF321324; AAK69606.1; -;
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR005829; Sug transporter.
 DR Pfam; PF00883; sugar_tr.1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
 KW Transport; Sugar transport; Transmembrane; Multigene family.
 FT NON_TER 1 1
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 15 35 5 (POTENTIAL).
 FT DOMAIN 36 38 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 39 59 6 (POTENTIAL).
 FT DOMAIN 60 113 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 114 134 7 (POTENTIAL).
 FT DOMAIN 135 149 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 150 170 8 (POTENTIAL).
 FT DOMAIN 171 176 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 177 197 9 (POTENTIAL).
 FT DOMAIN 198 224 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 225 245 10 (POTENTIAL).
 FT DOMAIN 246 261 11 (POTENTIAL).
 FT TRANSMEM 262 282 11 (POTENTIAL).
 FT DOMAIN 283 295 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 296 316 12 (POTENTIAL).
 FT DOMAIN 317 334 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 334 AA; 36699 MW; 0EE9B670ADAB71DD CRC64;
 Query Match 87.2%; Score 34; DB 1; Length 334;
 Best Local Similarity 83.3%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 35 LEWRWL 40
 RESULT 8
 GTR8_HUMAN STANDARD; PRT; 477 AA.
 ID GTR8_HUMAN

AC Q9NYG4; Q9NSC4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 DE (Glucose transporter type 8) (Glucose transporter type X1).
 GN SLC2A8 OR GLUT8 OR GLUTX1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=20283667; PubMed=10821868;
 RA Doege H., Schuermann A., Bahrenberg G., Brauers A., Joost H.-G.;
 RA "GLUT8, a novel member of the sugar transport facilitator family with
 RT glucose transport activity.";
 RL J. Biol. Chem. 275:16275-16280(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20138191; PubMed=10671487;
 RA Ibberson M.R., Uldry M.A., Thorens B.;
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the
 RT central nervous system and insulin-sensitive tissues.";
 RL J. Biol. Chem. 275:4607-4612(2000).
 CC -!- FUNCTION: Insulin-regulated facilitative glucose transporter.
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be
 CC a dual-specific sugar transporter as it is inhibitable by
 CC fructose (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Principally
 CC intracellular. May move between intracellular vesicles and the
 CC plasma membrane. The dileucine internalization motif is critical
 CC for intracellular sequestration (By similarity).
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis, but not in
 CC testicular carcinoma. Lower amounts present in most other tissues.
 CC -!- INDUCTION: In testis, downregulated by estrogen.
 CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
 CC TRANSPORTERS SUBFAMILY.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Y17801; CAB89809.1; -;
 DR EMBL; AJ245937; CAB75702.1; -;
 DR Genew; HGNC:13812; SLC2A8.
 DR MIM; 605245; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005355; F:glucose transporter activity; TAS.
 DR GO; GO:0005975; P:carbohydrate metabolism; TAS.
 DR GO; GO:0015758; P:glucose transport; TAS.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub_transporter.
 DR InterPro; IPR005829; Sug_transporter.
 DR InterPro; IPR003663; Sugar_transp.
 DR Pfam; PF00083; sugar_tr; 1.
 DR PRINTS; PR00171; SUGTRANSPORT.
 DR TIGRFAMs; TIGR00879; SP; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Transport; Sugar transport; Transmembrane; Glycoprotein;
 KW Multigene family.

FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 26 46 1 (POTENTIAL).
 FT DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 71 91 2 (POTENTIAL).
 FT DOMAIN 92 96 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 117 3 (POTENTIAL).

FT DOMAIN 118 127 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 128 148 4 (POTENTIAL).
 FT DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 157 177 5 (POTENTIAL).
 FT DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 183 203 6 (POTENTIAL).
 FT DOMAIN 204 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 7 (POTENTIAL).
 FT DOMAIN 278 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 8 (POTENTIAL).
 FT DOMAIN 314 319 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 320 340 9 (POTENTIAL).
 FT DOMAIN 341 367 10 (POTENTIAL).
 FT TRANSMEM 368 388 10 (POTENTIAL).
 FT DOMAIN 389 404 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 405 425 11 (POTENTIAL).
 FT DOMAIN 426 438 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 439 459 12 (POTENTIAL).
 FT DOMAIN 460 477 CYTOPLASMIC (POTENTIAL).
 FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF (BY
 FT SIMILARITY).
 FT CARBOHYD 349 N-LINKED (GLCNAC...) (By similarity).
 FT CONFLICT 377 S -> N (IN REF. 2).
 FT CONFLICT 456 FS -> LF (IN REF. 2).
 FT CONFLICT 462 T -> I (IN REF. 2).
 SQ SEQUENCE 477 AA; 50792 MW; 0B480F94B40AEE76 CRC64;
 Query Match 87.2%; Score 34; DB 1; Length 477;
 Best Local Similarity 83.3%; Fract. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 DB 179 LEWRWL 184
 RESULT 9
 ID GTR8 MOUSE STANDARD; PRT; 477 AA.
 AC Q9JUF3; Q9JUP4; Q9JUZ0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Solute carrier family 2, facilitated glucose transporter, member 8
 DE (Glucose transporter type 8) (Glucose transporter type X1).
 GN SLC2A8 OR GLUT8 OR GLUTX1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20138191; PubMed=10671487;
 RA Ibberson M.R., Uldry M.A., Thorens B.;
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the
 RT central nervous system and insulin-sensitive tissues.";
 RL J. Biol. Chem. 275:4607-4612(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=20283667; PubMed=10821868;
 RA Doege H., Schuermann A., Bahrenberg G., Brauers A., Joost H.-G.;
 RA "GLUT8, a novel member of the sugar transport facilitator family with
 RT glucose transport activity.";
 RL J. Biol. Chem. 275:16275-16280(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Embryonic carcinoma;
 RX MEDLINE=20319023; PubMed=10860996;
 RA Carayannopoulos M.O., Chi M.-Y., Cui Y., Pingsterhaus J.M.,
 RA McKnight R.A., Mueckler M., Devaskar S.U., Moley K.H.;
 RT "GLUT8 is a glucose transporter responsible for insulin-stimulated
 RT glucose uptake in the blastocyst.";

Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000).

[4]

SEQUENCE FROM N.A.

STRAIN=129/Ola, TISSUE=Spleen;

MEDLINE=21547794; PubMed=11889004;

Scheepers A., Doeghe H., Joost H.-G., Schuermann A.;

"Mouse GLUT8: genomic organization and regulation of expression in 3T3-L1 adipocytes by glucose.";

Biochem. Biophys. Res. Commun. 288:969-974(2001).

-!- FUNCTION: Insulin-regulated facilitative glucose transporter. Binds cytochalasin B in a glucose-inhibitable manner. Seems to be a dual-specific sugar transporter as it is inhibitable by fructose.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration (By similarity). Insulin induces a change in the intracellular localization and gives rise to insertion in the plasma membrane.

-!- TISSUE SPECIFICITY: Highest level of expression in placenta and testis. Highly expressed in adult and pubertal testis, but not prepubertal testis. Lower levels of expression in brain, liver, heart, kidney, fat and skeletal muscle.

-!- DEVELOPMENTAL STAGE: High expression in blastocysts.

-!- INDUCTION: Inhibited under glucose deprivation.

-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTERS SUBFAMILY.

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EMBL; AJ245936; CAB75719.1; -.

EMBL; Y17802; CAB89815.1; -.

EMBL; AF232061; AAF78366.1; -.

EMBL; AJ413951; CAC88690.1; -.

MGI; MGI:1860103; SLC2a8.

GO; GO:0005887; C: integral to plasma membrane; IDA.

GO; GO:0005336; F: glucose binding activity; IDA.

GO; GO:0005355; F: glucose transporter activity; IDA.

GO; GO:0015758; P: glucose transport; IDA.

GO; GO:0008286; P: insulin receptor signaling pathway; IDA.

GO; GO:0001666; P: response to hypoxia; IDA.

InterPro; IPR007114; MFS.

InterPro; IPR005828; Sub transporter.

InterPro; IPR005829; Sug transporter.

InterPro; IPR003663; Sugar transport.

Pfam; PF00083; sugar_tr; 1.

PRINTS; PR00171; SUGRTNSPOT.

TIGRFAMS; TIGR00879; SP; 1.

PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

Transport; Sugar transport; Transmembrane; Glycoprotein; Multigene family.

DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).

TRANSMEM 26 46 1 (POTENTIAL).

DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).

TRANSMEM 71 91 2 (POTENTIAL).

DOMAIN 92 96 CYTOPLASMIC (POTENTIAL).

TRANSMEM 97 117 3 (POTENTIAL).

DOMAIN 118 127 EXTRACELLULAR (POTENTIAL).

TRANSMEM 128 148 4 (POTENTIAL).

DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).

TRANSMEM 157 177 5 (POTENTIAL).

DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).

TRANSMEM 183 203 6 (POTENTIAL).

DOMAIN 204 257 CYTOPLASMIC (POTENTIAL).

TRANSMEM 258 278 7 (POTENTIAL).

DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	294	314	8 (POTENTIAL).
FT	DOMAIN	315	320	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	321	341	9 (POTENTIAL).
FT	DOMAIN	342	367	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	368	388	10 (POTENTIAL).
FT	DOMAIN	389	404	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	405	425	11 (POTENTIAL).
FT	DOMAIN	426	438	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	439	459	12 (POTENTIAL).
FT	DOMAIN	460	477	CYTOPLASMIC (POTENTIAL).
FT	SITE	12	13	DILEUCINE INTERNALIZATION MOTIF (BY SIMILARITY).
FT	CARBOHYD	350	350	N-LINKED (GLCNAC. . .) (By similarity).
FT	CONFLICT	39	39	S -> N (IN REF. 1).
FT	CONFLICT	94	94	S -> A (IN REF. 2 AND 4).
FT	CONFLICT	429	429	S -> N (IN REF. 1).
SEQ	SEQUENCE	477 AA; 51523 MW; A3753FB34E452F9A	CRC64;	

Query Match 87.2%; Score 34; DB 1; Length 477;

Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSML 6

DB 179 LEWRML 184

RESULT 10

GTR8 RAT

ID GTR8 RAT STANDARD; PRT; 478 AA.

AC Q9JZL1; Q9JMA6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Solute carrier family 2, facilitated glucose transporter, member 8 (Glucose transporter type 8) (Glucose transporter type X1).

GN SLC2A8 OR GLUT8 OR GLUTX1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF LEU-12 AND LEU-13.

RC TISSUE=Testis;

RX MEDLINE=20138191; PubMed=10671487;

RA Ibberson M.R., Uldry M.A., Thorens B.;

RT "GLUTX1, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";

RL J. Biol. Chem. 275:4607-4612(2000).

RP [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Ishibashi K.;

RT "Molecular cloning of a new putative glucose transporter.";

RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP TISSUE SPECIFICITY.

RX MEDLINE=20283667; PubMed=10821868;

RA Doeghe H., Schuermann A., Bahrenberg C., Brauers A., Joost H.-G.;

RT "GLUT8, a novel member of the sugar transport facilitator family with glucose transport activity";

RL J. Biol. Chem. 275:16275-16280(2000).

CC -!- FUNCTION: Insulin-regulated facilitative glucose transporter. Binds cytochalasin B in a glucose-inhibitable manner. Seems to be a dual-specific sugar transporter as it is inhibitable by fructose.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration.

CC -!- TISSUE SPECIFICITY: Highly expressed in adult and pubertal testis, but not prepubertal testis. Moderate expression in hypothalamus,

CC cerebellum, brainstem, hippocampus, and adrenal gland. Lower
 CC amounts present in most other tissues.
 CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
 CC TRANSPORTERS SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ245935; CAB75729.1; -;
 CC EMBL; AB033418; BAA94383.1; -;
 CC InterPro; IPR007114; MFS.
 CC InterPro; IPR005828; Sub transporter.
 CC InterPro; IPR005829; Sug transporter.
 CC InterPro; IPR003663; Sugar transport.
 CC Pfam; PF00083; sugar tr_1
 CC PRINTS; PR00171; SUGTRANSPORT.
 CC TIGRFAMs; TIGR00879; SP; 1.
 CC PROSITE; PS00216; SUGAR TRANSPORT 1; 2.
 CC PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
 CC Transport; Sugar transport; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 26 46
 FT DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 71 91
 FT DOMAIN 92 96 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 97 117
 FT DOMAIN 118 127
 FT TRANSMEM 128 148
 FT DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 157 177
 FT DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 183 203
 FT DOMAIN 204 257
 FT TRANSMEM 258 278
 FT DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 294 314
 FT DOMAIN 315 320 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 321 341
 FT DOMAIN 342 368
 FT TRANSMEM 369 389
 FT DOMAIN 390 405 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 406 426
 FT DOMAIN 427 439 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 440 460
 FT DOMAIN 461 478
 FT TRANSMEM 479 488
 FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF.
 FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (PROBABLE).
 FT MUTAGEN 12 13 LL->AA: CHANGES SUBCELLULAR LOCATION.
 FT FT MAINLY TO THE PLASMA MEMBRANE, THREEREBY
 FT INCREASING TRANSPORT ACTIVITY.
 FT FT GG -> QGA (IN REF. 2).
 FT CONFLICT 83 84
 FT SEQUENCE 478 AA; 51458 MW; 95841FC1F18C9EE9 CRC64;
 Query Match 87.2%; Score 34; DB 1; Length 478;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LEWSWL 6
 Db 179 LEWRWL 184
 RESULT 11
 ID RORI DROME STANDARD; PRT; 685 AA.
 AC Q24488;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor
 DE (EC 2.7.1.112) (OROR).
 DE ROR OR CG4926.
 OS Drosophila melanogaster (Fruit fly).
 GN Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RP STRAIN=Canton-S; TISSUE=Larval brain;
 RX MEDLINE=93348222; PubMed=8394009;
 RT "Wilson C., Guberhan D.C.I., Steller H.;
 RT "Dror, a potential neurotrophic receptor gene, encodes a Drosophila
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
 RT kinases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE OF 545-597 FROM N.A.
 RX MEDLINE=98401146; PubMed=9731193;
 RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
 RA "Sampling the genomic pool of protein tyrosine kinase genes using the
 RA polymerase chain reaction with genomic DNA.";
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -!- FUNCTION: Tyrosine-protein kinase receptor that functions during
 CC early stages of neuronal development.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).


```
RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- TISSUE SPECIFICITY: Testis and ovary specific.
CC -!- SIMILARITY: Contains 3 Tudor domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```
CC
CC EMBL; AF285591; AAK31970.1; -.
DR MGD; MGI:1933218; Tdrd1.
DR InterPro; IPR001097; Maternal_tudor.
DR InterPro; IPR002999; Tudor.
DR Pfam; PF00567; Tudor; 4.
DR SMART; SM00333; Tudor; 4.
DR PROSITE; PS50304; Tudor; 4.
KW Repeat.
FT DOMAIN 63 123 TUDOR 1.
FT DOMAIN 292 351 TUDOR 2.
FT DOMAIN 512 571 TUDOR 3.
FT DOMAIN 738 796 TUDOR 4.
SQ SEQUENCE 928 AA; 103050 MW; 9CCF0DBA3AF671AF CRC64;

Query Match 84.6%; Score 33; DB 1; Length 928;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6
Db 453 LEWTWV 458
||||:
SEQUENCE FROM N.A.

RESULT 15
Y076_HUMAN
ID Y076_HUMAN STANDARD; PRT; 1698 AA.
AC Q14999;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein KIAA0076.
GN KIAA0076.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 1:223-229(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC
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 CC -----

DR EMBL; D38548; BAA07551.1; -
 DR EMBL; BC033647; AAH33647.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 1698 AA; 191188 MW; 57B11CC478E3EEDA CRC64;

Query Match 84.6%; Score 33; DB 1; Length 1698;
 Best Local Similarity 66.7%; Pred. No. 7.5e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6
 | : | : |
 Db 1446 LQWTWL 1451

Search completed: February 18, 2004, 14:28:06
 Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-8
Perfect score: 39
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	645	2 T11137	NADH2 dehydrogenas
2	36	92.3	745	1 I49101	conserved helix-lo
3	35	89.7	150	2 PNO444	Ig heavy chain v r
4	35	89.7	242	2 T27590	hypothetical prote
5	35	89.7	371	2 S20075	promastigote surfa
6	35	89.7	387	2 AD3426	mannose-6-phosphat
7	35	89.7	391	2 AG2318	hypothetical prote
8	35	89.7	400	2 B64733	protein transport
9	35	89.7	474	1 G2MS11	Ig gamma-2b chain
10	35	89.7	522	2 A84606	hypothetical prote
11	35	89.7	1367	2 H82874	conserved hypothet
12	35	89.7	1379	2 JC4954	vascular endotheli
13	35	89.7	2054	2 T32413	probable acetyl-Co
14	34	87.2	116	2 T03472	conserved hypothet
15	34	87.2	117	2 S03289	Ig heavy chain pre
16	34	87.2	133	2 PC1155	Ig heavy chain pre
17	34	87.2	355	2 F70983	probable serine pr
18	34	87.2	395	2 E90438	hypothetical prote
19	34	87.2	398	2 S76763	hypothetical prote
20	34	87.2	685	1 A48289	neurotrophic recep
21	34	87.2	919	2 T37062	probable transcrip
22	34	87.2	1139	2 A10379	probable potassium
23	33	84.6	160	2 E71560	hypothetical prote
24	33	84.6	161	2 C81711	conserved hypothet
25	33	84.6	267	2 G90579	hypothetical prote
26	33	84.6	273	2 AH1696	PTS mannose-specif
27	33	84.6	273	2 AH1324	hypothetical prote
28	33	84.6	322	2 A13395	NADH2 dehydrogenas
29	33	84.6	358	2 AD2878	iron-chelator util

ALIGNMENTS

RESULT 1

T11137

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - acorn worm mitochondrion
C:Species: mitochondrion Balanoglossus carnosus
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T11137
R:Castresana, J.; Feldmaier-Fuchs, G.; Yokobori, S.; Satoh, N.; Paabo, S.
Genetics 150, 1115-1123, 1998
A:Title: The mitochondrial genome of the hemichordate Balanoglossus carnosus and the ev
A:Reference number: Z17250; MUID:99016090; PMID:9799263
A:Accession: T11137
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-645 <CAS>
A:Cross-references: EMBL:AF051097; NID:g3065680; PID:g3065682; PIDN:AAD11945.1
C:Genetics:

A:Genome: mitochondrion
A:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 92.3%; Score 36; DB 2; Length 645;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|||:|
DB 96 LEWTWL 101

RESULT 2

I49101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I49101
R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
A:Reference number: I49101; MUID:96044444; PMID:7558004
A:Accession: I49101
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-745 <RES>
A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C:Genetics:

A:Gene: CHUK
C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homol
C:Keywords: ATP; phosphotransferase
F:13-283/Domain: protein kinase homology <KIN>

Query Match 92.3%; Score 36; DB 1; Length 745;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;

mxCB protein (AF29
hypothetical prote
hypothetical prote
hypothetical prote
protein R09E10.3 l
hypothetical prote
hypothetical prote
hypothetical prote
gene 41 protein -
gp41 protein - Myc
probable phage-rel
Ig V-D-J region (M
mel-13a protein -
conserved hypothet
CT556 hypothetical
hypothetical prote

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LQMSWL 743

RESULT 3
PN0444
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PN0444
R:Kaluzs, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A>Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A:Reference number: PN0444; PMID:93138402; PMID:1339379
A:Accession: PN0444
A:Molecule type: mRNA
A:Residues: 1-150 <KAL>
A:Cross-references: GB:L02346
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-150/Product: Ig heavy chain V region #status predicted <MAT>
F:20-117/Domain: variable region <VRG>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 35; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. NO. 66;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
:||||
Db 1 MEWSWI 6

RESULT 4
T27590
hypothetical protein ZC47.13 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T27590
R:McMurray, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z20391
A:Accession: T27590
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-242 <WIL>
A:Cross-references: EMBL:Z81141; PIDN:CAB03488.1; CESP:ZC47.13
A:Experimental source: clone ZC47
C:Genetics:
A:Gene: CESP:ZC47.13
A:Introns: 172/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 89.7%; Score 35; DB 2; Length 242;
Best Local Similarity 83.3%; Pred. NO. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|||
Db 226 LEWEWL 231

RESULT 5
S20075
promastigote surface antigen P2 (clone 2.5) precursor - Leishmania major (fragment)
C:Species: Leishmania major
C>Date: 13-Jan-1995 #sequence_revision 06-Feb-1998 #text_change 31-Jan-2000
C:Accession: S20075; C41710
R:Murray, P.J.; Spithill, T.W.

J. Biol. Chem. 266, 24477-24484, 1991
A>Title: Variants of a Leishmania surface antigen derived from a multigenic family.
A:Reference number: A41710; PMID:92105105; PMID:1761547
A:Accession: S20075
A:Molecule type: mRNA
A:Residues: 1-371 <MUR>
A:Cross-references: EMBL:X57134; NID:g9580; PID:g9581
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F:1-343/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA>
F:344-371/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:343/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form

Query Match 89.7%; Score 35; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
|||||
Db 1 EWSWL 5

RESULT 6
AD3426
mannose-6-phosphate isomerase (EC 5.3.1.8) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AD3426
R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AD3426
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: GB:AB008917; PIDN:AAL52575.1; PID:gl7983392; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11394
A:Map position: 1
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 89.7%; Score 35; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
|||||
Db 245 EWSWL 249

RESULT 7
AG2318
hypothetical protein all4102 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG2318
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.;
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; PMID:21595285; PMID:11759840
A:Accession: AG2318
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA075801.1; PID:gl7133237; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4102

Query Match 89.7%; Score 35; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSWL 6
 |||||
 Db 37 LEWDWL 42

RESULT 8

B64733

protein transport protein hofC - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 01-Mar-2002

C;Accession: B64733; S45184; S45183

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: B64733

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-400 <BLAT>

A;Cross-references: GB:AE000119; GB:U00096; NID:g1786283; PIDN:AACT3217.1; PID:g1786295;

A;Experimental source: strain K-12, substrain MG1655

R;Fujita, N.

submitted to the EMBL Data Library, January 1994

A;Reference number: S45181

A;Accession: S45184

A;Molecule type: DNA

A;Residues: 'MGRE', 28-147, 'PK', 150-173, 'NHGGCGNAAFVCVRSPLSIRPSPVHRH' <FUJ>

A;Cross-references: EMBL:D26562; NID:g473770; PIDN:BR405563.1; PID:g473774

A;Experimental source: strain K-12

A;Accession: S45183

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 207-366, 'NRVADHNGRNYVAGGVNSANFPFRCCDEWDGITVACCSPTALGPDYRLKKRFSCTSR' <INVV

A;Cross-references: EMBL:D26562; NID:g473770; PIDN:BR405562.1; PID:g473773

A;Experimental source: strain K-12

C;Genetics:

A;Gene: hofC; hopC

C;Superfamily: secretion protein xcps

C;Keywords: protein transport; transmembrane protein

F;167-183/Domain: transmembrane #status predicted <TM>

F;219-235/Domain: transmembrane #status predicted <TM>

F;369-385/Domain: transmembrane #status predicted <TM>

Query Match 89.7%; Score 35; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6
 |||||
 Db 215 EWSWL 219

RESULT 9

G2MS11

Ig gamma-2b chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text_change 01-Dec-2000

C;Accession: S25057; A02157; A26232; A26233; A53598

R;Fischer, R.; Voss, A.; Niersbach, M.; Munsiker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m

A;Reference number: S25057

A;Accession: S25057

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-474 <FIS>

A;Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Ohta, M.; Honjo, T.

Nature 283, 786-789, 1980
 A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
 A;Reference number: A02157; MUID:80120716; PMID:6766534

A;Contents: a allele

A;Accession: A02157

A;Molecule type: DNA

A;Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>

A;Cross-references: GB:J00461

A;Note: the sequence was determined from the germline gene

R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979

A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he.

A;Reference number: A26235; MUID:80081501; PMID:117548

A;Contents: MPC 11

A;Accession: A26235

A;Molecule type: mRNA

A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>

A;Note: Lys-474 is probably removed posttranslationally

R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.

Science 206, 1303-1306, 1979

A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl

A;Reference number: A26232; MUID:80081502; PMID:117549

A;Accession: A26232

A;Molecule type: DNA

A;Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>

R;Ollo, R.; Rougeon, F.

Nature 296, 761-763, 1982

A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gam

A;Reference number: A26233; MUID:82173203; PMID:6803173

A;Contents: b allele

A;Accession: A26233

A;Molecule type: DNA

A;Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>

A;Cross-references: GB:J00461

R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yanamoto, K.; Irimura, T.; Takahashi

J. Biol. Chem. 269, 12345-12350, 1994

A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.

A;Reference number: A53598; MUID:94216359; PMID:7512967

A;Accession: A53598

A;Status: preliminary

A;Molecule type: protein

A;Residues: 234-251 <KIM>

C;Comment: The a allele sequence is shown.

C;Genetics:

A;Introns: 138/1; 236/1; 258/1; 368/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob

F;157-222/Domain: immunoglobulin homology <IMI>

F;236-257/Region: hinge

F;281-350/Domain: immunoglobulin homology <IM2>

F;387-454/Domain: immunoglobulin homology <IM3>

F;152/Disulfide bonds: interchain (to light chain) #status predicted

F;164-220, 288-348, 394-452/Disulfide bonds: #status predicted

F;247-250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted

F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.7%; Score 35; DB 1; Length 474;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6

|||||

Db 1 MEWSWI 6

RESULT 10

A84606

hypothetical protein At2g21860 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84606

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84606

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-522 <STO>

A;Cross-references: GB:AE002093; NID:G4417279; PIDN:AAD20404.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g21860

A;Map position: 2

Query Match 89.7%; Score 35; DB 2; Length 522;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSW 5

DB 341 LEWSW 345

RESULT 11

H82874

conserved hypothetical ATP/GTP-binding protein U0571 [imported] - *Ureaplasma urealyticum*

C;Species: *Ureaplasma urealyticum*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: H82874

R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a min

A;Reference number: A82870

A;Accession: H82874

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1367 <GLA>

A;Cross-references: GB:AE002155; GB:AF222894; NID:G6899572; PIDN:AAF30985.1; GSPDB:GN001

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: U0571

A;Genetic code: SGC3

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 1367;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6

DB 786 EWSWL 790

RESULT 12

JC4954

vascular endothelial growth factor receptor 2 precursor - Japanese quail

N;Alternate names: Quail endothelial kinase 2; Qek 2

C;Species: *Coturnix coturnix japonica* (Japanese quail)

C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999

C;Accession: JC4954

R;Richmann, A.; Marcille, C.; Breant, C.; Le Douarin, N.M.

Gene 174, 3-8, 1996

A;Title: Molecular cloning of Qek 1 and 2, two quail vascular endothelial growth factor

A;Reference number: JC4953; MUID:97017121; PMID:8863722

A;Accession: JC4954

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1379 <EIC>

A;Cross-references: EMBL:X83287; NID:G619865; PIDN:CAA58267.1; PID:e283815; PID:gi707416

C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;789-810/Domain: transmembrane #status predicted <TMM>
F;856-1188/Domain: protein kinase homology <KIN>
F;864-872/Region: protein kinase ATP-binding motif

Query Match 89.7%; Score 35; DB 2; Length 1379;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSW 5

DB 57 LEWSW 61

RESULT 13

T32413

probable acetyl-CoA carboxylase (EC 6.4.1.2) W0986.1 [similarity] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Aug-2000

C;Accession: T32413

R;Goela, D.; Maggi, L.; Andrews, S.

submitted to the EMBL Data Library, September 1997

A;Description: The sequence of *C. elegans* cosmid W0986.

A;Reference number: Z21162

A;Accession: T32413

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2054 <GOE>

A;Cross-references: EMBL:AF025469; PIDN:AAB71048.1; GSPDB:GN00020; CESP:W0986.1

A;Experimental source: strain Bristol N2; clone W0986

C;Genetics:

A;Gene: CESP:W0986.1

A;Map position: 2

A;Introns: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2

C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-

C;Keywords: ligase

Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 2054;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSW 5

DB 773 LEWSW 777

RESULT 14

T03472

conserved hypothetical protein - *Rhodobacter capsulatus*

C;Species: *Rhodobacter capsulatus*

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C;Accession: T03472

R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.

Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997

A;Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SB1003

A;Reference number: Z14955; MUID:97404404; PMID:9256491

A;Accession: T03472

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-116 <VLC>

A;Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16125.1; PID:g3128273

C;Genetics:

A;Map position: 1

Query Match

Best Local Similarity 87.2%; Score 34; DB 2; Length 116;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSWL 6

DB 63 LSWSWL 68

RESULT 15

S03289
 Ig heavy chain precursor V region (VAR100) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
 C:Accession: S03289
 R:Blankenstein, R.; Bonhomme, F.; Krawinkel, U.
 Immunogenetics 26, 237-248, 1987
 A:Title: Evolution of pseudogenes in the immunoglobulin V(H)-gene family of the mouse.
 A:Reference number: S03289; MOID:88006305; PMID:2820872
 A:Accession: S03289
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-117 <BLA>
 A:Cross-references: EMBL:X06866; NID:g52454; PIDN:CAA29991.1; PID:g758157
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	87.2%;	Score 34;	DB 2;	Length 117;
Best Local Similarity	66.7%;	Pred. NO. 74;		
Matches	4;	Conservative	2;	Mismatches 0; Indels 0; Gaps 0;

Qy	1 LEWSWL 6
	: :
Db	1 MEWSNV 6

 Search completed: February 18, 2004, 14:38:42
 Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-8
Perfect score: 39
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCFUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	454	4	US-09-252-991A-28780
2	36	92.3	745	2	US-08-887-518-3
3	36	92.3	745	2	US-09-023-321-3
4	36	92.3	745	2	US-08-890-853-4
5	36	92.3	745	2	US-09-032-475-3
6	36	92.3	745	2	US-09-039-125A-4
7	36	92.3	745	2	US-09-099-124A-4
8	36	92.3	745	3	US-09-032-476-4
9	36	92.3	745	3	US-08-890-854-4
10	36	92.3	745	3	US-09-023-324-4
11	36	92.3	745	3	US-09-168-629-2
12	36	92.3	745	3	US-08-910-820-10
13	36	92.3	745	3	US-08-810-131A-2
14	36	92.3	745	4	US-09-109-986-4
15	36	92.3	745	4	US-09-844-908-10
16	36	92.3	745	4	US-09-868-758-3
17	36	92.3	756	2	US-08-887-518-4
18	36	92.3	756	2	US-09-023-321-4
19	36	92.3	756	2	US-08-890-853-2
20	36	92.3	756	2	US-09-032-475-4
21	36	92.3	756	2	US-09-099-125A-2
22	36	92.3	756	2	US-09-099-124A-2
23	36	92.3	756	3	US-09-032-476-2
24	36	92.3	756	3	US-08-890-854-2
25	36	92.3	756	3	US-09-023-324-2
26	36	92.3	756	3	US-09-168-629-15
27	36	92.3	756	3	US-08-910-820-9

28	36	92.3	756	4	US-09-109-986-2	Sequence 2, Appli
29	36	92.3	756	4	US-09-844-908-9	Sequence 9, Appli
30	36	92.3	756	4	US-09-868-758-4	Sequence 4, Appli
31	36	92.3	956	4	US-09-417-197-123	Sequence 123, App
32	36	92.3	997	4	US-09-417-197-121	Sequence 121, App
33	35	89.7	137	1	US-08-392-419-2	Sequence 2, Appli
34	35	89.7	140	3	US-08-836-561-27	Sequence 27, Appl
35	35	89.7	140	3	US-08-836-561-63	Sequence 63, Appl
36	35	89.7	140	3	US-08-836-561-74	Sequence 74, Appl
37	35	89.7	140	3	US-08-836-561-78	Sequence 78, Appl
38	35	89.7	140	3	US-08-836-561-83	Sequence 83, Appl
39	35	89.7	140	3	US-08-579-378A-4	Sequence 4, Appli
40	35	89.7	140	4	US-09-434-122-27	Sequence 27, Appl
41	35	89.7	140	4	US-09-434-122-63	Sequence 63, Appl
42	35	89.7	140	4	US-09-434-122-74	Sequence 74, Appl
43	35	89.7	140	4	US-09-434-122-78	Sequence 78, Appl
44	35	89.7	140	4	US-09-434-122-83	Sequence 83, Appl
45	35	89.7	140	5	PCT-US93-11612-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-28780
; Sequence 28780, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28780
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28780

Query Match 100.0%; Score 39; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
| | | | |
DB 305 LEWSWL 310

RESULT 2
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-3

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 738 LDWSWL 743

RESULT 3
US-09-023-321-3
Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-023-321-3

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 738 LDWSWL 743

RESULT 4
US-08-890-853-4
Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-853-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 738 LDWSWL 743

RESULT 5
US-09-032-475-3
Sequence 3, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200

;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94104
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/032,475
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/887,518
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T97-008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-032-475-3

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

RESULT 6
US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-125A-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 343-4341
;; TELEFAX: (415) 343-4342
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 745 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-099-125A-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

RESULT 7
US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 92.3%; Score 36; DB 2; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

RESULT 8
US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-476-4
Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
Db 738 LDWSWL 743
RESULT 9
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-854-4
Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LEWSWL 6
Db 738 LDWSWL 743
RESULT 10
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 738 LDWSWL 743

RESULT 11

US-09-168-629-2
Sequence 2, Application US/09168629

Patent No. 6242253
GENERAL INFORMATION:

APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.

APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio

APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same

FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629

CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470

EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2

LENGTH: 745
TYPE: PRT

ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 738 LDWSWL 743

RESULT 12

US-08-910-820-10
Sequence 10, Application US/08910820

Patent No. 6258579
GENERAL INFORMATION:

APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi

APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gian

APPLICANT: Murray, Brion W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE

TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle

STATE: Washington
COUNTRY: USA

ZIP: 98104
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

US-08-910-820-10

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 738 LDWSWL 743

RESULT 13

US-08-810-131A-2
Sequence 2, Application US/08810131A

Patent No. 6268194
GENERAL INFORMATION:

APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.

APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio

APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using

TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego

STATE: California
COUNTRY: United States

ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A

FILING DATE: 25-FEB-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-810-131A-2

Query Match 92.3%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

RESULT 14
US-09-109-986-4
; Sequence 4, Application US/09109986
; Patent No. 6479266
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaoan
; APPLICANT: R guier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-109-986-4

Query Match 92.3%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

RESULT 15
US-09-844-908-10
; Sequence 10, Application US/09844908
; Patent No. 6576437
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; Zhu, Hengyi
; Barbosa, Miguel
; Li, Gian
; Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; COMPLEX AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,908
; FILING DATE: 27-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 522-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-844-908-10

Query Match 92.3%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
|:||||
Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:47
Job time : 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	1033	4 Q8N3S6	Q8N3S6 homo sapien
2	36	94.7	488	10 Q9SEJ7	Q9SEJ7 lupinus alb
3	36	94.7	675	17 O26849	O26849 methanobact
4	35	92.1	91	16 Q98C88	Q98C88 rhizobium l
5	35	92.1	116	2 O68039	O68039 rhodobacter
6	35	92.1	135	2 O05744	O05744 mycobacteri
7	35	92.1	145	5 Q810L0	Q810L0 drosophila
8	35	92.1	172	2 Q9KX81	Q9KX81 brevibacter
9	35	92.1	196	16 Q50005	Q50005 mycobacteri
10	35	92.1	197	2 Q8RSV7	Q8RSV7 uncultured
11	35	92.1	210	16 Q86317	Q86317 mycobacteri
12	35	92.1	321	5 Q94515	Q94515 drosophila
13	35	92.1	329	5 Q9VF18	Q9VF18 drosophila
14	35	92.1	398	16 Q8FWH6	Q8FWH6 bruceella su
15	35	92.1	422	16 Q92NU3	Q92NU3 rhizobium m
16	35	92.1	438	16 Q8UDU6	Q8UDU6 agrobacteri

17	35	92.1	441	16 Q8YBV0	Q8YBV0 bruceella me
18	35	92.1	966	11 Q8BRK2	Q8BRK2 mus musculus
19	35	92.1	1040	10 Q8GU52	Q8GU52 oryza sativ
20	35	92.1	1055	10 Q87222	Q87222 arabidopsis
21	35	92.1	1057	10 Q9F117	Q9F117 arabidopsis
22	35	92.1	1058	10 Q9FLR5	Q9FLR5 arabidopsis
23	34	89.5	50	2 Q49996	Q49996 mycobacteri
24	34	89.5	77	2 Q9XIK2	Q9XIK2 pseudomonas
25	34	89.5	88	12 Q88815	Q88815 eastern equ
26	34	89.5	88	12 Q88810	Q88810 eastern equ
27	34	89.5	88	12 Q88803	Q88803 eastern equ
28	34	89.5	88	12 Q88816	Q88816 eastern equ
29	34	89.5	88	12 Q88811	Q88811 eastern equ
30	34	89.5	88	12 Q88817	Q88817 eastern equ
31	34	89.5	88	12 Q88809	Q88809 eastern equ
32	34	89.5	88	12 Q88823	Q88823 eastern equ
33	34	89.5	88	12 Q88808	Q88808 eastern equ
34	34	89.5	88	12 Q88818	Q88818 eastern equ
35	34	89.5	88	12 Q88801	Q88801 eastern equ
36	34	89.5	88	12 Q88821	Q88821 eastern equ
37	34	89.5	88	12 Q88807	Q88807 eastern equ
38	34	89.5	88	12 Q88804	Q88804 eastern equ
39	34	89.5	88	12 Q88822	Q88822 eastern equ
40	34	89.5	88	12 Q88805	Q88805 eastern equ
41	34	89.5	88	12 Q88820	Q88820 eastern equ
42	34	89.5	88	12 Q88813	Q88813 eastern equ
43	34	89.5	88	12 Q88814	Q88814 eastern equ
44	34	89.5	88	12 Q88819	Q88819 eastern equ
45	34	89.5	88	12 Q88800	Q88800 eastern equ

ALIGNMENTS

RESULT 1

Q8N3S6 PRELIMINARY; PRT; 1033 AA.

AC Q8N3S6; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein (Fragment).

GN DKFZP451G202.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Wambutt R., Heubner D., Mewes H.W., Weil B., Wilmann S.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL031955; CAD38600.1; -.

KW Hypothetical protein.

FT NON TER 1

SQ SEQUENCE 1033 AA; 114395 MW; ED4F629A229CDB6B CRC64;

Query Match 100.0%; Score 38; DB 4; Length 1033;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
|||
Db 557 LAWSWL 562

RESULT 2

Q9SEJ7 PRELIMINARY; PRT; 488 AA.

AC Q9SEJ7; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE 1-aminocyclopropane-1-carboxylate synthase 3 (EC 4.4.1.14).

GN ACS3.
 OS Lupinus albus (White lupine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3870;
 RN [1]
 RQ SEQUENCE FROM N.A.
 RP STRAIN=cv. Ultra;
 RC MEDLINE=20539411; PubMed=11089679;
 RX Bekman E.P., Salbo N.U., Di Cataldo A., Regalado A.P., Ricardo C.P.,
 RA Rodriguez-Pousada C.;
 RA "Differential expression of four genes encoding 1-aminocyclopropane-1-
 RT carboxylate synthase in *Lupinus albus* during germination, and in
 RT response to indole-3-acetic acid and wounding.";
 RL *Planca* 211:663-672(2000).
 CC -|- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -|- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 DR EMBL; AF119413; AAF22111.1; -.
 DR HSSP; P37821; 1B8G.
 DR InterPro; IPR001176; ACC synthase.
 DR InterPro; IPR004839; Aminotransf1/2.
 DR InterPro; IPR004838; NHtransf1.
 DR Pfam; PF00155; aminotran1_2; 1.
 DR PRINTS; PR00753; ACCSYNTHASE.
 DR PROSITE; PS00105; AA_TRANSF_CLASS_1; 1.
 KW Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 488 AA; 55026 MW; 5BB0D640DD129970 CRC64;
 Query Match 94.7%; Score 36; DB 10; Length 488;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 479 IAWSWL 484
 RESULT 3
 O26849 PRELIMINARY; PRT; 675 AA.
 AC O26849;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Heavy-metal transporting CPX-type ATPase.
 GN MTH755.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RQ SEQUENCE FROM N.A.
 RP STRAIN=Delta H;
 RC MEDLINE=98037514; PubMed=9371463;
 RX Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT deltaH: functional analysis and comparative genomics.";
 RL *J. Bacteriol.* 179:7135-7155(1997).
 DR EMBL; AB00854; AAB85258.1; -.
 DR InterPro; IPR006403; ATPase-IB1_Cu.
 DR InterPro; IPR006416; ATPase-IB_HVY.
 DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR001756; Cu ATPase.
 DR InterPro; IPR005834; Hydrolase.
 DR Pfam; PF00122; E1-E2 ATPase; 1.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00943; CUATPASE.
 DR TIGRFAMs; TIGR01511; ATPase-IB1_Cu; 1.
 DR TIGRFAMs; TIGR01525; ATPase-IB_HVY; 1.
 DR TIGRFAMs; TIGR01494; ATPase_P-type; 3.
 DR PROSITE; PS00154; ATPase_E1-E2; 1.
 KW Complete proteome.
 SQ SEQUENCE 675 AA; 72337 MW; 56A5D4C175C0CC6F CRC64;
 Query Match 94.7%; Score 36; DB 17; Length 675;
 Best Local Similarity 83.3%; Pred. No. 8.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 299 IAWSWL 304
 RESULT 4
 Q98C88 PRELIMINARY; PRT; 91 AA.
 AC Q98C88;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Exopolysaccharide production repressor, ExoX.
 GN MLR5253.
 OS *Rhizobium loti* (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RQ SEQUENCE FROM N.A.
 RC STRAIN=MAPE303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT *Mesorhizobium loti*.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003006; BAB51733.1; -.
 KW Complete proteome.
 SQ SEQUENCE 91 AA; 9887 MW; 10F09237249B37F0 CRC64;
 Query Match 92.1%; Score 35; DB 16; Length 91;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAWSWL 6
 Db 18 VAWSWL 23
 RESULT 5
 O68039 PRELIMINARY; PRT; 116 AA.
 AC O68039;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 12.6 kDa protein.
 OS *Rhodospirillum rubrum* (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 OX NCBI_TaxID=1061;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=SB1003;
RX MEDLINE=97404404; PubMed=9256491;
RA Vleck C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.;
RT "Sequence of a 189-kb segment of the chromosome of Rhodobacter
RT capsulatus SB1003.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
DR EMBL; AF010496; AAC16125.1; -
DR InterPro; IPR005133; PhaG MnhG YufB.
DR Pfam; PF03334; PhaG MnhG YufB; 1.
DR TIGRfams; TIGR01300; CPA_mnhG_phaG; 1.
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 12553 MW; FFB91E726D421996 CRC64;

Query Match          92.1%; Score 35; DB 2; Length 116;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
   |::|||
Db 63 LSWSL 68

RESULT 6
ID 005744 PRELIMINARY; PRT; 135 AA.
AC 005744;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)
DE Hypothetical 14.5 kDa protein.
GN MLCB5.12.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
[1]
RP SEQUENCE FROM N.A.
RA Badcock K., Churcher C.M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188700; PubMed=8446027;
RA Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
RT "Use of an ordered cosmid library to deduce the genomic organization
RT of Mycobacterium leprae.";
RL Mol. Microbiol. 7:197-206(1993).
DR EMBL; Z95151; CAB08408.1; -
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14516 MW; E7B32B2379C4888C CRC64;

Query Match          92.1%; Score 35; DB 2; Length 135;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
   |::|||
Db 23 LSWSL 28

RESULT 7
Q810L0 PRELIMINARY; PRT; 145 AA.
AC Q810L0;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE CG32240-PA (GH04494p).
GN CG32240.

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J.P., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banron J., An H., Baldwin D., Banron J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galie R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragov S., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";

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RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.;
RA Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR003481; AAN11600.1; -
DR EMBL; BT001386; AAN71141.1; -
SQ SEQUENCE 145 AA; 17393 MW; 4EF7D500940F762A CRC64;

Query Match 92.1%; Score 35; DB 5; Length 145;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 36 LSWSWL 41

RESULT 8
Q9KK81 ID Q9KK81 PRELIMINARY; PRT; 172 AA.
AC Q9KK81;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 18.8 kDa protein.
GN CRTK.
OS Brevibacterium linens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococineae; Brevibacteriaceae; Brevibacterium.
OX NCBI_TaxID=1703;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20426;
RX MEDLINE=20279196; PubMed=10821176;
RA Krubasik P., Sandmann G.;
RT "A carotenogenic gene cluster from Brevibacterium linens with novel
RT lycopene cyclase genes involved in the synthesis of aromatic
RT carotenoids.";
RL Mol. Gen. Genet. 263:423-432(2000).
DR EMBL; AF139916; AAF65585.1; -
DR InterPro; IPR006032; Ribosomal_S12_23.
DR InterPro; IPR004307; Tspo_MBR.
DR Pfam; PF03073; Tspo_MBR; 1.
DR PROSITE; PS00055; RIBOSOMAL_S12; 1.
KW Hypothetical protein.
SQ SEQUENCE 172 AA; 18808 MW; 9F6BD848E95875F5 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 172;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 91 VAWSWL 96

RESULT 9
Q50005 ID Q50005 PRELIMINARY; PRT; 196 AA.
AC Q50005;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE U1764V (Hypothetical protein ML1041).
GN ML1041.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RL "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; U15181; AAA62925.1; -
DR EMBL; AL583920; CAC31422.1; -
DR Leproma; ML1041; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 196 AA; 21186 MW; 15D4AF7CDF653936 CRC64;

Query Match 92.1%; Score 35; DB 16; Length 196;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 109 VAWSWL 114

RESULT 10
Q8RSV7 ID Q8RSV7 PRELIMINARY; PRT; 197 AA.
AC Q8RSV7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Maturase (Fragment).
OS uncultured marine bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=56765;
RN [1]
RP SEQUENCE FROM N.A.
RA Podar M., Mullineaux L., Sogin M.I., Perlman P.S.;
RT "Bacterial group II introns in a deep sea hydrothermal vent
RT environment.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075118; AAL78689.1; -
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase; Transferase.
ET NON TER
SQ SEQUENCE 197 AA; 24010 MW; FA76F629B32D836A CRC64;

Query Match 92.1%; Score 35; DB 2; Length 197;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LAWSWL 6
Db 172 LAMNWL 177

RESULT 11
ID 086317 PRELIMINARY; PRT; 210 AA.
AC 086317;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein RV2680.
GN RV2680 OR MT2754 OR MT010.04.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horneby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Blehail W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z96072; CAB09496.1; -.
DR EMBL; AE007105; AAK47069.1; ALT_INIT.
DR TIGR; MT2754; -.
DR TubercuList; RV2680; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 210 AA; 22573 MW; 2D9429BF1FE0956A CRC64;

Query Match 92.18; Score 35; DB 16; Length 210;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LAWSWL 6
Db 123 VAMSWL 128

RESULT 12
ID 094515 PRELIMINARY; PRT; 321 AA.
AC 094515;
DT 01-FEB-1997 (TrEMBLrel. 02, Created).
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE IFC protein (LD15458P) (Sphingolipid delta 4 desaturase protein DES-
DE 1).
OS IFC OR DES1 OR CG9078.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
[1]_
NCBI_TaxID=7227;
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RX MEDLINE=97156918; PubMed=9003299;
RA Endo K., Akiyama T., Kobayashi S., Okada M.;
RT "Degenerative spermatocyte, a novel gene encoding a transmembrane
RT protein required for the initiation of meiosis in Drosophila
RT spermatogenesis.";
RL Mol. Gen. Genet. 253:157-165 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Terne P., Franke S., Zaehring U., Sperling P., Heinz E.;
RT "Identification and Characterization of a Sphingolipid Delta4-
RT Desaturase Family";
RL J. Biol. Chem. 0:0-0 (2002).
DR EMBL; AE003612; AAF52318.1; -.
DR EMBL; X94180; CAAG3889.1; -.
DR EMBL; AY061196; AAL28744.1; -.
DR EMBL; AF466379; AAM12535.1; -.

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DR FlyBase; FBgn0001941; ifc.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR005804; FA_desat fam.
DR InterPro; IPR006025; Zn_WTpeptidase.
DR Pfam; PF00487; FA_desaturase; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Transmembrane.
SQ SEQUENCE 321 AA; 37213 MW; B8DB13961B5F38E CRC64;

Query Match          92.1%; Score 35; DB 5; Length 321;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 64 LWSWL 69

RESULT 13
Q9VFX8 PRELIMINARY; PRT; 329 AA.
AC Q9VFX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG10148 protein.
GN CG10148.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos B.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houtin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimbel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassaman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

```

```

RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003698; AAF54907.1; -.
DR FlyBase; FBgn0038120; CG10148.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 4.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_Typ; 1.
DR PROSITE; PS05066; LRR_TYPICAL; 1.
SQ SEQUENCE 329 AA; 37165 MW; C41063485C334DA CRC64;

Query Match          92.1%; Score 35; DB 5; Length 329;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 17 LAWTWL 22

RESULT 14
Q8FWH6 PRELIMINARY; PRT; 398 AA.
AC Q8FWH6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pyridine nucleotide-disulphide oxidoreductase family protein.
GN BRA0479.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=122711122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettler H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
animal and plant pathogens and symbionts.";
RC Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014545; AAN33671.1; -.
DR TIGR; BRA0479; -.
KW Complete proteome.
SQ SEQUENCE 398 AA; 43624 MW; 574D95CA92B9E424 CRC64;

Query Match          92.1%; Score 35; DB 16; Length 398;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 370 VAWSWL 375

RESULT 15
Q92NU3 PRELIMINARY; PRT; 422 AA.
AC Q92NU3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative NADH dehydrogenase transmembrane protein (EC 1.6.99.3).
GN NDH OR R02079 OR SMC004452.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.

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OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021.
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591789; CAC46658.1; -;
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRDTASEI.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 422 AA; 46023 MW; 1490D9AC1EA517DB CRC64;

Query Match 92.1%; Score 35; DB 16; Length 422;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 394 VAWSWL 399

Search completed: February 18, 2004, 14:35:43
Job time : 19.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
 - 5: /cgn2_6/ptodata/1/iaa/PCRU COMB.pcp.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	92.1	136	4	US-08-311-731A-69
2	35	92.1	136	4	US-08-311-731A-319
3	34	89.5	56	4	US-09-205-258-359
4	34	89.5	63	4	US-08-311-731A-311
5	34	89.5	172	4	US-09-252-991A-17325
6	34	89.5	260	4	US-09-252-991A-21611
7	34	89.5	269	4	US-09-252-991A-31792
8	34	89.5	280	4	US-09-634-238-334
9	34	89.5	313	4	US-09-252-991A-28418
10	34	89.5	320	4	US-09-339-159B-22
11	34	89.5	331	4	US-09-339-159B-12
12	34	89.5	335	4	US-09-252-991A-23948
13	34	89.5	343	4	US-09-252-991A-26240
14	34	89.5	369	4	US-09-339-159B-16
15	34	89.5	468	4	US-09-485-648-4
16	34	89.5	468	4	US-09-503-565-4
17	34	89.5	468	4	US-09-485-649-4
18	34	89.5	468	4	US-09-339-159B-8
19	34	89.5	476	4	US-09-339-159B-4
20	34	89.5	490	4	US-09-339-159B-2
21	34	89.5	493	4	US-09-485-648-2
22	34	89.5	493	4	US-09-503-565-2
23	34	89.5	493	4	US-09-485-649-2
24	34	89.5	493	4	US-09-339-159B-6
25	34	89.5	545	4	US-09-252-991A-25304
26	33	86.8	95	4	US-09-252-991A-19590
27	33	86.8	355	3	US-08-818-112-79

28	33	86.8	355	4	US-08-818-111-80	Sequence 80, Appl
29	33	86.8	355	4	US-09-056-556-79	Sequence 79, Appl
30	33	86.8	355	4	US-09-072-596-80	Sequence 80, Appl
31	33	86.8	416	4	US-09-252-991A-23585	Sequence 23585, A
32	33	86.8	454	4	US-09-252-991A-28780	Sequence 28780, A
33	32	84.2	137	1	US-08-137-117D-31	Sequence 31, Appl
34	32	84.2	137	2	US-08-436-717-31	Sequence 31, Appl
35	32	84.2	187	6	5217891-4	Patent No. 5217891
36	32	84.2	193	4	US-09-252-991A-31699	Sequence 31699, A
37	32	84.2	224	4	US-09-465-901-30	Sequence 30, Appl
38	32	84.2	379	4	US-09-252-991A-26255	Sequence 26255, A
39	32	84.2	745	2	US-08-887-518-3	Sequence 3, Appl1
40	32	84.2	745	2	US-09-023-321-3	Sequence 3, Appl1
41	32	84.2	745	2	US-08-890-853-4	Sequence 3, Appl1
42	32	84.2	745	2	US-09-032-475-3	Sequence 3, Appl1
43	32	84.2	745	2	US-09-099-125A-4	Sequence 4, Appl1
44	32	84.2	745	2	US-09-099-124A-4	Sequence 4, Appl1
45	32	84.2	745	3	US-09-032-476-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1

US-08-311-731A-69

; Sequence 69, Application US/08311731A

; Patent No. 6583266

; GENERAL INFORMATION:

; APPLICANT: SMITH, DOUGLAS

; APPLICANT: MAO, JEN-I

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 411

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WOLF, GREENFIELD & SACKS, P. C.

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/311,731A

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: GATES, EDWARD R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: C0044/7125

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; INFORMATION FOR SEQ ID NO: 69:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 196 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: MYCOBACTERIUM LEPRAE

; US-08-311-731A-69

Query Match 92.1%; Score 35; DB 4; Length 196;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LAWSWL 6

EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 359
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (56)
OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-359

Query Match 89.5%; Score 34; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LAWSW 5
Db 9 LAWSW 13

RESULT 4
US-08-311-731A-311
Sequence 311, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-1
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 311:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
US-08-311-731A-311

Query Match 89.5%; Score 34; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AWSWL 6

Db 43 AWSWL 47

RESULT 5
US-09-252-991A-17325
Sequence 17325, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17325
LENGTH: 172
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17325

Query Match 89.5%; Score 34; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
Db 38 LAWSW 42

RESULT 6
US-09-252-991A-21611
Sequence 21611, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21611
LENGTH: 260
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21611

Query Match 89.5%; Score 34; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
Db 186 LAWSW 190

RESULT 7
US-09-252-991A-31792
Sequence 31792, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 31792
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-31792

Query Match 89.5%; Score 34; DB 4; Length 269;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 Db 232 LAWGWL 237

RESULT 8
 US-09-634-238-334
 ; Sequence 334, Application US/09634238
 ; Patent No. 6544772
 ; GENERAL INFORMATION:
 ; APPLICANT: Glenn, Matthew
 ; APPLICANT: Havukkala, Ilkka J.
 ; APPLICANT: Bloksberg, Leonard, N.
 ; APPLICANT: Lubbers, Mark W.
 ; APPLICANT: Dekker, James
 ; APPLICANT: Christenson, Anna C.
 ; APPLICANT: Holland, Ross
 ; APPLICANT: O'Toole, Paul W.
 ; APPLICANT: Reid, Julian R.
 ; APPLICANT: Coolbear, Timothy
 ; TITLE OF INVENTION: Polynucleotides, materials incorporating
 ; TITLE OF INVENTION: them and methods for using them.
 ; FILE REFERENCE: 11000.1043U1
 ; CURRENT APPLICATION NUMBER: US/09/634,238
 ; CURRENT FILING DATE: 2000-08-08
 ; NUMBER OF SEQ ID NOS: 422
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 334
 ; LENGTH: 280
 ; TYPE: PRT
 ; ORGANISM: Lactobacillus rhamnosus
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(280)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-634-238-334

Query Match 89.5%; Score 34; DB 4; Length 280;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 Db 170 LAWSW 174

RESULT 9
 US-09-252-991A-28418
 ; Sequence 28418, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 28418
 ; LENGTH: 313
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-28418

Query Match 89.5%; Score 34; DB 4; Length 313;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 Db 80 LAWSW 84

RESULT 10
 US-09-339-159B-22
 ; Sequence 22, Application US/09339159B
 ; Patent No. 6566114
 ; GENERAL INFORMATION:
 ; APPLICANT: Kauppinen, Markus
 ; APPLICANT: Schulein, Martin
 ; APPLICANT: Schnorr, Kirk
 ; APPLICANT: Andersen, Lene
 ; APPLICANT: Bjornvad, Mads
 ; TITLE OF INVENTION: No. 6566114el Mannanases
 ; FILE REFERENCE: 5440.204-US
 ; CURRENT APPLICATION NUMBER: US/09/339,159B
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Bacillus sp.
 US-09-339-159B-22

Query Match 89.5%; Score 34; DB 4; Length 320;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 Db 276 LAWSW 280

RESULT 11
 US-09-339-159B-12
 ; Sequence 12, Application US/09339159B
 ; Patent No. 6566114
 ; GENERAL INFORMATION:
 ; APPLICANT: Kauppinen, Markus
 ; APPLICANT: Schulein, Martin
 ; APPLICANT: Schnorr, Kirk
 ; APPLICANT: Andersen, Lene
 ; APPLICANT: Bjornvad, Mads
 ; TITLE OF INVENTION: No. 6566114el Mannanases
 ; FILE REFERENCE: 5440.204-US
 ; CURRENT APPLICATION NUMBER: US/09/339,159B
 ; CURRENT FILING DATE: 1999-06-24
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 331
 ; TYPE: PRT


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; ORGANISM: Bacillus sp.AA112
US-09-339-159B-12

Query Match      89.5%; Score 34; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
        |||||
Db      281 LAWSW 285

RESULT 12
US-09-252-991A-23948
; Sequence 23948, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23948
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23948

Query Match      89.5%; Score 34; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AWSWL 6
        |||||
Db      247 AWSWL 251

RESULT 13
US-09-252-991A-26240
; Sequence 26240, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26240
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26240

Query Match      89.5%; Score 34; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
        |||||
Db      299 LAWSW 303
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RESULT 14
US-09-339-159B-16
; Sequence 16, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schuelein, Martin
; APPLICANT: Schmorr, Kirk
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114el Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-339-159B-16

Query Match      89.5%; Score 34; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
        |||||
Db      318 LAWSW 322

RESULT 15
US-09-485-648-4
; Sequence 4, Application US/09485648
; Patent No. 6376445
; GENERAL INFORMATION:
; APPLICANT: Bettiol, Jean-Luc P.
; APPLICANT: Showell, Michael S.
; TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a
; FILE REFERENCE: Mannanase and protease
; CURRENT APPLICATION NUMBER: US/09/485,648
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/US98/11996
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-485-648-4

Query Match      89.5%; Score 34; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
        |||||
Db      280 LAWSW 284

Search completed: February 18, 2004, 14:41:47
Job time : 8.06579 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-7
Perfect score: 38
Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	89.5	338	1 GALE MYCPN	P75517 mycoplasma
2	34	89.5	1239	1 POLS EREV	P08768 eastern equ
3	34	89.5	1240	1 POLS EREV3	P27284 eastern equ
4	34	89.5	1402	1 N160 MOUSE	Q920w3 mus musculus
5	33	86.8	118	1 YE16 HAEIN	P44186 haemophilus
6	33	86.8	685	1 ROR1 DROME	Q24488 drosophila
7	33	86.8	1053	1 HMDH SCHPO	Q10283 schizosacch
8	33	86.8	1564	1 N184 SCHPO	Q9p7m8 schizosacch
9	32	84.2	60	1 YMFR ECOLI	P75979 escherichia
10	32	84.2	107	1 YNFA RHIL0	Q984u2 rhizobium l
11	32	84.2	136	1 Y07C BPT4	P13323 bacterioph
12	32	84.2	252	1 Y410 RHISN	P55498 rhizobium s
13	32	84.2	446	1 N4M CERCA	Q34048 ceratitidis c
14	32	84.2	471	1 MELE KLEPN	Q07366 enterobacte
15	32	84.2	471	1 MELB KLEPN	Q02581 klebsiella
16	32	84.2	586	1 S132 MOUSE	Q9es88 mus musculus
17	32	84.2	587	1 S132 RAT	P70545 rattus norv
18	32	84.2	592	1 S132 HUMAN	Q13183 homo sapien
19	32	84.2	745	1 IKKA HUMAN	Q15111 h inhibitor
20	32	84.2	745	1 IKKB MOUSE	Q60680 m inhibitor
21	32	84.2	756	1 IKKB HUMAN	O14920 homo sapien
22	32	84.2	757	1 IKKB MOUSE	O88351 mus musculus
23	32	84.2	757	1 IKKB RAT	Q9qy78 rattus norv
24	32	84.2	842	1 AMPN_LACDL	P37896 lactobacilli
25	32	84.2	981	1 RRPO AHNVV	Q9dics atlantic ha
26	32	84.2	982	1 RRPO GGNV	Q993m1 greasy grou
27	31	81.6	51	1 LHB2 ECTHA	P80105 ectothiorho
28	31	81.6	53	1 LHB1 ECTHA	P80104 ectothiorho
29	31	81.6	54	1 LHB5 RHOAC	P35098 rhodopseudo
30	31	81.6	54	1 LHB7 RHOAC	P35099 rhodopseudo
31	31	81.6	247	1 YJ83 YEAST	P47150 saccharomyc
32	31	81.6	255	1 UNG HSVE2	P53765 equine herp
33	31	81.6	262	1 CTE2_MOUSE	P59266 mus musculus

34 31 81.6 278 1 CYST SYN7
35 31 81.6 300 1 Y223_HAEIN
36 31 81.6 326 1 NUJM_ASTPE
37 31 81.6 343 1 YSC2_THETH
38 31 81.6 367 1 NODX_RHILV
39 31 81.6 443 1 FD6C_BRANA
40 31 81.6 447 1 FD6C_SPIOL
41 31 81.6 448 1 FD6C_ARATH
42 31 81.6 467 1 SIL5_MOUSE
43 31 81.6 483 1 VE2_HPV14
44 31 81.6 493 1 VE2_HPV19
45 31 81.6 497 1 VE2_HPV20

ALIGNMENTS

RESULT 1
ID_GALE MYCPN STANDARD; PRT; 338 AA.
AC P75517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-
galactose 4-epimerase).
GN GALE OR MPN257 OR MP576.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RT Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -|- CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose.
CC -|- COFACTOR: NAD.
CC -|- PATHWAY: Galactose metabolism; third step.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.
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CC -----
CC EMBL; AF000056; AAB96224.1; -.
CC PIR; S73902; S73902.
CC HSP; P09147; 1KVS.
CC InterPro; IPR001509; Epimerase_Dh.
CC InterPro; IPR005886; GALE.
CC Pfam; PF01370; Epimerase; 1.
CC TIGRFAMs; TIGR01179; gale; 1.
CC Isomerase; NAD; Galactose metabolism; Complete proteome.
FT NP_BIND 7 38 NAD (POTENTIAL).
SQ SEQUENCE 338 AA; 38132 MW; 9C50FF3856E68C03 CRC64;

Query Match 89.5%; Score 34; DB 1; Length 338;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAWSWL 6
Db 244 LAWKWL 249

RESULT 2
POLY_EEVV STANDARD; PRT; 1239 AA.
AC P08768;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
DE 6 kDa peptide; Spike glycoprotein E1].
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11021;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=82V-2137;
RA MEDLINE=87282265; PubMed=2886548;
RX Chang G.-J., Trent D.W.;
RT "Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus and the deduced amino acid sequence of the viral structural proteins."; J. Gen. Virol. 68:2129-2142(1987).
CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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CC EMBL; X05916; CAA29261.1; -.
CC PIR; A26816; VHWVEE.
CC HSSP; P03315; 1VCP.
CC MEROPS; S03.001; -.
CC InterPro; IPR002548; Alpha_E1_glycop.
CC InterPro; IPR000936; Alpha_E2_glycop.
CC InterPro; IPR002533; Alpha_E3_glycop.
CC InterPro; IPR000930; Togavirin.
CC Pfam; PF00944; Alpha_core; 1.
CC Pfam; PF01589; Alpha_E1_glycop; 1.
CC Pfam; PF00943; Alpha_E2_glycop; 1.
CC Pfam; PF01563; Alpha_E3_glycop; 1.
CC PRINTS; PR00798; TOGAVIRIN.
KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
KW Serine protease.
FT CHAIN 1 259 COAT PROTEIN C.
FT CHAIN 260 322 SPIKE GLYCOPROTEIN E3.
FT CHAIN 323 742 SPIKE GLYCOPROTEIN E2.
FT CHAIN 743 798 6 kDa PEPTIDE.
FT CHAIN 799 1239 SPIKE GLYCOPROTEIN E1.
FT ACT SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 142 142 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 210 210 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT TRANSMEM 261 277 POTENTIAL.
FT TRANSMEM 684 701 POTENTIAL.
FT TRANSMEM 727 737 POTENTIAL.
FT TRANSMEM 777 798 POTENTIAL.
FT TRANSMEM 1211 1235 POTENTIAL.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 932 932 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1239 AA; 137431 MW; 8C7664A405D2D41C CRC64;

Query Match

89.5%; Score 34; DB 1; Length 1239;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AWSWL 6
DB 1205 AWSWL 1209
RESULT 3
POLY_EEVV3 STANDARD; PRT; 1240 AA.
AC P27284;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
DE 6 kDa peptide; Spike glycoprotein E1].
OS Eastern equine encephalitis virus (strain va33[ten broeck]) (Eastern equine encephalomyelitis virus).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11022;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91220727; PubMed=2024496;
RA Weaver S.C., Scott T.W., Rico-Hesse R.;
RT "Molecular evolution of eastern equine encephalomyelitis virus in North America."; Virol. 182:774-784(1991).
CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
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CC EMBL; M69094; AAA42980.1; -.
CC PIR; A39992; VHWVEV.
CC HSSP; P03315; 1VCP.
CC MEROPS; S03.001; -.
CC InterPro; IPR002548; Alpha_E1_glycop.
CC InterPro; IPR000936; Alpha_E2_glycop.
CC InterPro; IPR002533; Alpha_E3_glycop.
CC InterPro; IPR000930; Togavirin.
CC Pfam; PF00944; Alpha_core; 1.
CC Pfam; PF01589; Alpha_E1_glycop; 1.
CC Pfam; PF00943; Alpha_E2_glycop; 1.
CC Pfam; PF01563; Alpha_E3_glycop; 1.
CC PRINTS; PR00798; TOGAVIRIN.
KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
KW Serine protease.
FT CHAIN 1 260 COAT PROTEIN C.
FT CHAIN 261 323 SPIKE GLYCOPROTEIN E3.
FT CHAIN 324 743 SPIKE GLYCOPROTEIN E2.
FT CHAIN 744 799 6 kDa PEPTIDE.
FT CHAIN 800 1240 SPIKE GLYCOPROTEIN E1.
FT ACT SITE 137 137 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 143 143 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 211 211 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT TRANSMEM 259 276 POTENTIAL.
FT TRANSMEM 695 712 POTENTIAL.
FT TRANSMEM 722 738 POTENTIAL.
FT TRANSMEM 781 799 POTENTIAL.
FT TRANSMEM 1212 1236 POTENTIAL.

FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 933 933 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1240 AA; 13790 MW; ABBEB1599D083045 CRC64;
 Query Match 89.5%; Score 34; DB 1; Length 1240;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AWSWL 6
 DB 1206 AWSWL 1210
 RESULT 4
 ID N160_MOUSE STANDARD; PRT; 1402 AA.
 AC Q920W3; Q9CZD9;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa
 DE nucleoporin) (Gene trap locus 1-13) (GTL-13).
 GN NUP160 OR GTL1-13 OR KIAA0197.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Van de Putte T., Cozijnsen M., Dewulf N., Tylzanowski P., Lonnoy O.,
 RA Huylebroeck D.;
 RT "Mus musculus mRNA for gtl-13 (gene trap locus-13), similar to human
 RT KIAA0197 gene (D83781), complete cds.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE OF 1151-1402 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontecki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RN IDENTIFICATION, SUBUNIT, AND SUBCELLULAR LOCATION.
 RX MEDLINE=21448620; PubMed=11564755;
 RA Beigah N., Rabut G., Bai S.W., van Overbeek M., Beaudouin J.,
 RA Daigle N., Zatepina O.V., Pasteau F., Labas V., Fromont-Racine M.,
 RA Ellenberg J., Doye V.;
 RT "An evolutionarily conserved NPC subcomplex, which redistributes in
 RT part to kinetochores in mammalian cells.";
 RL J. Cell Biol. 154:1147-1160(2001).
 RN [4]
 RN IDENTIFICATION, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
 RP MEDLINE=21541555; PubMed=11684705;
 RX

RA Vasu S., Shah S., Orjalo A., Park M., Fischer W.H., Forbes D.J.;
 RT "Novel vertebrate nucleoporins Nup133 and Nup160 play a role in mRNA
 RT export";
 RL J. Cell Biol. 155:339-354(2001).
 CC -|- SUBUNIT: Involved in poly(A)+ RNA transport.
 CC -|- SUBUNIT: Forms part of the Nup160 subcomplex in the nuclear pore
 CC which is composed of Nup160, Nup133, Nup107 and Nup96. This
 CC complex plays a role in RNA export and in tethering Nup98 and
 CC Nup153 to the nucleus.
 CC -|- SUBCELLULAR LOCATION: Nuclear pore complex.
 CC -|- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 1157 and a stop codon in position 1396.
 CC -----
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 CC -----
 DR EMBL; AF104415; AAD17922.2; -;
 DR EMBL; AK012715; BAB28429.1; ALT_FRAME.
 DR MGD; MGI:1326227; Nup160.
 DR GO; GO:0005643; C:nuclear pore; IDA.
 DR GO; GO:0005487; P:nucleocytoplasmic transporter activity; IDA.
 DR GO; GO:0006406; P:mRNA-nucleus export; IDA.
 KW Nuclear protein; Transport.
 FT CONFLICT 1156 1156 A -> T (IN REF. 2).
 FT CONFLICT 1314 1314 E -> G (IN REF. 2).
 FT CONFLICT 1368 1368 N -> D (IN REF. 2).
 SQ SEQUENCE 1402 AA; 158230 MW; 3BF5D9F057D28772 CRC64;
 Query Match 89.5%; Score 34; DB 1; Length 1402;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AWSWL 6
 DB 1230 AWSWL 1234
 RESULT 5
 YE16_HAEIN STANDARD; PRT; 118 AA.
 ID YE16_HAEIN STANDARD; PRT; 118 AA.
 AC P44188;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein H11416 precursor.
 GN H11416
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]_TaxID=727;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
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DR EMBL; U32821; AAC23067.1; -;
 DR PIR; I64028; I64028.
 DR TIGR; H11416; -;
 DR InterPro; IPR006481; Holin_lambda.
 DR Pfam; PF05106; Phage_holin_3; 1.
 DR TIGRFAMs; TIGR01594; holin_lambda; 1.
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 27 POTENTIAL
 FT CHAIN 28 118 HYPOTHETICAL PROTEIN H11416.
 SQ SEQUENCE 118 AA; 13516 MW; 96C5D469F8E2EB CRC64;

Query Match 86.8%; Score 33; DB 1; Length 118;
 Best Local Similarity 83.3%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 DB 11 LIWSWL 16

RESULT 6

ID ROR1_DROME STANDARD; PRT; 685 AA.
 AC Q24488;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor
 DE (EC 2.7.1.112) (dRor).
 GN ROR OR CG4926.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=Canton-S; TISSUE=Larval brain;
 RX MEDLINE=93348222; PubMed=8394009;
 RA Wilson C., Guberhan D.C.I., Steller H.;
 RT "Dror", a potential neurotrophic receptor gene, encodes a Drosophila
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
 RT kinases."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gilbert W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE OF 545-597 FROM N.A.
 RX MEDLINE=98401146; PubMed=9731193;
 RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA."
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -!- FUNCTION: Tyrosine-protein kinase receptor that functions during
 CC early stages of neuronal development.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
 CC system.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR
 CC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -----
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EMBL; L20297; AAA28860.1; -;
 EMBL; AE003628; AAF52885.1; -;
 EMBL; AJ002908; CAA05743.1; -;
 PIR; A48289; A48289.
 HSP; F11362; IFGK.
 DR Flybase; FBgn0010407; Ror.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004713; F:protein tyrosine kinase activity; NAS.
 DR GO; GO:0007417; P:central nervous system development; IEP.
 DR GO; GO:0006458; P:protein amino acid phosphorylation; NAS.
 DR InterPro; IPR000024; FZ domain.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002011; RTK_naseI.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000395; Kringle; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 KW Transferase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;
 KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
 KW Developmental protein.
 FT SIGNAL 1 24
 FT CHAIN 25 685
 FT
 FT DOMAIN 25 317
 FT TRANSMEM 318 338
 FT DOMAIN 339 685
 FT DOMAIN 36 225
 FT DOMAIN 236 310
 FT DOMAIN 410 677
 FT NP_BIND 416 424
 FT BINDING 442 442
 FT ACT_SITE 539 539
 FT MOD_RES 565 565
 FT MOD_RES 569 569
 FT MOD_RES 570 570
 FT CARBOHYD 45 45
 FT CARBOHYD 63 63
 FT CARBOHYD 129 129
 FT CARBOHYD 144 144
 FT CARBOHYD 250 250
 SQ SEQUENCE 685 AA; 78142 MW; 526162D27D5PD7C7 CRC64;

Query Match 86.88; Score 33; DB 1; Length 685;
 Best Local Similarity 83.38; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 |
 |
 |
 |
 Db 259 LRWSWL 264

RESULT 7
 HMDH SCHPO STANDARD; PRT; 1053 AA.
 AC Q10283; O74425;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 18-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA reductase).
 DE HMG1 OR SPCC162.09C.
 GN Schizosaccharomyces pombe (Fission yeast).
 OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97051601; PubMed=8896278;
 RA Lum P.Y., Edwards S., Wright R.;
 RT "Molecular, functional and evolutionary characterization of the gene encoding HMG-CoA reductase in the fission yeast, Schizosaccharomycetes pombe."
 RT pombe."
 RL Yeast 12:1107-1124 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras J., Peat N., Hayles J., Baker S., Basham S., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeall C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Fohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe."
 RL Nature 415:871-880 (2002).
 CC -1- FUNCTION: INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS. IT
 IS THE RATE-LIMITING ENZYME OF THE STEROL BIOSYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: (R)-mevalonate + CoA + 2 NADP(+) = (S)-3-
 hydroxy-3-methylglutaryl-CoA + 2 NADPH.
 CC -1- PATHWAY: Cholesterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 reticulum.
 CC -1- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.
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 DR EMBL; L76979; AAB39277.1; -;
 DR EMBL; AL023860; CAA19589.1; -;
 DR PIR; S72194; S72194.
 DR GeneDB.SPombe; SPCC162.09c; -;
 DR InterPro; IPR002202; HMG-CoA red.
 DR InterPro; IPR004554; HMG CoA R_NADP.
 DR InterPro; IPR000731; SSD_5TM.
 DR Pfam; PF00368; HMG-CoA_red; 1.
 DR PRINTS; PR00071; HMGCOARDTASE.
 DR TIGRFAMs; TIGR00533; HMG CoA R_NADP; 1.
 DR PROSITE; PS00066; HMG CoA REDUCTASE 1; 1.
 DR PROSITE; PS00318; HMG CoA REDUCTASE 2; 1.
 DR PROSITE; PS01192; HMG CoA REDUCTASE 3; FALSE_NEG.
 DR PROSITE; PS00065; HMG CoA REDUCTASE 4; 1.
 DR PROSITE; PS0156; SSD; 1.
 KW Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;
 KW Cholesterol biosynthesis; NADP.
 FT DOMAIN 1 547
 FT DOMAIN 548 615
 FT LINKER
 FT DOMAIN 616 1053
 FT CATALYTIC
 FT TRANSMEM 9 29
 FT TRANSMEM 204 224
 FT TRANSMEM 233 253
 FT TRANSMEM 259 279
 FT TRANSMEM 321 341
 FT TRANSMEM 342 362
 FT TRANSMEM 418 438
 FT TRANSMEM 527 547
 FT TRANSMEM 570 578
 FT ACT_SITE 712 712
 FT ACT_SITE 922 922
 FT ACT_SITE 1018 1018
 FT CARBOHYD 137 137
 FT CARBOHYD 399 399
 FT CARBOHYD 518 518
 FT CARBOHYD 578 578

BY SIMILARITY.
 GENERAL BASE (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 751 751 N -> D (IN REF. 1).
SQ SEQUENCE 1053 AA; 114876 MW; 33E5C2365222D238 CRC64;

Query Match 86.8%; Score 33; DB 1; Length 1053;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 177 ILSWSL 182

RESULT 8
N184-SCHPO STANDARD; PRT; 1564 AA.
AC Q9P7M8; Q9Y8G4;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nucleoporin nup184 (Nuclear pore protein nup184).
GN NUP184 OR SPAP27G11.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=972;
RX MEDLINE=99318821; PubMed=10388805;
RA Whalen W.A., Yoon J.H., Shen R., Dhar R.;
RT "Regulation of mRNA export by nutritional status in fission yeast.";
RL Genetics 152:827-838(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voiclaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wamburt R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: INTERACTS WITH POM152 IN THE CORE STRUCTURE OF THE
CC NUCLEAR PORE COMPLEX (NPC). INVOLVED IN THE EXPORT OF MRNA.
CC -!- SUBCELLULAR LOCATION: Nuclear pore complex.
CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1560
CC ONWARD AND IS LONGER (1628 AA) DUE TO A FRAMESHIFT.
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-----
DR EMBL; AF055035; AAD43830.1; ALT_FRAME.
DR EMBL; AL157917; CAB76031.1; -.
DR GensDB_SPombe; SPAP27G11.10C; -.
KW Nuclear protein; Transport.
FT CONFLICT 1219 1219
SQ SEQUENCE 1564 AA; 176962 MW; 248F3AEF338C30B7 CRC64;

Query Match 86.8%; Score 33; DB 1; Length 1564;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
DB 6 LSWSWI 11

RESULT 9
YMF8-ECOLI STANDARD; PRT; 60 AA.
AC P75979;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ymf8.
GN YMF8 OR B1150.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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-----
DR EMBL; AE000214; AAC74234.1; -.
DR EMBL; D90749; BAA35976.1; -.
DR EMBL; D90750; BAA35988.1; -.
DR PIR; C64860; C64860.
DR EcoGene; EGI14336; ymfR.
```



```

KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 5 25 POTENTIAL.
FT TRANSMEM 26 46 POTENTIAL.
SQ SEQUENCE 60 AA; 6381 MW; . A41487AAFEED364A CRC64;

Query Match      84.2%; Score 32; DB 1; Length 60;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
   | |||
Db 39 LFWSWL 44

RESULT 10
YNFA RHILQ
ID _YNFA RHILQ STANDARD; PRT; 107 AA.
AC Q984U2; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hypothetical protein mll7841.
GN MLL7841.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE UPF0060 FAMILY.
CC -----
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CC -----
DR EMBL; AP003012; BAB54221.1; -.
DR HAMAP; MF_00010; -.
DR InterPro; IPR003844; UPF0060.
DR Pfam; PF02694; UPF0060; 1.
DR ProDom; PD015609; UPF0060; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
SQ SEQUENCE 107 AA; 11591 MW; 0C666D85212C16C3 CRC64;

Query Match      84.2%; Score 32; DB 1; Length 107;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
   | |||
Db 71 LAWLWL 76

RESULT 11
Y07C_BPT4
ID Y07C_BPT4 STANDARD; PRT; 136 AA.
AC P13323;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE Hypothetical 16.0 kDa protein in segB-ipi intergenic region (ORF3).
GN Y07C OR IPI.-2 OR TRNA.3.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86037230; PubMed=4057254;
RA Broida J., Abelson J.;
RT "Sequence organization and control of transcription in the
RT bacteriophage T4 trNA region.";
RL J. Mol. Biol. 185:545-563(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Taugita A., Mosig G.,
RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X03016; CA26805.1; -.
DR EMBL; AF158101; AAD42681.1; -.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 16034 MW; 02ED3B4D8D274D9A CRC64;

Query Match      84.2%; Score 32; DB 1; Length 136;
Best Local Similarity 80.0%; Pred. No. 16+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWSWL 6
   ||||
Db 35 AWSWI 39

RESULT 12
Y4IO RHISN
ID _Y4IO RHISN STANDARD; PRT; 252 AA.
AC P55498;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 28.6 kDa protein Y4IO.
GN Y4IO
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: LOW SIMILARITY TO THE IS1111A/IS1328/IS1533 FAMILY OF
CC TRANSPOSASES.
CC -1- SIMILARITY: HIGH TO F13; SOME, TO Y4PF/Y4SB AND Y4QE.
CC -----
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CC -----
 DR EMBL; A5000079; AAB91710.1; -;
 DR InterPro; IPR003346; Transposase_20;
 DR Pfam; PF02371; Transposase_20; 1;
 KW Hypochemical protein; Plasmid.
 SQ SEQUENCE 252 AA; 28552 MW; D993C7DA03E15190 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 252;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 |||||
 Db 190 LAWLWL 195

RESULT 13
 NU4M CERCA STANDARD; PRT; 446 AA.
 ID NU4M CERCA Q34053;
 AC Q34053; Q34053;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
 GN ND4.
 OS Ceratitidis capitata (Mediterranean fruit fly).

OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Tephritidae; Tephritidae; Ceratitidis.
 OX NCBI_TaxID=7213;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Guatemala laboratory colony, and Hawaii laboratory colony;
 RX MEDLINE=95261546; PubMed=7742977;
 RA Gasparich G.E., Sheppard W.S., Han H.Y., McPherson B.A., Steck G.J.;
 RT "Analysis of mitochondrial DNA and development of PCR-based
 RT diagnostic molecular markers for Mediterranean fruit fly (Ceratitidis
 RT capitata) populations.";
 RL Insect Mol. Biol. 4:61-67(1995).

CC -! CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -----
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CC -----
 DR EMBL; U12925; AAA85797.1; -;
 DR EMBL; U12924; AAA85796.1; -;
 DR InterPro; IPR003918; NADHub_oxred4.
 DR InterPro; IPR001750; Oxidored q1.
 DR InterPro; IPR000260; Oxidored q5 N.
 DR Pfam; PF00361; oxidored q1; 1_1_5_N.
 DR Pfam; PF01059; oxidored q5 N; 1.
 DR PRINTS; PR01437; NUOXDRDTS4.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 446 AA; 50967 MW; E9AAAC06796897FD CRC64;

Query Match 84.2%; Score 32; DB 1; Length 446;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 ::|||

Db 374 VSWSWL 379
 RESULT 14
 MELB ENTAE STANDARD; PRT; 471 AA.
 ID MELB ENTAE AC 007366;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melibiose carrier protein (Thiomethylgalactoside permease II)
 DE (Melibiose permease) (Na+ (Li+)/melibiose symporter) (Melibiose
 DE transporter).
 GN MELB.
 OS Enterobacter aerogenes (Aerobacter aerogenes).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxID=548;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97332569; PubMed=9188803;
 RA Okazaki N., Kuroda M., Shimamoto T., Shimamoto T., Tsuchiya T.;
 RT "Characteristics of the melibiose transporter and its primary
 RT structure in Enterobacter aerogenes.";
 RL Biochim. Biophys. Acta 1326:83-91(1997).
 CC -! FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS
 CC CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS
 CC FOR COTRANSPORT, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED
 CC (SYMPORT SYSTEM).
 CC -! SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -! SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
 CC (SGF).
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; D86576; BAA20461.1; -;
 DR InterPro; IPR001927; Na/Gal symport.
 DR TIGRFAMs; TIGR00792; gph; 1_
 DR PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
 KW Transport; Sugar transport; Transmembrane; Inner membrane; Symport.
 FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 12 32 POTENTIAL.
 FT DOMAIN 33 36 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 37 57 POTENTIAL.
 FT DOMAIN 58 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 100 POTENTIAL.
 FT DOMAIN 101 106 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 107 127 POTENTIAL.
 FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 150 170 POTENTIAL.
 FT DOMAIN 171 175 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 176 196 POTENTIAL.
 FT DOMAIN 197 234 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 255 POTENTIAL.
 FT DOMAIN 256 266 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 267 287 POTENTIAL.
 FT DOMAIN 288 296 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 297 317 POTENTIAL.
 FT DOMAIN 318 323 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 324 344 POTENTIAL.
 FT DOMAIN 345 373 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 374 394 POTENTIAL.
 FT DOMAIN 395 411 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 412 432 POTENTIAL.
 FT DOMAIN 433 471 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 471 AA; 52214 MW; 9755D85D91828106 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 471;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 |||||
 Db 106 LAWVWL 111

RESULT 15

MELB_KLEPN STANDARD; PRT; 471 AA.
 AC Q02581;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melibiose carrier protein (Thiomethylgalactoside permease II)
 DE (Melibiose permease) (Na+ (Li+)/melibiose symporter) (Melibiose
 transporter).
 GN MELB.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2002;
 RX MEDLINE=92406738; PubMed=1339436;
 RA Hama H., Wilson T.H.;
 RT "Primary structure and characteristics of the melibiose carrier of
 Klebsiella pneumoniae.";
 RL J. Biol. Chem. 267:18371-18376(1992).
 CC -I- FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS
 CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS
 FOR COTRANSPORT, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED
 (SYMPORT SYSTEM). IT CATALYZES HYDROGEN CATION-MELIBIOSE, LITHIUM
 CATION-LACTOSE, & HYDROGEN/LITHIUM CATIONS-METHYL-1-THIO-BETA-D-
 GALACTOPYRANOSIDE (TMG) COTRANSPORT. THIS PROTEIN SEEMS TO BE
 LACKING THE ABILITY TO RECOGNIZE SODIUM CATIONS.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -I- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
 (SGP).

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 CC ENBL; M97257; AAA25067.1; --
 DR PIR; B44166.
 DR InterPro; IPR001927; Na/Gal_symport.
 DR TIGRFAMs; TIGR00792; gph; 1.
 DR PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
 KW Transport; Sugar transport; Transmembrane; Inner membrane; Symport.
 FT DOMAIN 1 11
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 12 32
 FT POTENTIAL.
 FT DOMAIN 33 36
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 37 57
 FT POTENTIAL.
 FT DOMAIN 58 79
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 100
 FT POTENTIAL.
 FT DOMAIN 101 106
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 107 127
 FT POTENTIAL.
 FT DOMAIN 128 149
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 150 170
 FT POTENTIAL.
 FT DOMAIN 171 175
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 176 196
 FT POTENTIAL.
 FT DOMAIN 197 234
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 235 255
 FT POTENTIAL.
 FT DOMAIN 256 266
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 267 287
 FT POTENTIAL.

FT DOMAIN 288 296
 FT TRANSMEM 297 317
 FT POTENTIAL.
 FT DOMAIN 318 323
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 324 344
 FT POTENTIAL.
 FT DOMAIN 345 373
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 374 394
 FT POTENTIAL.
 FT DOMAIN 395 411
 FT PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 412 432
 FT POTENTIAL.
 FT DOMAIN 433 471
 FT CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 471 AA; 52329 MW; 6D373D09BF4BAEC7 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 471;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 |||||
 Db 106 LAWVWL 111

Search completed: February 18, 2004, 14:28:05
 Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-7
Perfect score: 38
Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	94.7	675	2 H69200	heavy-metal transp
2	35	92.1	116	2 T03472	conserved hypotet
3	35	92.1	172	2 T51122	crkK protein limpo
4	35	92.1	196	2 C87039	conserved hypotet
5	35	92.1	210	2 C70528	hypothetical prote
6	35	92.1	421	2 A12824	NADH dehydrogenase
7	35	92.1	438	2 H97602	probable NADH dehy
8	35	92.1	441	2 A13607	NADH2 dehydrogenas
9	34	89.5	136	2 A10124	probable prephilin
10	34	89.5	151	2 AE2249	hypothetical prote
11	34	89.5	162	2 B83635	conserved hypotet
12	34	89.5	207	2 A48608	E1 glycoprotein -
13	34	89.5	224	2 C48652	transfer protein s
14	34	89.5	264	2 H83224	phosphonate transp
15	34	89.5	266	2 C83602	prolipoprotein dia
16	34	89.5	296	2 E83292	conserved hypotet
17	34	89.5	338	2 S73902	UDP-glucose 4-epim
18	34	89.5	357	2 C97564	hypothetical prote
19	34	89.5	446	2 A83355	hypothetical prote
20	34	89.5	516	2 JE0134	mannan endo-1,4-be
21	34	89.5	709	2 F75584	hypothetical prote
22	34	89.5	1147	2 T35781	hypothetical prote
23	34	89.5	1239	1 VHWVEE	structural polypro
24	34	89.5	1240	1 VHWVEV	genome polypeptide
25	34	89.5	1241	2 S26373	structural polypro
26	34	89.5	1242	2 S72350	structural polypro
27	34	89.5	1242	2 A56605	hypothetical prote
28	34	89.5	1315	2 T05300	hypothetical prote
29	34	89.5	1411	2 T48529	hypothetical prote

30	34	89.5	4924	2 T50176	probable peptide s
31	33	86.8	65	2 E83492	hypothetical prote
32	33	86.8	72	2 AD2464	hypothetical prote
33	33	86.8	118	2 I64028	hypothetical prote
34	33	86.8	306	2 G82256	conserved hypotet
35	33	86.8	311	2 AE3169	hypothetical prote
36	33	86.8	355	2 F70983	probable serine pr
37	33	86.8	420	2 E72357	sugar ABC transpor
38	33	86.8	433	2 E70968	hypothetical prote
39	33	86.8	440	2 D87076	probable conserved
40	33	86.8	661	2 F83342	probable cation-tr
41	33	86.8	685	1 A48289	neurotrophic recep
42	33	86.8	919	2 T37062	probable transcrip
43	33	86.8	1053	2 S72194	hydroxymethylgluta
44	33	86.8	1628	2 T43682	nucleoporin - fiss
45	33	86.8	2121	2 T27406	hypothetical prote

ALIGNMENTS

RESULT 1

H69200 heavy-metal transporting CPx-type ATPase - Methanobacterium thermoautotrophicum (strain C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C; Accession: H69200
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: H69200
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-675 <MTH>
A; Cross-references: GB:AE000854; GB:AE000666; NID:G2621839; PIDN:AAB85258.1; PID:G26218
A; Experimental source: Strain Delta H
C; Genetics:
A; Gene: MTH755
C; Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding
F; 76-413/Domain: ATPase transduction domain homology <ATT>
F; 484-626/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 94.7%; Score 36; DB 2; Length 675;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6

Db 299 IAWSWL 304

RESULT 2

T03472 conserved hypothetical protein - Rhodobacter capsulatus
C; Species: Rhodobacter capsulatus
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C; Accession: T03472
R; Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A; Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB100
A; Reference number: Z14955; MUID:97404404; PMID:9256491
A; Accession: T03472
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-116 <VLC>

A; Cross-references: EMBL:AF010496; NID:G3128256; PIDN:AAC16125.1; PID:G3128273
C; Genetics:
A; Map position: 1

Query Match 92.1%; Score 35; DB 2; Length 116;

Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
:|||||
Db 63 LSWSWL 68

RESULT 3
T51122
crkK protein [imported] - Brevibacterium linens
C:Species: Brevibacterium linens
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
A:Accession: T51122
R:Krubasik, P.; Sandmann, G.
Mol. Gen. Genet. 263, 423-432, 2000
A:Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cyc
A:Reference number: Z25303; MUID:20279196; PMID:10821176
A:Accession: T51122
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-172 <KRU>
A:Cross-references: EMBL:AF139916; PIDN:AAF65585.1
A:Experimental source: DSM 20426; ATCC9175
C:Genetics:
A:Gene: crkK

Query Match 92.1%; Score 35; DB 2; Length 172;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
:|||||
Db 91 VAWSWL 96

RESULT 4
C87039
conserved hypothetical protein ML1041 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: C87039
R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: C87039
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <STO>
A:Cross-references: GB:AL450380; NID:gl3093055; PIDN:CAC31422.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML1041
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

Query Match 92.1%; Score 35; DB 2; Length 196;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
:|||||
Db 109 VAWSWL 114

RESULT 5
C70528
hypothetical protein Rv2680 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2000
C:Accession: C70528

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rejandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70528
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <COL>
A:Cross-references: GB:Z96072; GB:AL123456; NID:g3261793; PIDN:CAB09496.1; PID:el300031.
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv2680
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

Query Match 92.1%; Score 35; DB 2; Length 210;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
:|||||
Db 123 VAWSWL 128

RESULT 6
A12824
NADH dehydrogenase ndh [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: A12824
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: A12824
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <KUP>
A:Cross-references: GB:AE008688; PIDN:AAL43015.1; PID:gl7740478; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: ndh
A:Map position: circular chromosome
C:Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
:|||||
Db 393 VAWSWL 398

RESULT 7
H97602
probable NADH dehydrogenase (Y09899) [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: H97602
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: H97602
A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-438 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK87777.1; PID:gl51517148; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_3667
 A:Map position: circular chromosome
 C:Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 438;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 :|||||
 Db 410 VAWSWL 415

RESULT 8
 AI3607
 NADH2 dehydrogenase (EC 1.6.99.3) [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
 C:Accession: AI3607
 R:DeiVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujez, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688

A:Accession: AI3607
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-441 <KUR>
 A:Cross-references: GB:AE008918; PIDN:AAL54028.1; PID:gl7984981; GSPDB:GN00191
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME110786
 A:Map position: 11
 C:Superfamily: NADH dehydrogenase
 C:Keywords: oxidoreductase

Query Match 92.1%; Score 35; DB 2; Length 441;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 :|||||
 Db 413 VAWSWL 418

RESULT 9
 AI0124
 probable prepilin peptidase dependent protein YP01017 [imported] - Yersinia pestis (stra
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AI0124
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; PMID:21470413; PMID:11586360

A:Accession: AI0124
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC89860.1; PID:gl5979085; GSPDB:GN00175
 C:Genetics:
 A:Gene: YP01017

Query Match 89.5%; Score 34; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWSWL 6
 :|||||
 Db 68 AWSWL 72

RESULT 10

AE2249
 hypothetical protein alr3548 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AE2249
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; PMID:21595285; PMID:11759840
 A:Accession: AE2249
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BAB75247.1; PID:gl7132681; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr3548

Query Match 89.5%; Score 34; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 :|||||
 Db 18 LAWSW 22

RESULT 11

B83635
 conserved hypothetical protein PA0085 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: B83635
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lin,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A:Reference number: AB2950; PMID:20437337; PMID:10984043
 A:Accession: B83635
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-162 <STO>
 A:Cross-references: GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AAG03475.1; GSPDB:GN001

A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA0085

Query Match 89.5%; Score 34; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 :|||||
 Db 28 LAWSW 32

RESULT 12

A48608
 E1 glycoprotein - eastern equine encephalomyelitis virus (fragment)
 C:Species: eastern equine encephalomyelitis virus
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
 C:Accession: A48608
 R:Weaver, S.C.; Bellow, L.A.; Gousset, L.; Repik, P.M.; Scott, T.W.; Holland, J.J.
 Virology 195, 700-709, 1993

A:Title: Diversity within natural populations of eastern equine encephalomyelitis virus.
 A:Reference number: A48608; MUID:93331728; PMID:8101674
 A:Contents: 215-85, MD85B
 A:Accession: A48608
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-207 <WEA>
 A:Cross-references: GB:S63996; NID:g400551; PIDN:AA827576.1; PID:g400552
 A>Note: sequence extracted from NCBI backbone (NCBIN:135481, NCBI:P:135482)
 C:Superfamily: togavirus structural polyprotein
 C:Keywords: glycoprotein

Query Match 89.5%; Score 34; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AWSWL 6
 Db 173 AWSWL 177

RESULT 13
 C48652
 transfer protein spdA - Streptomyces ambofaciens plasmid pSAM2
 C:Species: Streptomyces ambofaciens
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 22-Oct-1999
 C:Accession: C48652; S33428
 R:Haeghe, J.; Pernodet, J.L.; Sezouov, G.; Gerbaud, C.; Friedmann, A.; Guerineau, M.
 J. Bacteriol. 175, 5529-5538, 1993
 A:Title: Transfer functions of the conjugative integrating element pSAM2 from Streptomyces
 A:Reference number: A48652; MUID:93374848; PMID:8366038
 A:Accession: C48652
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-224 <HAG>
 A:Cross-references: EMBL:Z19593; NID:g298051; PIDN:CAA79641.1; PID:g298054
 C:Genetics:
 A:Genome: plasmid

Query Match 89.5%; Score 34; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 Db 66 LAWSW 70

RESULT 14
 H83224
 phosphonate transport protein PhnE PA3382 [imported] - Pseudomonas aeruginosa (strain PA
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83224
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83224
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <STO>
 A:Cross-references: GB:AE004759; GB:AE004091; NID:g9949500; PIDN:AA806770.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: phnE; PA3382
 C:Superfamily: phnE protein

Query Match 89.5%; Score 34; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSW 5
 Db 31 LAWSW 35

RESULT 15
 C83602

prolipoprotein diacylglycerol transferase PA0341 [imported] - Pseudomonas aeruginosa (st
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: C83602
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: C83602
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-266 <STO>
 A:Cross-references: GB:AE004472; GB:AE004091; NID:g9946188; PIDN:AA803730.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: lgt; PA0341
 C:Superfamily: prolipoprotein diacylglycerol transferase

Query Match 89.5%; Score 34; DB 2; Length 266;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
 Db 229 LAWSWL 234

Search completed: February 18, 2004, 14:38:40
 Job time : 7.5921 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	236	3 Q8NJY9	Q8njy9 bionectria
2	37	92.5	274	16 Q8G659	Q8g659 bifidobacte
3	37	92.5	437	16 Q92K30	Q92k30 rhizobium m
4	37	92.5	548	16 Q92M15	Q92m15 rhizobium m
5	37	92.5	581	5 Q8MSH3	Q8msh3 drosophila
6	37	92.5	597	5 Q9VGP2	Q9vgp2 drosophila
7	37	92.5	610	16 Q86712	Q86712 streptomyce
8	37	92.5	885	16 Q9I389	Q9i389 pseudomonas
9	36	90.0	205	16 Q9ACR5	Q9acr5 streptomyce
10	36	90.0	227	4 Q8IXK8	Q8ixk8 homo sapien
11	36	90.0	242	12 Q919K8	Q919k8 culex nigri
12	36	90.0	355	11 Q8BIT9	Q8bit9 mus musculu
13	36	90.0	358	10 O50002	O50002 prunus arme
14	36	90.0	374	16 Q9HZ10	Q9hz10 pseudomonas
15	36	90.0	433	16 Q8P4A1	Q8p4a1 xanthomonas
16	36	90.0	438	16 Q8PFV8	Q8pfv8 xanthomonas

17	36	90.0	452	4 Q96AB7	Q96ab7 homo sapien
18	36	90.0	463	5 Q8MMJ0	Q8mmj0 apis cerana
19	36	90.0	477	11 Q9CYU6	Q9cyu6 mus musculu
20	36	90.0	484	4 Q9BTU6	Q9btu6 homo sapien
21	36	90.0	686	16 Q8FQZ9	Q8fqz9 corynebacte
22	36	90.0	889	16 Q9AAZ6	Q9aaz6 caulobacter
23	36	90.0	1005	10 Q9XGZ2	Q9xgz2 arabidopsis
24	36	90.0	5435	2 Q9L4X2	Q9l4x2 streptomyce
25	34	85.0	166	4 Q8NBW1	Q8nbw1 homo sapien
26	34	85.0	273	10 Q94JM4	Q94jm4 arabidopsis
27	34	85.0	273	10 Q94OD6	Q94od6 arabidopsis
28	34	85.0	275	10 Q65710	Q65710 arabidopsis
29	34	85.0	376	3 Q9UVL4	Q9uvl4 penicillium
30	34	85.0	617	10 P93050	P93050 arabidopsis
31	34	85.0	1074	16 Q8PJ70	Q8pj70 xanthomonas
32	34	85.0	1842	3 Q96WT6	Q96wt6 schizosacch
33	34	85.0	1842	3 Q96WT7	Q96wt7 schizosacch
34	34	85.0	1842	3 Q96WT8	Q96wt8 schizosacch
35	33	82.5	49	6 Q8SPL6	Q8spl6 equus caball
36	33	82.5	98	5 Q9VB45	Q9vb45 drosophila
37	33	82.5	136	2 Q8KZ39	Q8kz39 uncultured
38	33	82.5	154	11 Q8BGD2	Q8bgd2 mus musculu
39	33	82.5	161	6 Q8MUT3	Q8mjt3 oryctolagus
40	33	82.5	161	11 Q921P9	Q921p9 rattus norv
41	33	82.5	198	16 Q9PA54	Q9pa54 xylella fas
42	33	82.5	213	12 Q9ELI7	Q9eli7 meleagrid h
43	33	82.5	213	12 Q9DPT1	Q9dpt1 meleagrid h
44	33	82.5	234	3 Q8NJY6	Q8njy6 hypocrea sc
45	33	82.5	234	3 O00095	O00095 trichoderma

ALIGNMENTS

RESULT 1

Q8NJY9 PRELIMINARY; PRT; 236 AA.
ID Q8NJY9
AC Q8NJY9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Endoglucanase.
GN CEL12C.
OS Bionectria ochroleuca
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Bionectriaceae; Bionectria.
OX NCBI_TaxID=29856;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22067395; PubMed=12073090;
RA Goedegebuur P., Fowler T., Phillips J., van der Kley P.,
van Solingen P., Dankmeyer L., Power S.D.;
RT "Cloning and relational analysis of 15 novel fungal endoglucanases
from family 12 glycosyl hydrolase.",
RL Curr. Genet. 41:89-98(2002).
DR EMBL: AF435065; AM77708.1;
DR InterPro: IPR002594; Glyco_hydro_12.
DR PFam: PF01670; Glyco_hydro_12; 1.
DR ProDom: PD004316; Glyco_hydro_12; 1.
SQ SEQUENCE 236 AA; 26024 MW; C308A7E33F0C41D8 CRC64;

Query Match 92.5%; Score 37; DB 3; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

Db 63 ADMSWS 68

RESULT 2

Q8G659 PRELIMINARY; PRT; 274 AA.
ID Q8G659

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AC Q8G59;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable dithydroorotate dehydrogenase electron transfer subunit.
GN PYRK OR BL0790.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Fessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RA "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014701; AA24605.1; -.
KW Complete proteome.
SQ SEQUENCE 274 AA; 29978 MW; 971E0016E79636DB CRC64;

Query Match 92.5%; Score 37; DB 16; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 171 ADMSWS 176
|||||

RESULT 3
Q92K30
ID Q92K30 PRELIMINARY; PRT; 437 AA.
AC Q92K30;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein R02283.
GN R02283 OR SMC01671.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591791; CAC47210.1; -.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00211; ABC TRANSPORTER; 1.
DR PROSITE; PS00455; AMP BINDING; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 235 ADMSWA 240
|||||

RESULT 5
Q8MSH3
ID Q8MSH3 PRELIMINARY; PRT; 581 AA.
AC Q8MSH3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GH24640p.
GN CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118818; AAM50678.1; -.
DR FlyBase; FBgn0037896; CG6728.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00732; GMC_oxred; 3.
DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.
DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.
SQ SEQUENCE 581 AA; 63475 MW; A3F13BEC25B496D CRC64;

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ID Q92MI5 PRELIMINARY; PRT; 548 AA.
AC Q92MI5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative fatty-acid-CoA ligase protein (EC 6.-.-.-).
GN R02631 OR SMC00741.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591791; CAC47210.1; -.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00211; ABC TRANSPORTER; 1.
DR PROSITE; PS00455; AMP BINDING; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 235 ADMSWA 240
|||||

RESULT 5
Q8MSH3
ID Q8MSH3 PRELIMINARY; PRT; 581 AA.
AC Q8MSH3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GH24640p.
GN CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118818; AAM50678.1; -.
DR FlyBase; FBgn0037896; CG6728.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00732; GMC_oxred; 3.
DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.
DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.
SQ SEQUENCE 581 AA; 63475 MW; A3F13BEC25B496D CRC64;

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Query Match      92.5%; Score 37; DB 5; Length 581;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWA 6
Db      158 SDMSWA 163

RESULT 6
Q9VGP2 PRELIMINARY; PRT; 597 AA.
ID Q9VGP2
AC Q9VGP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE C66728 protein.
GN C66728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benton P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foele C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003691; AAF54634.1; -.
DR FlyBase; FBgn0037896; GMC 6728.
DR InterPro; IPR000172; GMC oxid.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00732; GMC oxid; 1.
DR PROSITE; PS00624; GMC OXRED; 2; 1.
DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.
SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFA0902A CRC64;

Query Match      92.5%; Score 37; DB 16; Length 610;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWA 6
Db      83 ADMSWA 88

RESULT 7
Q9I389 PRELIMINARY; PRT; 885 AA.
ID Q9I389
AC Q9I389;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Two-component sensor KdpD.
GN KDPD OR PA1636.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RC MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

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RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen.";
 CC Nature 406:959-964 (2000).
 RL -I- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
 DR EMBL; AB004591; AAG05025.1; --
 DR HSSP; P02933; IJOY.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR004338; GAF.
 DR InterPro; IPR003018; GAF_sens_pr_C.
 DR InterPro; IPR003661; His_kinA.
 DR InterPro; IPR005467; His_kinase.
 DR InterPro; IPR003852; KdpD.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00512; HiskA_1.
 DR PRINTS; PR00344; BCTR1SENSOR.
 DR SMART; SM00065; GAF; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00388; HiskA_1.
 DR PROSITE; PS0109; HIS_KIN; 1.
 KW Kinase; Phosphorylation; Sensory transduction; Transferase;
 KW Complete proteome.
 SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
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 DB 563 ADWAWA 568

RESULT 9
 Q9ACR5 PRELIMINARY; PRT; 205 AA.
 AC Q9ACR5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein SCPI.253.
 GN SCPI.253.
 OS Streptomyces coelicolor.
 OG Flammid SCPI.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT coelicolor A3(2).";
 RL Nature 417:141-147 (2002).
 DR EMBL; AL590464; CAC36779.1; --
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
 |||||
 DB 10 ADWSW 14

RESULT 10
 Q8IXK8 PRELIMINARY; PRT; 227 AA.
 AC Q8IXK8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to hypothetical protein BC017335.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040173; AAH40173.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
 |||||
 DB 113 ADWSW 117

RESULT 11
 Q919K8 PRELIMINARY; PRT; 242 AA.
 AC Q919K8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CUN068 hypothetical protein.
 GN CUN068.
 OS Culex nigripalpus baculovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
 OX NCBI_TaxID=130556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Florida1997;
 RX MEDLINE=21488685; PubMed=11602755;
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Becnel J.J., Rock D.L., Kutish G.F.;
 RT "Genome Sequence of a Baculovirus Pathogenic for *Culex nigripalpus*.";
 RL J. Virol. 75:11157-11165 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Florida1997;
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Becnel J.J., Rock D.L., Kutish G.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF403738; AAK94146.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
 |||||
 DB 80 DWSWA 84

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RESULT 12
Q8BIT9
ID Q8BIT9 PRELIMINARY; PRT; 355 AA.
AC Q8BIT9
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK087998; BAC40084.1; -.
SQ SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 215 ADMSW 219

RESULT 13
OS0002
ID OS0002 PRELIMINARY; PRT; 358 AA.
AC OS0002;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cysteine protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Bergon; TISSUE=Mesocarp, and Exocarip;
RA Mbequie-A-Mbequie D., Gomez R.-M., Fils-Lycaon B.;
RT "Sequence of APTPL, a Cysteine Proteinase From Apricot Fruit
RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
RT 179).";
RL Plant Physiol. 115:1730-1730(1997).
DR EMBL; U93166; AAB97142.1; -.
DR HSSP; P07711; 1CJL.
DR MEROPS; C01.041;
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00845; Pept_C1; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 358;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 215 ADMSW 219

RESULT 14
Q9HZ10
ID Q9HZ10 PRELIMINARY; PRT; 374 AA.
AC Q9HZ10;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Hypothetical protein PAJ230.
GN PAJ230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004746; AAG06618.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 81 DMSWA 85

RESULT 15
Q8P4A1
ID Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=1204217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
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RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities";
 RL Nature 417:459-463(2002).
 DR EMBL; AE012502; AAW43483.1; -.
 DR InterPro; IPR002293; AA/rei_permease1.
 DR InterPro; IPR004841; Permease.
 DR Pfam; PF0324; aa_permeases; 1.
 KW Complete proteome.
 SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 433;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
 Db 181 DMSWA 185

Search completed: February 18, 2004, 14:35:41
 Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	470	1 NRAM_IADBU	Q07570 influenza a
2	36	90.0	470	1 NRAM_IADCH	Q07571 influenza a
3	36	90.0	470	1 NRAM_IADH2	Q07572 influenza a
4	36	90.0	470	1 NRAM_IADM2	Q07573 influenza a
5	36	90.0	470	1 NRAM_IADU3	Q07599 influenza a
6	36	90.0	470	1 NRAM_IAGFN	Q07574 influenza a
7	36	90.0	470	1 NRAM_IAGHD	Q07577 influenza a
8	36	90.0	470	1 NRAM_IAHJI	Q07578 influenza a
9	36	90.0	470	1 NRAM_IAMAE	Q07583 influenza a
10	36	90.0	470	1 NRAM_IATKL	Q07585 influenza a
11	36	90.0	598	1 MRJ5_APIME	Q97432 apis mellif
12	34	85.0	376	1 EGLR_PENGR	Q93883 penicillium
13	34	85.0	1842	1 PAS2_SCHPO	Q10289 s fatty aci
14	33	82.5	99	1 NOS3_SHEEP	P79209 ovis aries
15	33	82.5	220	1 Y132_METJA	Q57596 methanococ
16	33	82.5	232	1 C1B3_SHEEP	P80943 ovis aries
17	33	82.5	333	1 C1B2_SHEEP	Q29422 ovis aries
18	33	82.5	410	1 Y801_DEIRA	Q9rwe8 deinococcus
19	33	82.5	421	1 PNK1_SCHPO	Q13911 schizosacch
20	33	82.5	470	1 NRAM_IAQIT	Q07584 influenza a
21	33	82.5	479	1 EGLA_BACSU	P42973 bacillus su
22	33	82.5	492	1 AERA_AERTR	P09166 aeromonas t
23	33	82.5	529	1 GUAA_WCLE	P46810 mycobacteri
24	33	82.5	578	1 YC20_METJA	Q58610 methanococ
25	33	82.5	579	1 YC12_KLEPN	Q48458 klebsiella
26	33	82.5	817	1 PHK_STRCO	Q8ck51 streptomyce
27	33	82.5	914	1 GUX2_CLOS	P50900 clostridium
28	33	82.5	1201	1 NOS3_MOUSE	P70313 mus musculu
29	33	82.5	1202	1 NOS3_HUMAN	P29474 homo sapien
30	33	82.5	1204	1 NOS3_BOVIN	P29473 bos taurus
31	33	82.5	1204	1 NOS3_PIG	Q28969 sus scrofa
32	32	80.0	100	1 NOS3_CAVPO	P97270 cavia porce
33	32	80.0	107	1 STEL_RHVE	P00302 rhus vernic

ALIGNMENTS

RESULT 1

ID	NRAM_IADBU	STANDARD;	PRT;	470 AA.
AC	Q07570;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuraminidase (EC 3.2.1.18)			
GN	NA.			
OS	Influenza A virus (strain A/Duck/Burjatis/652/88).			
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC	Influenza A viruses; Influenzavirus A.			
OX	NCBI_TaxID=38956;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93212520; PubMed=8460490;			
RA	Saito T., Kawoka Y., Webster R.G.;			
RT	"Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."			
RL	Virology 193:868-876(1993).			
CC	- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.			
CC	- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.			
CC	- SUBUNIT: Homotetramer.			
CC	- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.			
CC	- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.			
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CC	EMBL; L06572; AAA43365.1; -			
DR	HSSP; P06820; 2BAT.			
DR	InterPro; IPR001860; Glyco_hydro_34.			
DR	Pfam; PF00064; neur_1			
DR	ProDom; PD000431; Glyco_hydro_34; 1.			
KW	Hydrolase; Glycosidase; Glycoprotein; Transmembrane.			
FT	TRANSMEM 7 38 ANCHOR (BY SIMILARITY).			
FT	DOMAIN 39 88 HYPERVARIABLE STALK REGION.			
FT	DOMAIN 89 470 HEAD OF NEURAMINIDASE.			
FT	ACT_SITE 273 275 BY SIMILARITY.			
FT	ACT_SITE 275 275 BY SIMILARITY.			
FT	CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).			

O64253 mycobacteri
P23135 rhodospirill
P04395 escherichia
Q9871 homo sapien
P27250 escherichia
P34889 caenorhabdi
P32347 saccharomyc
P58882 xanthomonas
P57265 buchnera ap
Q99289 vibrio para
P03470 influenza a
P03468 influenza a

34 32 80.0 125 1 VG61_BPM2
35 32 80.0 272 1 CY1_RHOU
36 32 80.0 282 1 3MG2_ECOLI
37 32 80.0 295 1 X769_HUMAN
38 32 80.0 339 1 YGGB_ECOLI
39 32 80.0 360 1 WNT2_CABEL
40 32 80.0 362 1 DCUP_YEAST
41 32 80.0 375 1 HIS7_XANCP
42 32 80.0 411 1 FOJC_BUCAL
43 32 80.0 418 1 HLT_VIBPA
44 32 80.0 453 1 NRAM_IATIL
45 32 80.0 454 1 NRAM_IAPUE

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FT CARBOHYD 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51989 MW; DLAGF07460F6F8AD CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 1; Length 470;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 453 ADWSW 457

RESULT 2
NRAM_IADCH
ID NRAM_IADCH STANDARD; PRT; 470 AA.
AC Q07571;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC -----
CC EMBL; L06573; AAA43367.1; -.
CC HSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.
CC ACT_SITE 273 273 BY SIMILARITY.
CC ACT_SITE 275 275 BY SIMILARITY.
CC FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 470 AA; 52070 MW; 169AB9FB8806DC CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 1; Length 470;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 453 ADWSW 457
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Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 453 ADWSW 457

RESULT 3
NRAM_IADH2
ID NRAM_IADH2 STANDARD; PRT; 470 AA.
AC Q07572;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC -----
CC EMBL; L06574; AAA43372.1; -.
CC HSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.
CC ACT_SITE 273 273 BY SIMILARITY.
CC ACT_SITE 275 275 BY SIMILARITY.
CC FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 470 AA; 52015 MW; E1C1D3E2C650B93C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
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Db 453 ADMSW 457
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RESULT 4
NRAM_IADM2
ID NRAM_IADM2 STANDARD; PRT; 470 AA.
AC Q07573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18)
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L06575; AAA43404.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.
CC ACT SITE 89 470 HEAD OF NEURAMINIDASE.
CC ACT SITE 273 273 BY SIMILARITY.
CC ACT SITE 275 275 BY SIMILARITY.
CC CARBOHYD 46 45 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 470 AA; 52146 MW; 30P5P9FE364C1F49 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSW 5
|||||
Db 453 ADMSW 457
RESULT 6
NRAM_IAGFN
ID NRAM_IAGFN STANDARD; PRT; 470 AA.
AC Q07574;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.

OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 RT viruses.";
 RL Virology 133:868-876(1993).

CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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DR EMBL; L06584; AAA43428.1; -.
 DR HSP; P06820; 2BAT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
 FT ACT_SITE 273 275 BY SIMILARITY.
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 |||||
 Db 453 ADMSW 457

RESULT 7
 NRAM IAHGD STANDARD; PRT; 470 AA.
 ID NRAM IAHGD
 AC Q07577;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.

OS Influenza A virus (strain A/Herring gull/DE/677/88).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38964;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 RT viruses.";
 RL Virology 133:868-876(1993).

CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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DR EMBL; L06585; AAA43368.1; -.
 DR HSP; P06820; 2BAT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
 FT ACT_SITE 273 275 BY SIMILARITY.
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
 |||||
 Db 453 ADMSW 457

RESULT 8
 NRAM IAHJI STANDARD; PRT; 470 AA.
 ID NRAM IAHJI
 AC Q07578;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Equine/Jililin/1/89).
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11401;

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RN SEQUENCE FROM N.A.
RP MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
CC EMBL; L06579; AAA3374.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC TransMem 7 38
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
CC DOMAIN 39 88
CC ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
CC ACT_SITE 275 275 BY SIMILARITY.
CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 453 ADWSW 457

RESULT 9
NRAM_IAMAE STANDARD; PRT; 470 AA.
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06579; AAA3374.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC TransMem 7 38
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
CC DOMAIN 39 88
CC ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
CC ACT_SITE 275 275 BY SIMILARITY.
CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 453 ADWSW 457

RESULT 9
NRAM_IAMAE STANDARD; PRT; 470 AA.
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side

```

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RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L06586; AAA43369.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC TransMem 7 38
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
CC DOMAIN 39 88
CC ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
CC ACT_SITE 275 275 BY SIMILARITY.
CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 470 AA; 52070 MW; 557630C3E1F2765 CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 453 ADWSW 457

RESULT 10
NRAM_IATKL STANDARD; PRT; 470 AA.
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side

```

CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL; L06588; AAA43410.1; --
 CC HSP; P06820; 2BAT.
 CC InterPro; IPR001860; Glyco_hydro_34.
 CC Pfam; PF00064; neur; 1.
 CC ProDom; PD000431; Glyco_hydro_34; 1.
 CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
 CC TRANSMEM 7 38
 CC DOMAIN 39 88
 CC HEAD OF NEURAMINIDASE.
 CC BY SIMILARITY.
 CC ACT SITE 273 273
 CC ACT SITE 275 275
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 46 46
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 54 54
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 84 84
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 144 144
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 293 293
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 398 398
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 470 AA; 52352 MW; D573742ABFF1E6B CRC64;
 SQ

Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
 DB 453 ADWSW 457
 |||||

RESULT 11
 MRJ5 APIPE
 ID MRJ5 APIPE STANDARD; PRT; 598 AA.
 AC O97432;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
 GN MRJP5.
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7460;
 RN [1]_TaxID=7460;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=99373663; PubMed=10441680;
 RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;
 RT "The family of major royal jelly proteins and its evolution.";
 RL J. Mol. Evol. 49:290-297(1999).
 CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
 CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
 CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
 CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE

CC HONEYBEE QUEEN.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
 CC -!- DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF
 CC THE NURSE HONEY BEE.
 CC -!- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF004842; AAD01205.1; --
 CC InterPro; IPR003534; Royaljelly.
 CC Pfam; PF03022; MRJP; 2.
 CC PRINTS; PR01366; ROYALJELLY.
 CC Signal; Repeat; Glycoprotein.
 CC SIGNAL 1 17
 CC POTENTIAL.
 CC CHAIN 18 598
 CC MAJOR ROYAL JELLY PROTEIN 5.
 CC CARBOHYD 148 148
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 164 164
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 181 181
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 324 324
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 598 AA; 70236 MW; 2C603C77B7ACDF63 CRC64;
 SQ

Query Match 90.0%; Score 36; DB 1; Length 598;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
 DB 113 DWSWA 117
 |||||

RESULT 12
 PGLR PENG
 ID PGLR PENG STANDARD; PRT; 376 AA.
 AC O93983;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
 GN PGG1.
 OS Penicillium griseoforme.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 OX NCBI_TaxID=84562;
 RN [1]_TaxID=84562;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCT 6421;
 RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
 RT "Cloning and characterization of a gene encoding the
 RT endopolygalacturonase of Penicillium griseoforme";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
 CC galactosiduronic linkages in pectate and other galacturonans.
 CC -!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
 CC (POLYGALACTURONASES).
 CC -----
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 CC -----
 CC EMBL; AF085238; AAC83692.1; --
 CC InterPro; IPR000743; Glyco_hydro_28.
 CC InterPro; IPR006626; Pbh1.

DR Pfam; PF00295; Glyco_hydro_28; 1.
 DR SMART; SM00710; Pbh1; 5.
 DR PROSITE; PS00502; POLYGACTURONASE; 1.
 KW Hydrolase; Glycosidase; Cell wall; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 376 POLYGACTURONASE.
 SQ SEQUENCE 376 AA; 38068 MW; 1EDBIEC56ED56928 CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 376;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWA 6
 Db 349 SDMSWS 354
 RESULT 13
 FAS2_SCHPO STANDARD; PRT; 1842 AA.
 AC Q10289; O14163; P78973;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fatty acid synthase subunit alpha (SC 2.3.1.86) (p190/210) [Includes:
 DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase
 DE (SC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier
 DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
 GN FAS2 OR LSD1 OR SPAC4A8.11C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=96354912; PubMed=8769419;
 RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,
 RA Hirata A., Yanagida M.;
 RT "Aberrant mitosis in fission yeast mutants defective in fatty acid
 RT synthetase and acetyl CoA carboxylase";
 RL J. Cell Biol. 134:949-961(1996).
 [2]
 SEQUENCE FROM N.A.
 RX MEDLINE=21363051; PubMed=11470243;
 RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
 RA Teguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
 RT "Very long-chain fatty-acid-containing phospholipids accumulate in
 RT fatty acid synthase temperature-sensitive mutant strains of the
 RT fission yeast Schizosaccharomyces pombe fae2/lisd1";
 RL Biochim. Biophys. Acta 1532:223-233(2001).
 [3]
 SEQUENCE FROM N.A.
 RP STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gatties S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,
 RA Woltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzyl K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Certutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 [4]
 RN SEQUENCE OF 1-215 FROM N.A.
 RP Koken M.H.M., de Rooij J.;
 RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE OF 1-20.
 RP MEDLINE=94245730; PubMed=8188691;
 RX Kaeslin E., Heyer W.-D.;
 RA "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand
 RT exchange in vitro";
 RL J. Biol. Chem. 269:14103-14110(1994).
 CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
 CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
 CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,
 CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-
 CC CARRIER-PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING
 CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
 CC long-chain acyl-CoA + N CoA + N CO(2) + 2N NADP(+).
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + Co(2) +
 CC [acyl-carrier protein].
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- SUBUNIT: [Alpha(6)beta(6)] hexamers of two multifunctional
 CC subunits (alpha and beta).
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
 CC OTHER FUNGI.

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 CC EMBL; D83412; BAAL1913.1; -;
 DR EMBL; AB013747; BAB62029.1; -;
 DR EMBL; Z98762; CAB11481.1; -;
 DR EMBL; U82216; AAB39943.1; -;
 DR PIR; A54083; A54083;
 DR PIR; T38781; T38781;
 DR PIR; T43409; T43409;
 DR GenBank; SPombe; SPAC4A8.11c; -;
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR InterPro; IPR004568; Pantethn_trn.
 DR InterPro; IPR006182; Pantethn_attach.
 DR Pfam; PF01648; ACPS; 1.
 DR Pfam; PF02109; ketoacyl-synt; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRfam; TIGR00556; pantethn_trn; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
 DR Transferase; NADP; Phosphopantetheine.
 KW DOMAIN 1 ?
 FT DOMAIN ? ? ACYL CARRIER (ACP).
 FT DOMAIN ? 1842 BETA-KETOACYL REDUCTASE.
 FT BINDING 180 180 BETA-KETOACYL SYNTHASE.
 FT ACT SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT CONFLICT 107 107 S -> A (IN REF. 4).
 FT CONFLICT 422 422 K -> R (IN REF. 1).

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SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133BE571 CRC64;
Query Match 85.0%; Score 34; DB 1; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
   |||:|
Db 400 SDNWA 405

RESULT 14
NOS3 SHEEP STANDARD; PRT; 99 AA.
AC P79209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS)
DE (Fragment)
GN NOS3 OR ENOS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RA Aguan K., Weiner C.P.;
RT "Effect of hypoxia on the microvasculature of developing fetal
RT brain of sheep: a studies on the expression pattern of
RT constitutive forms of nitric oxide synthase.";
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
CC VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A cGMP-MEDIATED SIGNAL
CC TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
CC FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
CC PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF PAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME (BY SIMILARITY).
CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
CC SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U76738; AAB40705.1; -.
CC HSSP; P29473; ID0C.
CC InterPro: IPR004030; NO synthase.
CC Pfam; PF02898; NO_synthase; 1.
CC PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
FT Heme; Multigene family.
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 43;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ADWSW 5
   |||:|
Db 65 ADWAW 69

RESULT 15
Y132 METJA STANDARD; PRT; 220 AA.
AC Q57596;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0132.
GN MJ0132.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Furmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT jannaschii";
RT Science 273:1058-1073(1996).
RL -!- SIMILARITY: TO M.JANNASCHII MJ1220 AND MJECL42.
CC -!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
CC (M SUBUNIT).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U67470; AAB98113.1; -.
CC PIR; D64316; D64316.
CC TIGR; MJ0132; -.
CC InterPro: IPR003356; N6 DNA_Mtase.
CC Pfam; PF02384; N6_Mtase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 220 AA; 25766 MW; 710DDAE4C7A47954 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 220;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
   |||:|
Db 33 ADWAW 37

Search completed: February 18, 2004, 14:28:04
Job time : 3.55263 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	610	2 T35222	hypothetical prote
2	37	92.5	885	2 C83441	two-component sens
3	36	90.0	374	2 B83241	conserved hypothet
4	36	90.0	889	2 E87304	TonB-dependent rec
5	34	85.0	275	2 T05822	hypothetical prote
6	34	85.0	617	2 C84922	probable protein k
7	34	85.0	1842	2 T43409	probable fatty-aci
8	34	85.0	1842	2 T38781	fatty acid synthas
9	33	82.5	132	2 S65785	mel-13a protein -
10	33	82.5	198	2 B82531	conserved hypothet
11	33	82.5	220	2 D64316	restriction modifi
12	33	82.5	232	2 S58353	CD1b protein - she
13	33	82.5	239	2 D90470	hypothetical prote
14	33	82.5	237	2 D87152	conserved hypothet
15	33	82.5	276	2 B75337	hypothetical prote
16	33	82.5	304	2 F83632	probable cytochrom
17	33	82.5	310	2 JC7853	L-fucose-specific
18	33	82.5	324	2 AB3548	vegetatible incomp
19	33	82.5	328	2 E72424	oligopeptide ABC t
20	33	82.5	333	2 S47446	gene CDI protein -
21	33	82.5	350	2 S71923	cysteine proteinas
22	33	82.5	368	2 H90998	probable proteinas
23	33	82.5	410	2 D75475	lycopene cyclase -
24	33	82.5	415	2 AE1844	hypothetical prote
25	33	82.5	418	2 AE1460	sugar ABC transpor
26	33	82.5	418	2 AF1097	sugar ABC transpor
27	33	82.5	421	2 T38242	probable phosphata
28	33	82.5	433	2 T31511	hypothetical prote
29	33	82.5	467	2 G82697	hypothetical prote

30	33	82.5	478	2 E89790	6-phospho-beta-glu
31	33	82.5	479	2 I39953	6-phospho-beta-glu
32	33	82.5	492	2 S03098	aerolysin precurs
33	33	82.5	529	2 C86958	probable GMP synth
34	33	82.5	539	2 T15256	hypothetical prote
35	33	82.5	578	2 C64452	restriction modifi
36	33	82.5	590	2 S72813	GMP synthase (glut
37	33	82.5	616	2 C69226	type I restriction
38	33	82.5	623	2 E75221	type I restriction
39	33	82.5	765	2 S76795	hypothetical prote
40	33	82.5	836	2 D82177	conserved hypothet
41	33	82.5	1202	2 S71424	nitric-oxide synth
42	33	82.5	1203	1 A47501	nitric-oxide synth
43	33	82.5	1205	1 A38943	nitric-oxide synth
44	33	82.5	1329	2 D87226	conserved hypothet
45	33	82.5	1409	2 S74916	alkaline phosphata

ALIGNMENTS

RESULT 1

T35222
hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35222
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21572
A:Accession: T35222
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-610 <SEE>
A:Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCOEDB:SC5C7.15
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC5C7.15

Query Match 92.5%; Score 37; DB 2; Length 610;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

DB 83 ADWAWA 88

RESULT 2

C83441
two-component sensor kdpD PA1636 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83441
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path:
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: C83441
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-885 <STO>
A:Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AAG05025.1; GSPDB:GN00
A:Experimental source: strain PA01
C:Genetics:
A:Gene: kdpD; PA1636

Query Match 92.5%; Score 37; DB 2; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|||:|
Db 563 ADWAWA 568

RESULT 3
B83241
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83241
R:Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83241
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||:|
Db 81 DWSWA 85

RESULT 4
E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87304
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87304
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-889 <STO>
A:Cross-references: GB:AE005673; NID:gl3421615; PIDN:AAK22433.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 618 ADWSW 622

RESULT 5
T05822
hypothetical protein TSK18.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C:Accession: T05822
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15453

A:Accession: T05822
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: EMBL:AL022580
A:Experimental source: cultivar Columbia; BAC clone TSK18
C:Genetics:
A:Map position: 4
A:Introns: 103/3; 141/3; 169/1; 206/3
A>Note: TSK18.170

Query Match 85.0%; Score 34; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:|:|:|
Db 57 SDWSWS 62

RESULT 6
C84922
probable protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84922
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84922
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-617 <STO>
A:Cross-references: GB:AE002093; NID:g4249408; PIDN:AAD13705.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g48010
A:Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|||:|
Db 500 ADWAWA 505

RESULT 7
T43409
probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomy
N:Alternate names: fatty acid synthetase alpha subunit
C:Species: Schizosaccharomyces pombe
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43409
R:Saton, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.; Yar
J. Cell Biol. 134, 949-961, 1996
A:Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase ar
A:Reference number: Z22493; MUID:96354912; PMID:8769419
A:Accession: T43409
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1842 <SAI>
A:Cross-references: EMBL:D83412; NID:gl199959; PIDN:BAAL1913.1; PID:gl199960
C:Genetics:
A>Note: lsdl+
C:Superfamily: yeast fatty-acid synthase
C:Keywords: acyltransferase; coenzyme A

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:||:|
Db 400 SDNWA 405

RESULT 8

T38781
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T38781
R:Skellerton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21751
A:Accession: T38781
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1842 <SKE>
A:Cross-references: EMBL:Z98762; PIDN:CAB11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c
A:Experimental source: strain 972h-; cosmid c4A8
C:Genetics:
A:Gene: SPDB:SPAC4A8.11c
A:Map position: 1
C:Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 56.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
:||:|
Db 400 SDNWA 405

RESULT 9

S65785
mel-13a protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S65785
R:Tetou, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A:Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A:Reference number: S65785; MUID:96180310; PMID:8597592
A:Accession: S65785
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TET>
A:Cross-references: EMBL:U35309
C:Genetics:
A:Gene: mel-13
C:Superfamily: mouse mel-13a protein
C:Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
:||:|
Db 57 SDWSW 61

RESULT 10

B82531
conserved hypothetical protein XP2666 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C:Accession: B82531
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: B82531
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <SIM>
A:Cross-references: GB:AE004072; GB:AE003849; NID:G9107884; PIDN:AAF85463.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Laig
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, I.
as-Neco, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranee, E.B.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins,
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawas
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
M.; Tauhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2666
C:Superfamily: conserved hypothetical protein MJ1677

Query Match 82.5%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
:||:|
Db 135 DWNWA 139

RESULT 11

D64316
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002
C:Accession: D64316
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: D64316
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-220 <BUL>
A:Cross-references: GB:U67470; GB:L77117; NID:G2826247; PIDN:AAB98113.1; PID:G1592267;
C:Genetics:
A:Map position: REV127472-126810
A:Start codon: TTG
C:Superfamily: type I site-specific deoxyribonuclease chain hcdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 33 ADWA 37

RESULT 12

S58353
Cdb protein - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58353

R.Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.
submitted to the EMBL Data Library, July 1995
A:Description: The ovine CD1 gene family contains at least four CD1B homologues.
A:Reference number: S58353

A:Accession: S58353

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-232 <PER>

A:Cross-references: EMBL:X90567; NID:g945010; PIDN:CAA62187.1; PID:g945011

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 156 ADWTW 160

RESULT 13

D90470

hypothetical protein cysH [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001

C:Accession: D90470

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

gong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: D90470

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-239 <KUR>

A:Cross-references: GB:AE006661; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155

C:Genetics:

A:Gene: cysH

C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 172 ADWTW 176

RESULT 14

D87152

conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: D87152

R:Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq-

A>Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: D87152

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AL450380; NID:g13093601; PIDN:CAC30900.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML1945

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSW 6

Db 11 ATWSWA 16

RESULT 15

B75337

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: B75337

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: B75337

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-276 <WHI>

A:Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF11479.1; PID:g645971

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1923

A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 84 ADWAW 88

Search completed: February 18, 2004, 14:38:39

Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	938	4	US-09-252-991A-23882
2	36	90.0	68	4	US-09-252-991A-18367
3	36	90.0	142	4	US-09-252-991A-31533
4	36	90.0	174	4	US-09-325-932A-163
5	36	90.0	225	4	US-09-325-932A-162
6	36	90.0	242	4	US-09-345-2368-3
7	36	90.0	378	4	US-09-325-932A-158
8	36	90.0	445	4	US-09-252-991A-22368
9	36	90.0	462	4	US-09-252-991A-21704
10	34	85.0	44	3	US-08-905-223-274
11	33	82.5	74	1	US-08-379-538-2
12	33	82.5	136	2	US-08-774-065-2
13	33	82.5	164	4	US-09-252-991A-23817
14	33	82.5	218	1	US-08-032-848C-10
15	33	82.5	218	1	US-08-438-870-10
16	33	82.5	218	2	US-08-169-948B-34
17	33	82.5	218	2	US-08-448-873-34
18	33	82.5	218	3	US-08-382-452D-34
19	33	82.5	218	3	US-09-216-295-1
20	33	82.5	218	4	US-08-507-362A-18
21	33	82.5	232	3	US-09-146-770-1
22	33	82.5	232	4	US-09-633-084-1
23	33	82.5	232	4	US-10-075-872-1
24	33	82.5	232	4	US-10-261-997-1
25	33	82.5	234	1	US-08-032-848C-9
26	33	82.5	234	1	US-08-438-870-9
27	33	82.5	234	3	US-09-146-770-3

28	33	82.5	234	3	US-09-146-770-4	Sequence 4, Appli
29	33	82.5	234	3	US-09-216-295-3	Sequence 3, Appli
30	33	82.5	234	3	US-09-216-295-4	Sequence 4, Appli
31	33	82.5	234	4	US-09-633-084-3	Sequence 3, Appli
32	33	82.5	234	4	US-09-633-084-4	Sequence 4, Appli
33	33	82.5	234	4	US-10-075-872-3	Sequence 3, Appli
34	33	82.5	234	4	US-10-075-872-4	Sequence 4, Appli
35	33	82.5	234	4	US-10-261-997-3	Sequence 3, Appli
36	33	82.5	234	4	US-10-261-997-4	Sequence 4, Appli
37	33	82.5	239	3	US-09-216-295-15	Sequence 15, Appli
38	33	82.5	316	4	US-09-252-991A-17312	Sequence 17312, A
39	33	82.5	467	1	US-08-140-104A-2	Sequence 2, Appli
40	33	82.5	670	4	US-09-252-991A-22079	Sequence 22079, A
41	33	82.5	1205	1	US-07-908-245-2	Sequence 2, Appli
42	33	82.5	1205	2	US-08-319-866-10	Sequence 10, Appli
43	33	82.5	1205	3	US-09-123-708-6	Sequence 6, Appli
44	33	82.5	1205	3	US-09-123-624-6	Sequence 6, Appli
45	32	80.0	5	6	5217869-75	Patent No. 5217869

ALIGNMENTS

RESULT 1
US-09-252-991A-23882
; Sequence 23882, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23882
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23882

Query Match 92.5%; Score 37; DB 4; Length 938;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
Db 581 ADMAWA 586

RESULT 2
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT

; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 128 ADMSW 132

RESULT 8

US-09-252-991A-22368
; Sequence 22368, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22368
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

Query Match 90.0%; Score 36; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 304 DMSWA 308

RESULT 9

US-09-252-991A-21704
; Sequence 21704, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21704
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 169 DMSWA 173

RESULT 10

US-08-905-223-274
; Sequence 274, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 274:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 26...1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 9.6
; OTHER INFORMATION: seq WLIALASWSWALC/RI
US-08-905-223-274

Query Match 85.0%; Score 34; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
Db 19 ADMSWA 24

RESULT 11

US-08-379-538-2
; Sequence 2, Application US/08379538
; Patent No. 5804554
; GENERAL INFORMATION:
; APPLICANT: Volkman, Robert A.
; APPLICANT: Saccamano, Nicholas A.
; APPLICANT: Nason II, Deane M.

APPLICANT: Heck, Steven D.
APPLICANT: Ronau, Robert T.
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pfizer Inc
STREET: 235 East 42nd Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,538
FILING DATE: 3-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887073
FILING DATE: 21-MAY-1992
APPLICATION NUMBER: PCT/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Zielinski, Bryan
REGISTRATION NUMBER: 34,462
REFERENCE/DOCKET NUMBER: PC8175A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 573-4585
TELEFAX: (212) 573-1939
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Filistata hibernalis
TISSUE TYPE: venom
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 52 DWSWS 56

RESULT 12
US-08-774-065-2
Sequence 2, Application US/08774065
Patent No. 5989899
GENERAL INFORMATION:
APPLICANT: Bower, Benjamin
APPLICANT: Clarkson, Kathleen
APPLICANT: Larenas, Edmond
APPLICANT: Ward, Michael
TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS
TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND
TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL
STREET: 925 PAGE MILL ROAD
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,065

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Glalster, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-846-7620
TELEFAX: 415-845-6504
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 62 ADWQWS 67

RESULT 13
US-09-252-991A-23817
Sequence 23817, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23817
LENGTH: 164
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 132 AGWSWA 137

RESULT 14
US-08-032-848C-10
Sequence 10, Application US/08032848C
Patent No. 5475101

GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of
EG III Cellulase
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,848C
FILING DATE: MAR 17 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7356
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-032-848C-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 46 ADMQWS 51

RESULT 15
US-08-438-870-10
Sequence 10, Application US/08438870
Patent No. 5753484
GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of EG
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,870
FILING DATE: May 10, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7555
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-870-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 46 ADMQWS 51

Search completed: February 18, 2004, 14:41:46
Job time : 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-5
Perfect score: 40
Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	362	1 DCUP YEAST	P32347 saccharomyc
2	36	90.0	598	1 MRJ5 APIME	O97432 apis mellif
3	36	90.0	745	1 IKKA HUMAN	O15111 h inhibitor
4	36	90.0	745	1 IKKA MOUSE	O60680 m inhibitor
5	36	90.0	756	1 IKKB HUMAN	O14920 homo sapien
6	36	90.0	757	1 IKKB MOUSE	O88351 mus musculu
7	36	90.0	757	1 IKKB RAT	O9qy78 rattus norv
8	36	90.0	983	1 EPA3 CHICK	P29318 gallus gall
9	36	90.0	983	1 EPA3 HUMAN	P29320 homo sapien
10	36	90.0	983	1 EPA3 MOUSE	P29319 mus musculu
11	36	90.0	984	1 EPA3 RAT	O08680 rattus norv
12	34	85.0	411	1 FOLC_BUCAI	P57265 buchnera ap
13	33	82.5	376	1 PGLR PENGH	O93883 penicillium
14	33	82.5	453	1 NRAM IAWIL	P03470 influenza a
15	33	82.5	454	1 NRAM IAPUE	P03468 influenza a
16	33	82.5	492	1 AERA AERTR	P09166 aeromonas t
17	33	82.5	524	1 CP72 CATRO	O05047 catharanthu
18	33	82.5	656	1 VEXE SALT1	P43112 salmonella
19	33	82.5	840	1 VPPI YEAST	P32563 saccharomyc
20	33	82.5	1842	1 FAS2 SCHPO	Q10289 s fatty aci
21	32	80.0	86	1 YZX5 HUMAN	O9y530 homo sapien
22	32	80.0	107	1 STEL RHUVE	P00302 rhus vernic
23	32	80.0	191	1 GDIF CAEEL	Q20496 caenorhabdi
24	32	80.0	210	1 KTHV SCHPO	P36590 schizosacch
25	32	80.0	272	1 CY1 RHORU	P23135 rhodospiril
26	32	80.0	282	1 3MG2 ECOLI	P04395 escherichia
27	32	80.0	295	1 X769 HUMAN	O99871 homo sapien
28	32	80.0	296	1 CYOA_BUCAI	P57544 buchnera ap
29	32	80.0	307	1 QOX2_ACEAC	P50653 acetobacter
30	32	80.0	314	1 CYOA_PSEPU	O9wrl1 pseudomonas
31	32	80.0	360	1 WNT2 CAEEL	P34889 caenorhabdi
32	32	80.0	375	1 HIS7_XANCP	P58882 xanthomonas
33	32	80.0	418	1 HLT_VIBPA	O99289 vibrio para

34	32	80.0	470	1 NRAM_IADBU	Q07570 influenza a
35	32	80.0	470	1 NRAM_IADCH	Q07571 influenza a
36	32	80.0	470	1 NRAM_IADH2	Q07572 influenza a
37	32	80.0	470	1 NRAM_IADM2	Q07573 influenza a
38	32	80.0	470	1 NRAM_IADU3	Q07599 influenza a
39	32	80.0	470	1 NRAM_IAGFN	Q07574 influenza a
40	32	80.0	470	1 NRAM_IAGHD	Q07577 influenza a
41	32	80.0	470	1 NRAM_IAGJI	Q07578 influenza a
42	32	80.0	470	1 NRAM_IAMAE	Q07583 influenza a
43	32	80.0	470	1 NRAM_IATKL	Q07585 influenza a
44	32	80.0	479	1 BGUA_BACSU	P42973 bacillus su
45	32	80.0	500	1 PROP_ECOLI	P30848 escherichia

ALIGNMENTS

RESULT 1
DCUP YEAST
ID DCUP YEAST STANDARD; PRT; 362 AA.
AC P32347;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
GN HEM12 OR HEM6 OR POP3 OR YD9609.03.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249304; PubMed=1576986;
RA Carey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,
RA Kushner J., Labbe P.;
RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12
RT gene sequence and evidence for two conserved glycines essential for
RT enzymatic activity.";
RL Eur. J. Biochem. 205:1011-1016 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93348774; PubMed=8346678;
RA Diflumeri C., Laroque R., Keng T.;
RT "Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the
RT gene for uroporphyrinogen decarboxylase.";
RL Yeast 9:613-623 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP MUTANTS.
RX MEDLINE=93111946; PubMed=1471989;
RA Chelstowska A., Zosdek T., Kushner J., Rytka J.,
RA Labbe-Bois R.;
RT "Identification of amino acid changes affecting yeast
RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
RT mutant alleles.";
RL Biochem. J. 288:753-757 (1992).
RN [5]
RP CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
CO(2).
RN [6]
RP PATHWAY: Porphyrin and heme biosynthesis.
RN [7]
RP SUBCELLULAR LOCATION: Cytoplasmic.
RN [8]
RP SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
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CC or send an email to licensee@isb-sib.ch).

CC EMBL; X63721; CAA45253.1; -
DR EMBL; Z19089; CAA79514.1; -
DR EMBL; Z49209; CAA89078.1; -
DR FIR; S23471; S23471.
DR HSP; P06132; IURO.
DR SGD; S0002454; HEM12.
DR GO; GO:0004853; P:uroporphyrinogen decarboxylase activity; IMP.
DR GO; GO:0006783; P:heme biosynthesis; IMP.
DR InterPro; IPR006361; HemeE.
DR InterPro; IPR000257; Uro decarboxylase.
DR Pfam; PF01208; URO-D; 1.
DR ProDom; PD003225; Uro decarboxylase; 1.
DR TIGRFAMs; TIGR01464; Heme5; 1.
DR PROSITE; PS00906; UROD_1; 1.
DR PROSITE; PS00907; UROD_2; 1.
KW Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
FT VARIANT 59 S -> F (IN HEM12-6 AND HEM12-12).
FT VARIANT 62 T -> I (IN HEM12-14).
FT VARIANT 107 L -> S (IN HEM12-3 AND HEM12-13).
FT VARIANT 215 S -> N (IN HEM12-2 AND HEM12-11).
FT MUTAGEN 33 G -> D: INACTIVATION.
FT MUTAGEN 300 G -> D: INACTIVATION.
SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48E62BC277 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
DB 279 LDMSW 283

RESULT 2
ID MRJ5 APIME STANDARD; PRT; 598 AA.
AC O97432;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;
RT "The family of major royal jelly proteins and its evolution.";
RL J. Mol. Evol. 49:290-297(1999).
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
CC -!- DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF
CC THE NURSE HONEY BEE.
CC -!- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.
CC
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CC EMBL; AF004842; AAD01205.1; -
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal; Repeat; Glycoprotein.
FT SIGNAL 1 17
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C7B7E7ACDF63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
DB 113 DWSWA 117

RESULT 3
ID IKKA HUMAN STANDARD; PRT; 745 AA.
AC O15111; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97384661; PubMed=9244310;
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT "Identification and characterization of an IkappaB kinase.";
RL Cell 90:373-383(1997).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97394468; PubMed=9252186;
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT "A cytokine-responsive IkappaB kinase that activates the transcription
RT factor NF-kappaB.";
RL Nature 388:548-554(1997).
RN [3]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP SER-176.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX Hu M.C.-T., Wang Y.-P.;
RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [5]
RP SEQUENCE OF 32-745 FROM N.A.

RC TISSUE=Cervical carcinoma;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RN PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RT Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RN PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RP MEDLINE=99413720; PubMed=10485710;
 RX Ozes O.N., Mayo L.D., Guetin J.A., Pfeiffer S.R., Pfeiffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RN [8]
 RN IKK- α -IKK β BINDING.
 RP MEDLINE=99212141; PubMed=10195894;
 RX Delhase M., Hayakawa M., Chen Y., Karin M.;
 RA "Positive and negative regulation of ikkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [9]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RX Nemoto S., DiDonato J.A., Lin A.;
 RA "Coordinate regulation of ikkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RN REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 RN [11]
 RN SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKK γ .
 RX MEDLINE=21968797; PubMed=11971985;
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase.";
 RL Mol. Cell. Biol. 22:3549-3561(2002).
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -I- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKK γ and CREBBP.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- TISSUE SPECIFICITY: Widely expressed.
 CC -I- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC -----
 DR EMBL; AF012890; AAC51662.1; -
 DR EMBL; AF009225; AAC51671.1; -
 DR EMBL; AF080157; AAD08996.1; -
 DR EMBL; U22512; AAC50713.1; -
 DR HSSP; Q63450; IAU6.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0008384; P:IkappaB kinase activity; TAS.
 DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
 DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT D01 455 LEUCINE-ZIPPER (POTENTIAL).
 FT D02 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 176 176 K->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
 FT ACTIVITY.
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 FT CONFLICT 543 543 E -> G (IN REF. 2).
 FT CONFLICT 604 604 L -> R (IN REF. 5).
 FT CONFLICT 679 680 TS -> AV (IN REF. 5).
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 FT CONFLICT 684 684 TS -> DL (IN REF. 5).
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 Db 738 LDMSW 742
 RESULT 4
 ID IKKA MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.1-)
 DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous

DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId:10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/C;
 RX MEDLINE=96044444; PubMed=7558004;
 RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RT chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BALB/C;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
 RA Geleziunas R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]

RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
 CC -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U12473; AAC52589.1; -;
 CC EMBL; AK018671; BAB31335.1; -;
 CC PIR; I49101; I49101.
 CC HSP; Q63450; I406.
 CC MGI; MGI:99484; Chuk.
 CC InterPro; IPR000719; Prot kinase.
 CC InterPro; IPR002290; Ser thr_pkinase.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00069; pkinase; 1
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; P0000001; Prot kinase; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Phosphorylation; Alternative splicing.
 CC DOMAIN 15 300 PROTEIN KINASE.
 CC DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 CC DOMAIN 738 743 NEMO-BINDING.
 CC NP_BIND 21 29 ATP (BY SIMILARITY).

FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)
 (BY SIMILARITY).
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
 (BY SIMILARITY).
 FT VARSPLIC 452 471 MSLLRYNALTQKNTLIS -> IFRKNVKSMEGRKRGH
 SLF (in isoform 2).
 FT VARSPLIC 472 745 Missing (in isoform 2).
 /FTId=VSP 004866.
 FT VARSPLIC 577 584 DHLYSDST -> GKTIQSQY (in isoform 3).
 /FTId=VSP 004867.
 FT VARSPLIC 585 745 Missing (in isoform 3).
 /FTId=VSP 004869.
 FT CONFLICT 236 236 K -> E (IN REF. 3).
 FT CONFLICT 400 400 S -> Y (IN REF. 3).
 SQ SEQUENCE 745 AA; 84728 MW; 3F5F582AF92233 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQSW 5
 DB 738 LQSW 742

RESULT 5
 IKKB_HUMAN
 ID IKKB_HUMAN STANDARD; PRT; 756 AA.
 AC O14920; O75327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008913; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 NF-kappaB activation."; Science 278:860-866 (1997).
 RL [2]
 RN SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RX MEDLINE=98008914; PubMed=9346485;
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 "IkappaB kinase-beta: NF-kappaB activation and complex formation with
 IkappaB kinase-alpha and NIK."; Science 278:866-869 (1997).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 embryonic tissues but localized to different human chromosomes."; Gene
 222:31-40 (1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 9p12-->p11 by in situ hybridization.";

RL Cytogenet. Cell Genet. 82:32-33 (1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388957; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywicki M.I., Skaleka U., Smalhus D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [6]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RX Nemoto S., DiDonato J.A., Lin A.;
 "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343 (1998).
 RL [7]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RX Jobin C., Sartor R.B.;
 "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection."; Am. J. Physiol. 278:C451-C462 (2000).
 RL [8]
 RN IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKBG.
 RP MEDLINE=21968797; PubMed=11971985;
 RX Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 O'Malley B.W.;
 "Regulation of SRC-3 (pCIP/ACTR/ATB-1/RAC-3/TRAM-1) coactivator
 activity by I kappa B kinase."; Mol. Cell. Biol. 22:3549-3561 (2002).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3 (by similarity).
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P50-P50
 complex. Phosphorylated IKB-alpha is further released from the
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 and CREBBP.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
 muscle, kidney, pancreas, spleen, thymus, prostate, testis and
 peripheral blood.
 CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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CC CC -----
DR EMBL; AF029684; AAC51860.1; -
DR EMBL; AF080158; AAD08997.1; -
DR EMBL; AF031416; AAC64675.1; -
DR EMBL; BC006231; AAH06231.1; -
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:5960; IKKB.
DR MIM; 603258; -; Cytosolasm; NAS.
DR GO; GO:0005737; F:ATP binding activity; NAS.
DR GO; GO:0005524; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:004674; F:transcriptional activator activity; NAS.
DR GO; GO:0016563; P:protein amino acid phosphorylation; NAS.
DR GO; GO:0006468; P:protein kinase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR ProDom; PD000001; Prot_kinase; 1.
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DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 PHOSPHORYLATION.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
FT MUTAGEN 177 177 EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
FT CONFLICT 231 285 WSKVRQKSEVDIVVSEDLNGVVKF -> CVRMWPGTVVHS
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FT CONFLICT 425 425 Q -> H (IN REF. 1).
SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
Query Match 90.0%; Score 36; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSW 5
Db 737 LDWSW 741
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RESULT 6
ID IKKB_MOUSE STANDARD; PRT; 757 AA.
AC Q88351; Q9R1J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,

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RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]
RP DEVELOPMENTAL STAGE.
RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of Ikb.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DEVELOPMENTAL STAGE.
RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
RT developmentally regulated protein kinase.";
RL Oncogene 18:5514-5524(1999).
RN [4]
RP IKK PHOSPHORYLATION.
RA MEDLINE=99038238; PubMed=9819420;
RX Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [5]
RP REVIEW.
RA MEDLINE=20178139; PubMed=10712233;
RX Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP (by similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC -!- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
CC the mouse embryo, at E9.5 day its expression begins to be
CC localized to the brain, neural ganglia, neural tube, and in liver
CC at E12.5 day. At E15.5 day, the expression is further restricted
CC to specific tissues of the embryo.
CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
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CC -----
DR EMBL; AF026524; AAC23557.1; -
DR EMBL; AF088910; AAD52095.1; -
DR HSSP; Q63450; 1A06.
DR MGD; MGI:1338071; Ikbb.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.

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ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDSWMLQMEDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
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 Db 737 LDWSW 741
 RESULT 7
 IKKB_RAT
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of Ikbppab kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -/- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -/- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but

also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBBP (By similarity).
 CC -/- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -/- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 CC -----
 CC EMBL; AF115282; AAF21978.1; -;
 DR HSSP; Q63450; 1A06.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFPE46A7DF91P9C CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 |||||
 Db 737 LDWSW 741
 RESULT 8
 EPA3_CHICK
 ID EPA3_CHICK STANDARD; PRT; 983 AA.
 AC P29318;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (CEK4).
 GN EPA3 OR ETK1 OR CEK4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92031278; PubMed=1657122;
 RA Sajjadi F.G., Pasquale E.B., Subramani S.;
 RT "Identification of a new eph-related receptor tyrosine kinase gene

RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor.";
 RL New Biol. 3:769-778(1991).
 CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC -!- EPHRIN-A2, -A3, -A4 AND -A5.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN-
 CC RECEPTOR SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; M68514; AAA48666.1; --
 CC PIR; B45583; B45583.
 CC HSP; P00523; 2PTK.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR001090; Ephrin receptor.
 CC InterPro; IPR003961; FN III.
 CC InterPro; IPR003962; FnIII subd.
 CC InterPro; IPR000719; Prot_Kinase.
 CC InterPro; IPR001660; SAM.
 CC InterPro; IPR001245; Tyr_kinase.
 CC InterPro; IPR001426; YKase_receptorV.
 CC Pfam; PF01404; EPH_lbd; 1.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00536; SAM; 1.
 CC PRINTS; PR00014; FNTYPEIII.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD001495; Ephrin_receptor; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00615; EPH_lbd; 1.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00454; SAM; 1.
 CC SMART; SM00219; TyRK; 1.
 CC PROSITE; PS01186; EGF 2; UNKNOWN 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V; 1.
 CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC PROSITE; PS0105; SAM_DOMAIN; 1.
 CC Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 20 540 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 541 564 POTENTIAL.
 FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 188 321 CYS-RICH.
 FT DOMAIN 322 431 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 432 529 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 621 882 PROTEIN KINASE.
 FT DOMAIN 911 975 SAM.
 FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 627 635 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).

FT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 983 AA; 109910 MW; E8895F0BDF77651E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 DB 342 LDMSW 346
 RESULT 9
 ID EPA3 HUMAN STANDARD; PRT; 983 AA.
 AC P29320; Q9H2V3; Q9H2V4;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (HEK) (HEK4).
 GN EPHA3 OR ETK1 OR ETK OR HEK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92179233; PubMed=1311845;
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
 RT kinase expressed by human lymphoid tumor cell lines."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Melanoma;
 RA Chiori R., Hames G., Stroobant V., Maillere B., Texier C., Mach B.,
 RA Boon T., Coulie P.G.;
 RT "Identification of a tumor specific shared antigen derived from an
 RT Eph-receptor and presented to CD4 T cells on HLA class II
 RT molecules."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
 RX MEDLINE=92147681; PubMed=1737782;
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
 RA Welch K., Loudovaris M., Rockman S., Busmanis I.;
 RT "Isolation and characterization of a novel receptor-type protein
 RT tyrosine kinase (hek) from a human pre-B cell line."
 RL J. Biol. Chem. 267:3262-3267(1992).
 CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
 CC FUNCTION.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
 CC SECRETED (ISOFORM 2).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P29320-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P29320-2; Sequence=VSP 002995, VSP 002996;
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN

RECEPTOR SUBFAMILY.

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EMBL; MG3941; AAS8633.1; --
DR DR EMBL; AF213459; AAC43576.1; --
DR DR EMBL; AF213460; AAC43577.1; --
DR DR EMBL; A28003; CAA01906.1; --
DR DR PIR; A38224; A38224.
DR DR HSSP; PO0523; 2PTK.
DR DR Genew; HGNC:3387; EPHA3.
DR MIM; 179611; --
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPRO06209; EGf_like.
DR InterPro; IPRO01090; Ephrin_receptor.
DR InterPro; IPRO03961; FN_III.
DR InterPro; IPRO03962; FnIII_subd.
DR InterPro; IPRO00719; Prot_kinase.
DR InterPro; IPRO01660; SAM.
DR InterPro; IPRO01245; Tyr_kinase.
DR InterPro; IPRO01426; Ykase_receptorv.
DR Pfam; PF01404; EFH_lbd; 1.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEI.III.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3_2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; Tyrc_KC; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00730; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1
DR Transfraser; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 983
FT FT DOMAIN 21 541
FT TRANSMEM 542 565
FT FT DOMAIN 566 983
CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 189 322
CYS-RICH.
FT FT DOMAIN 323 432
FIBRONECTIN TYPE-III 1.
FT FT DOMAIN 433 530
FIBRONECTIN TYPE-III 2.
FT FT DOMAIN 621 882
PROTEIN KINASE.
FT FT DOMAIN 911 975
SAM.
FT SITE 981 983
PDZ-BINDING MOTIF (POTENTIAL).
FT FT NP_BIND 627 635
ATP (BY SIMILARITY).
FT FT BINDING 653 653
ATP (BY SIMILARITY).
FT ACT_SITE 746 746
BY SIMILARITY.
FT MOD_RES 596 596
PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 602 602
PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 779 779
PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 232 232
N-LINKED GLCNAC.. (POTENTIAL).
FT CARBOHYD 337 337
N-LINKED GLCNAC.. (POTENTIAL).
FT CARBOHYD 391 391
N-LINKED GLCNAC.. (POTENTIAL).
FT CARBOHYD 404 404
N-LINKED GLCNAC.. (POTENTIAL).
FT VARSPHC 493 493
N-LINKED GLCNAC.. (POTENTIAL).
SFISGS -> CYMFENAV (in isoform 2).
FT 532 539

```

FT  VARSPLIC 540 983 /FTid=VSP_002995.
FT  Missing (in isoform 2).
FT  /FTid=VSP_002996.
FT  P -> L (IN REF. 1; CAA01906).
FT  CONFLICT 507 507
FT  CONFLICT 724 724 V -> L (IN REF. 1; CAA01906).
FT  CONFLICT 911 911 S -> T (IN REF. 2).
FT  CONFLICT 924 924 R -> W (IN REF. 2).
SQ  SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSW 5
    |||||
Db 343 LDWSW 347

RESULT 10
EPA3 MOUSE
ID EPA3 MOUSE STANDARD; PRT; 983 AA.
AC P29319;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor ETK1) (MEK4).
DS EPA3 OR ETK1 OR MEK4 OR TYRO4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=ICR X Swiss Webster; TISSUE=Embryo;
RX MEDLINE=92031278; PubMed=1657122;
RA Sajjadi F.G.; Pasquale E.B.; Subramani S.;
RT Identification of a new eph-related receptor tyrosine kinase gene
RT from mouse and chicken that is developmentally regulated and encodes
RT at least two forms of the receptor.";
RT New Biol. 3:769-778(1991).
RL
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC -1- EPHRIN-A2, -A3, -A4 AND -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM
CC IS SECRETED.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Names=Long;
CC IsoIds=P29319-1; Sequence=Displayed;
CC Names=Short;
CC IsoIds=P29319-2; Sequence=VSP_002997;
CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
CC BRAIN, ALSO DETECTED IN TESTIS.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
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EMBL; M68513; AAA39521.1; -.
EMBL; M68515; AAA39522.1; ALT_SEQ.
PIR; A45583; A45583.
HSP; P00523; 2PTK.
MGD; MGI:99612; EphA3.

```

DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003962; FNIII_subd.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR001426; Ykase_receptorV.
 DR Pfam: PF01404; EPH_lbd; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 541 564 POTENTIAL.
 FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).
 FT CYS-RICH 321 321 FIBRONECTIN TYPE-III 1.
 FT FIBRONECTIN TYPE-III 322 431 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 432 529 PROTEIN KINASE.
 FT DOMAIN 621 882 SAM.
 FT DOMAIN 911 975 SAM.
 FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 627 635 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 530 983 Missing (in isoform Short).
 FT SQ SEQUENCE 983 AA; 10995 MW; BE44A655D8107A2 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 Db 342 LDWSW 346
 RESULT 11
 ID EPA3 RAT STANDARD; PRT; 984 AA.
 AC O08680;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein

DE kinase receptor REK4) (TYRO-4).
 GN EPHA3 OR REK4 OR TYRO4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98120505; PubMed=9458884;
 RA Li Y.Y., McTierman C.F., Feldman A.M.;
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene
 r-Epha3 in neonatal rat cardiomyocytes.";
 RL Am. J. Physiol. 274:H331-H341(1998)
 CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 EPHRIN-A2, -A3, -A4 AND -A5.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN AND LUNG.
 CC -!- INDUCTION: DOWN-REGULATED BY ILL-BETA IN NEONATAL CARDIAC
 MYOCYTES.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 RECEPTOR SUBFAMILY.
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 EMBL; U69278; AAC06273.1; -.
 HSP; P00523; 2PTK.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR001426; Ykase_receptorV.
 DR Pfam: PF01404; EPH_lbd; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 984 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 984 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 189 322 CYS-RICH.
 FT DOMAIN 328 431 FIBRONECTIN TYPE-III 1.

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FT DOMAIN 436 528 FIBRONECTIN TYPE-III 2.
FT DOMAIN 622 883 PROTEIN KINASE.
FT SITE 912 976 SAM.
FT SITE 982 984 PDZ-BINDING MOTIF (POTENTIAL).
FT NP BIND 628 636 ATP (BY SIMILARITY).
FT BINDING 654 654 ATP (BY SIMILARITY).
FT ACT_SITE 747 747 BY SIMILARITY.
FT MOD_RES 597 597 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 603 603 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 780 780 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
DB 343 LDMSW 347

RESULT 12
FOLC_BUCAI STANDARD; PRT; 411 AA.
AC PS7265;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE FOLC bifunctional protein [Includes: Polyisoprenylglutamate synthase
DE (EC 6.3.2.11) (Polyisoprenyl-glutamate synthetase) (PPGS);
DE Dihydrofolate synthase (EC 6.3.2.12)].
FOLC OR BU167.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OC NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10930377;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.
CC -1- CATALYTIC ACTIVITY: ATP + {tetrahydrofolyl-[Glu]}(N) + L-glutamate
CC = ADP + phosphate + {tetrahydrofolyl-[Glu]}(N+1).
CC -1- CATALYTIC ACTIVITY: ATP + dihydropterate + L-glutamate = ADP +
CC phosphate + dihydrofolate.
CC -1- PATHWAY: BACTERIA REQUIRE FOLATE FOR THE BIOSYNTHESIS OF GLYCINE,
CC METHIONINE, FORMYL-MET-TRNA, THYMIDYLATES, PURINES, AND
CC PANTOTHENATE.
CC -1- SIMILARITY: Belongs to the folylpolyglutamate synthase family.
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EMBL; AP001118; BAB12885.1; -
DR HSPSP; P15925; IFGS.
DR InterPro; IPR001645; Fpolygl_synthase.
DR Pfam; PF01225; Mur_ligase; 1.
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DR TIGRFAMS; TIGR01499; folC; 1.
DR PROSITE; PS01011; FOLYPOLYGLU_SYNT_1; 1.
DR PROSITE; PS01012; FOLYPOLYGLU_SYNT_2; FALSE NEG.
KW Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
KW Folate biosynthesis; Complete proteome.
FT NP_BIND 50 56 ATP (BY SIMILARITY).
SQ SEQUENCE 411 AA; 46970 MW; 5DDC2DC66539935A CRC64;

Query Match 85.0%; Score 34; DB 1; Length 411;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
DB 219 LDMSW 223

RESULT 13
FGLR_PENGR STANDARD; PRT; 376 AA.
AC O93883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGG1
OS Penicillium griseoroseum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OC NCBI_TaxID=84562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT 6421;
RA Ribon A.B., Cosiho J.L.C., Barros E.G., Araujo E.F.;
RT "Cloning and characterization of a gene encoding the
RT endopolygalacturonase of Penicillium griseoroseum.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
CC (POLYGLACTURONASES).
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-----
EMBL; AF085238; AAC83692.1; -
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; PbH1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; PbH1_5.
DR PROSITE; PS00502; POLYGLACTURONASE; 1.
KW Hydrolase; Glycosidase; Cell wall; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 376 POLYGLACTURONASE.
SQ SEQUENCE 376 AA; 38068 MW; 1EDB1EC56ED56928 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 376;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 350 DMSWS 354

RESULT 14
NRAM_IAMIL STANDARD; PRT; 453 AA.
ID_NRAM_IAMIL
```

AC P03470;
 DT 21-JUL-1986 (Rel. 01, Last Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18)
 GN NA.
 OS Influenza A virus (strain A/Wilson-Smith/33).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OC NCBI_TaxID=11487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82192605; PubMed=7077751;
 RA Hiti A.L., Nayak D.P.;
 RT "Complete nucleotide sequence of the neuraminidase gene of human
 influenza virus A/WSN/33";
 RT J. Virol. 41:730-734(1982).
 RL CC
 CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 chains of the host cell surface proteins and from the viral
 envelope. Such a reaction prevents self-aggregation and facilitate
 the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J02177; AAA43397.1; ALT_SEQ.
 DR HSSP; P03472; QWMC.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 35 ANCHOR.
 FT DOMAIN 36 74 HYPERVARIABLE STALK REGION.
 FT DOMAIN 75 453 HEAD OF NEURAMINIDASE.
 FT ACT_SITE 259 259 PROBABLE.
 FT ACT_SITE 261 261 PROBABLE.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 453 AA; 49623 MW; 7DC56A4416A47BE8 CRC64;
 Query Match 82.5%; Score 33; DB 1; Length 453;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 Db 437 VDWSW 441
 RESULT 15
 ID NRAM IAPUE STANDARD; PRT; 454 AA.
 AC P03470;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18)
 GN NA.

OS Influenza A virus (strain A/Puerto Rico/8/34).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OC NCBI_TaxID=11455;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81148841; PubMed=7010182;
 RA Fields S., Winter G., Brownlee G.G.;
 RT "Structure of the neuraminidase gene in human influenza virus
 A/PR/8/34";
 RT Nature 290:213-217(1981).
 RL CC
 CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 chains of the host cell surface proteins and from the viral
 envelope. Such a reaction prevents self-aggregation and facilitate
 the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
 alpha-(2-8)-glycosidic linkages of terminal sialic residues in
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 CC
 CC EMBL; J02146; AAA43412.1; -.
 DR HSSP; P03472; QWMC.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 35 ANCHOR.
 FT DOMAIN 36 75 HYPERVARIABLE STALK REGION.
 FT DOMAIN 76 454 HEAD OF NEURAMINIDASE.
 FT ACT_SITE 260 260 PROBABLE.
 FT ACT_SITE 262 262 PROBABLE.
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 454 AA; 50143 MW; A0DC4C08A2B53705 CRC64;
 Query Match 82.5%; Score 33; DB 1; Length 454;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 Db 438 VDWSW 442

Search completed: February 18, 2004, 14:28:04
 Job time : 4.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDWSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapi:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	242	12 Q919K8	Q919K8 culex nigri
2	37	92.5	304	16 Q91719	Q91719 pseudomonas
3	37	92.5	433	16 Q8P4A1	Q8P4A1 xanthomonas
4	37	92.5	438	16 Q8P4V8	Q8P4V8 xanthomonas
5	36	90.0	258	5 Q45498	Q45498 caenorhabdi
6	36	90.0	361	16 Q8P955	Q8P955 xanthomonas
7	36	90.0	374	16 Q9H210	Q9H210 pseudomonas
8	36	90.0	409	10 Q9W3F6	Q9W3F6 arabidopsis
9	36	90.0	463	5 Q8MAJ0	Q8MAJ0 apis cerana
10	36	90.0	538	11 Q8C9K6	Q8C9K6 mus musculus
11	36	90.0	581	5 Q8MSH3	Q8MSH3 drosophila
12	36	90.0	597	5 Q9VGP2	Q9VGP2 drosophila
13	36	90.0	740	6 Q9SKV1	Q9SKV1 bos taurus
14	36	90.0	745	11 Q8CBT3	Q8CBT3 mus musculus
15	36	90.0	756	6 Q95KV0	Q95KV0 bos taurus
16	36	90.0	984	11 Q8C3U1	Q8C3U1 mus musculus

17	36	90.0	984	11 Q8BRB1	Q8BRB1 mus musculus
18	34	85.0	85	16 Q8FBL8	Q8FBL8 escherichia
19	34	85.0	211	9 Q8O148	Q8O148 bacterioph
20	34	85.0	211	9 Q8O148	Q8O148 bacterioph
21	34	85.0	237	10 Q8H2P9	Q8H2P9 oryza sativ
22	34	85.0	245	4 Q8N241	Q8N241 homo sapien
23	34	85.0	297	11 Q8BG50	Q8BG50 mus musculu
24	34	85.0	309	2 Q9F163	Q9F163 amycolatops
25	34	85.0	323	12 Q9QTE2	Q9QTE2 marek's dia
26	34	85.0	328	2 Q8KPM8	Q8KPM8 saccharopol
27	34	85.0	394	5 Q9U2T2	Q9U2T2 caenorhabdi
28	34	85.0	611	16 Q8DKF5	Q8DKF5 synchococcc
29	34	85.0	616	2 Q33749	Q33749 synchococcc
30	34	85.0	1139	16 Q8ZC91	Q8ZC91 versinia pe
31	34	85.0	1941	16 Q8G751	Q8G751 bifidobacte
32	33	82.5	97	12 Q9QTI1	Q9QTI1 svse2 plect
33	33	82.5	110	16 Q8DYI4	Q8DYI4 streptococc
34	33	82.5	173	16 Q8E5U2	Q8E5U2 streptococc
35	33	82.5	173	16 Q8E065	Q8E065 streptococc
36	33	82.5	178	10 Q8LHJ6	Q8LHJ6 oryza sativ
37	33	82.5	198	16 Q9PA54	Q9PA54 xylella fas
38	33	82.5	232	17 Q8ZSR8	Q8ZSR8 pyrobaculum
39	33	82.5	234	16 Q9X897	Q9X897 streptomyce
40	33	82.5	236	3 Q9P527	Q9P527 neurospora
41	33	82.5	236	3 Q8NJY9	Q8NJY9 bionectria
42	33	82.5	240	3 Q8NJZ1	Q8NJZ1 bionectria
43	33	82.5	246	16 Q8CWD6	Q8CWD6 escherichia
44	33	82.5	270	4 Q8NCJ2	Q8NCJ2 homo sapien
45	33	82.5	273	10 Q94JM4	Q94JM4 arabidopsis

ALIGNMENTS

RESULT 1

Q919K8 ID Q919K8 PRELIMINARY; PRT; 242 AA.
AC Q919K8; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_taxid=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Floridal997;
RX MEDLINE=21488685; PubMed=11602755;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RA "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus."
RT J. Virol. 75:11157-11165(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Floridal997;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF403738; AAK94146.1; -
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 100.0%; Score 40; DB 12; Length 242;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6

|||||

79 LDWSWA 84

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RESULT 2
Q91719 ID Q91719 PRELIMINARY; PRT; 304 AA.
AC Q91719;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable cytochrome c oxidase assembly factor.
GN PA0113.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004449; AG03503.1; -.
DR InterPro; IPR006369; CysC_CtaB.
DR InterPro; IPR000537; Ubia.
DR Pfam; PF01040; Ubia; 1.
DR TIGRFAMs; TIGR01473; cyoE ctaB; 1.
DR PROSITE; PS00943; Ubia; 1.
KW Complete proteome.
SQ SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 92.5%; Score 37; DB 16; Length 304;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
DB 259 LDWSWA 264
|||||

RESULT 3
Q8P4A1 ID Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cicarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 438;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
DB 182 VDWSWA 187
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RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012502; AAM43483.1; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 433;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
DB 180 VDWSWA 185
|||||

RESULT 4
Q8PFV8 ID Q8PFV8 PRELIMINARY; PRT; 438 AA.
AC Q8PFV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XAC3864.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cicarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarotti R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 438;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
DB 182 VDWSWA 187
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RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.",
 RL Nature 417:459-463(2002).
 DR EMBL; AE012305; AAM41300.1; -.
 DR InterPro; IPR002656; Acyl_transf_3; 1.
 DR Pfam; PF01757; Acyl_transf_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;

 Query Match 90.0%; Score 36; DB 16; Length 361;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
 QY 1 LDWSW 5
 DB 117 LDWSW 121

 RESULT 7
 Q9HZ10
 ID Q9HZ10 PRELIMINARY; PRT; 374 AA.
 AC Q9HZ10;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical protein PA3230.
 GN PA3230.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas;
 OX NCBI_TaxID=287;
 [1]
 RN R
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RT opportunistic pathogen.",
 RL Nature 406:959-964(2000).
 DR EMBL; AE004746; AAG06618.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

 Query Match 90.0%; Score 36; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
 QY 2 DWSWA 6
 DB 81 DWSWA 85

 RESULT 8
 Q9M3F6
 ID Q9M3F6 PRELIMINARY; PRT; 409 AA.
 AC Q9M3F6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative replication protein.
 GN T14K23.110.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.",
 RL Nature 417:459-463(2002).
 DR EMBL; AE012305; AAM41300.1; -.
 DR InterPro; IPR002656; Acyl_transf_3; 1.
 DR Pfam; PF01757; Acyl_transf_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;

 Query Match 90.0%; Score 36; DB 16; Length 361;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
 QY 1 LDWSW 5
 DB 117 LDWSW 121

 RESULT 7
 Q9HZ10
 ID Q9HZ10 PRELIMINARY; PRT; 374 AA.
 AC Q9HZ10;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical protein PA3230.
 GN PA3230.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas;
 OX NCBI_TaxID=287;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.",
 RL Nature 406:959-964(2000).
 DR EMBL; AE004746; AAG06618.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

 Query Match 90.0%; Score 36; DB 16; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
 QY 2 DWSWA 6
 DB 81 DWSWA 85

 RESULT 8
 Q9M3F6
 ID Q9M3F6 PRELIMINARY; PRT; 409 AA.
 AC Q9M3F6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative replication protein.
 GN T14K23.110.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC eukaryotes II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
 RA Quetier F., Salanoubat M.,
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL132909; CAB87732.1; -.
 DR InterPro; IPR003871; DUF223.
 DR Pfam; PF02721; DUF223; 2
 SQ SEQUENCE 409 AA; 45738 MW; ADDC4EPF5597E4EE4 CRC64;
 Query Match 90.0%; Score 36; DB 10; Length 409;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 Db 190 LDWSW 194
 RESULT 9
 Q8MMJ0 PRELIMINARY; PRT; 463 AA.
 ID Q8MMJ0
 AC Q8MMJ0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Major royal jelly protein MRJP2 precursor.
 DE MRJP2.
 GN Apis cerana (Indian honeybee).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
 OC Apoidea; Apis.
 OX NCBI_TaxID=7461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Nurse heads;
 RA Sittipranes S., Imjongjirak C.;
 RA "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
 RT cerana in Thailand";
 RT Cerana in Thailand";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF525777; AAM8282.1; -.
 DR InterPro; IPR003534; Royaljelly.
 DR Pfam; PF03022; MRJP; 1.
 DR PRINTS; PR01366; ROYALJELLY.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;
 Query Match 90.0%; Score 36; DB 5; Length 463;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWA 6
 Db 110 DWSWA 114
 RESULT 10
 Q8C9K6 PRELIMINARY; PRT; 538 AA.
 ID Q8C9K6
 AC Q8C9K6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Eph receptor A3.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK041935; BAC31104.1; -.
 SQ SEQUENCE 538 AA; 60659 MW; EEDAB12E0369E419 CRC64;
 Query Match 90.0%; Score 36; DB 11; Length 538;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 Db 343 LDWSW 347
 RESULT 11
 Q8MSH3 PRELIMINARY; PRT; 581 AA.
 ID Q8MSH3
 AC Q8MSH3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE GH24640p.
 GN CG6728.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY118818; AAM50678.1; -.
 DR FlyBase; FBgn0037896; CG6728.
 DR InterPro; IPR000172; GMC_oxred.
 DR InterPro; IPR000169; SHprot_acsite.
 DR Pfam; PF00732; GMC_oxred; 3.
 DR PROSITE; PS00639; THIOI PROTEASE HIS; 1.
 SQ SEQUENCE 581 AA; 63475 MW; A2F13BEB2C5B496D CRC64;
 Query Match 90.0%; Score 36; DB 5; Length 581;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWA 6
 Db 159 DWSWA 163
 RESULT 12
 Q9VGP2 PRELIMINARY; PRT; 597 AA.
 ID Q9VGP2
 AC Q9VGP2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG6728 protein.

GN CG6728.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtie K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foele C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mileshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003691; AAF54634.1; -;
 DR FlyBase; FBgn0037896; CG6728.
 DR InterPro; IPR000172; GMC_oxred.
 DR InterPro; IPR000169; SHPtot_acsite.
 DR Pfam; PF00732; GMC_oxred; 1.
 DR PROSITE; PS00624; GMC_OXRED.2; 1.
 DR PROSITE; PS00639; THIOLE PROTEASE HIS; 1.
 SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFFA0902A CRC64;
 Query Match 90.0%; Score 36; DB 5; Length 597;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWA 6
 DB 159 DWSWA 163
 RESULT 13
 ID Q95KV1 PRELIMINARY; PRT; 740 AA.
 AC Q95KV1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Ikb kinase-alpha.
 GN BIKKALPHA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
 RT "Identification and characterisation of the bovine Ikb kinases (IKKs)
 RT alpha, beta and gamma.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: BLASTING TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ414555; CAC93686.1; -;
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00669; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F4D176 CRC64;
 Query Match 90.0%; Score 36; DB 6; Length 740;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 DB 733 LDMSW 737
 RESULT 14
 ID Q8CBT3 PRELIMINARY; PRT; 745 AA.
 AC Q8CBT3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved helix-loop-helix ubiquitous kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK035326; BAC29034.1; -;
 SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;
 Query Match 90.0%; Score 36; DB 11; Length 745;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDMSW 5
 DB 738 LDMSW 742
 RESULT 15
 ID Q95KV0 PRELIMINARY; PRT; 756 AA.
 AC Q95KV0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-beta.
GN BIKKBEIA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKks)
RT alpha, beta and gamma."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ414556; CAC93687.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match          90.0%; Score 36; DB 6; Length 756;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSW 5
DB      737 LDWSW 741

```

Search completed: February 18, 2004, 14:35:40
 Job time : 19.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDWSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	304	2 F83632	probable cytochrome
2	36	90.0	258	2 T21987	hypothetical prote
3	36	90.0	382	2 S23471	uroporphyrinogen d
4	36	90.0	374	2 B83241	conserved hypotet
5	36	90.0	409	2 T47298	probable replicati
6	36	90.0	745	1 I49101	conserved helix-lo
7	36	90.0	983	2 B45583	receptor tyrosine
8	36	90.0	983	2 A38224	protein-tyrosine k
9	36	90.0	983	2 A45583	receptor tyrosine
10	34	85.0	211	2 T03355	gene e12 protein -
11	34	85.0	411	2 E84949	tetrahydrofolylpol
12	34	85.0	433	2 T31511	hypothetical prote
13	34	85.0	616	2 T14235	NADH2 dehydrogenas
14	34	85.0	1139	2 A10379	probable potassium
15	33	82.5	198	2 B82531	conserved hypotet
16	33	82.5	234	2 T36162	probable integral
17	33	82.5	275	2 T05922	hypothetical prote
18	33	82.5	316	2 AB2931	hypothetical prote
19	33	82.5	316	2 D98351	dipeptide ABC tran
20	33	82.5	342	2 A13395	NADH2 dehydrogenas
21	33	82.5	344	2 AB3548	vegetatable incomp
22	33	82.5	360	2 S60888	ferric exochelin b
23	33	82.5	415	2 AE1844	hypothetical prote
24	33	82.5	421	2 T31787	hypothetical prote
25	33	82.5	436	2 E69371	bile acid-inducibl
26	33	82.5	454	1 NMIV3	exo-alpha-sialidas
27	33	82.5	454	1 NMIV	hypothetical prote
28	33	82.5	464	2 S75362	aerolysin precurs
29	33	82.5	492	2 S03098	

30	33	82.5	516	2 T10000	cytochrome P450 (C
31	33	82.5	524	2 T09999	cytochrome P450 -
32	33	82.5	524	2 T09944	probable cytochrom
33	33	82.5	539	2 T15256	hypothetical prote
34	33	82.5	610	2 T35222	hypothetical prote
35	33	82.5	656	2 A56975	VI polysaccharide
36	33	82.5	656	2 AF1040	VI polysaccharide
37	33	82.5	836	2 D82177	conserved hypotet
38	33	82.5	840	1 A42970	H+-exporting ATPas
39	33	82.5	885	2 C83441	two-component sens
40	33	82.5	1334	2 T50568	probable multi-dom
41	33	82.5	1575	2 T18545	lysoactin synthet
42	33	82.5	1842	2 T43409	probable fatty-aci
43	33	82.5	1842	2 T38781	fatty acid synthas
44	32	80.0	53	2 T11353	H+-transporting tw
45	32	80.0	83	2 S24712	IG alpha chain - h

ALIGNMENTS

RESULT 1

F83632

Probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginos
C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F83632

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83632

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-304 <STO>

A:Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03503.1; GSPDB:GN0001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0113

C:Superfamily: heme O synthase

Query Match 92.5%; Score 37; DB 2; Length 304;
Best Local Similarity 83.3%; Pred No. 50;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6

Db 259 LDWSWA 264

RESULT 2

T21987

hypothetical protein F39B2.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21987

R:Dobson, R.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19498

A:Accession: T21987

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-258 <MIL>

A:Cross-references: EMBL:Z92834; PIDN:CAB07386.1; GSPDB:GN00019; CESP:F39B2.5

A:Experimental source: clone F39B2

C:Genetics:

A:Gene: CESP:F39B2.5

A:Map position: 1

A:Introns: 16/2; 58/1; 97/3

Query Match 90.0%; Score 36; DB 2; Length 258;

Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWA 6
|||
Db 21 LDWKWA 26

RESULT 3
S23471
uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YD9609.03; protein YDR047w
C:Species: *Saccharomyces cerevisiae*
C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 22-Jun-1999
C:Accession: S23471; S33965; S54033; S20190; S27348; S3312
C:Garay, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytko, J.; Harrison, L.; Kushner, J.; La
Eur. J. Biochem. 205, 1011-1016, 1992
A:Title: Uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence
A:Reference number: S23471; MUID:92249304; PMID:1576986
A:Accession: S23471
A:Molecule type: DNA
A:Residues: 1-362 <GAR>
A:Cross-references: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
R:DiFlumeri, C.; Larocque, R.; Keng, T.
Yeast 9, 613-623, 1993
A:Title: Molecular analysis of HEM6 (HEM12) in *Saccharomyces cerevisiae*, the gene for u
A:Reference number: S33965; MUID:93348774; PMID:8346678
A:Accession: S33965
A:Molecule type: DNA
A:Residues: 1-362 <DIF>
A:Cross-references: EMBL:Z19089; NID:g4775; PIDN:CAA79514.1; PID:g4776
R:Hunt, S.; Bowman, S.; Harris, D.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54031
A:Accession: S54033
A:Molecule type: DNA
A:Residues: 1-362 <HUN>
A:Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAA89078.1; PID:g798900; MIPS:YDR047w
C:Genetics:
A:Gene: HEM12; HEM6; POP3
A:Cross-references: MIPS:YDR047w; SGD:S0002454
A:Map position: 4R
C:Superfamily: uroporphyrinogen decarboxylase
C:Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||
Db 279 LDWSW 283

RESULT 4
B83241
conserved hypothetical protein PA3230 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C>Date: 15-Sep-2000 #sequence revision 15-Sep-2000 #text change 31-Dec-2000
C:Accession: B83241
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: B82950; MUID:20437337; PMID:10984043
A:Accession: B83241
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:

A:Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||
Db 81 DWSWA 85

RESULT 5
T47298
probable replication protein - *Arabidopsis thaliana*
N:Alternate names: protein T14K23.110
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 20-Apr-2000
C:Accession: T47298
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24458
A:Accession: T47298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <NYA>
A:Cross-references: EMBL:AL132909
A:Experimental source: cultivar Columbia; BAC clone T14K23
C:Genetics:
A:Map position: 3
A:Introns: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3
A>Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||
Db 190 LDWSW 194

RESULT 6
I49101
conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
C:Species: *Mus musculus* (house mouse)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C:Accession: I49101
R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
A:Reference number: I49101; MUID:96044444; PMID:7558004
A:Accession: I49101
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <RES>
A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C:Genetics:
A:Gene: CHUK
C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||
Db 738 LDWSW 742

RESULT 7

B45583
 receptor tyrosine kinase Cek4 - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 22-Apr-1993 #sequence_revision 18-Jun-1999
 C:Accession: B45583
 R:Sajjadi, F.G.; Paquale, E.B.; Subramani, S.
 New Biol. 3, 769-778, 1991
 A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
 A:Reference number: A45583; MUID:92031278; PMID:1657122
 A:Accession: B45583
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-983 <SAJ>
 A:Cross-references: GB:M68514; NID:9454809; PIDN:AAA48665.1; PID:9211447
 A:Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIP:62411)
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif

Query Match 90.0%; Score 36; DB 2; Length 983;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 342 LDMSW 346

RESULT 8
 A:38224
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
 C:Accession: A38224; B38224
 R:Wicks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
 A:Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed
 A:Reference number: A38224; MUID:92179233; PMID:1311845
 A:Accession: A38224
 A:Molecule type: mRNA
 A:Residues: 1-983 <WIC>
 A:Cross-references: GB:M83941; NID:9183931; PIDN:AAA58633.1; PID:9183932
 A:Experimental source: pre-B-cell leukemia cell line LK63
 A:Note: sequence extracted from NCBI backbone (NCBIP:86627)
 A:Accession: B38224
 A:Molecule type: protein
 A:Residues: 21-39;810-860 <W12>
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
 F:542-565/Domain: transmembrane #status predicted <TMW>
 F:519-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif
 F:232,337,391,404,493/Binding site: carbohydrate (Asn) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 983;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 343 LDMSW 347

RESULT 9
 A:45583
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Apr-1993 #sequence_revision 18-Jun-1999
 C:Accession: A45583
 R:Sajjadi, F.G.; Paquale, E.B.; Subramani, S.

New Biol. 3, 769-778, 1991
 A:Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse
 A:Reference number: A45583; MUID:92031278; PMID:1657122
 A:Accession: A45583
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-983 <SAJ>
 A:Cross-references: GB:M68513; NID:919119; PIDN:AAA39521.1; PID:9199120
 A:Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
 F:619-885/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif

Query Match 90.0%; Score 36; DB 2; Length 983;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
 |||||
 Db 342 LDMSW 346

RESULT 10
 T03355
 gene el2 protein - Lactococcus phage bIL170
 C:Species: Lactococcus phage bIL170
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
 C:Accession: T03355
 R:Crutz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin,
 submitted to the EMBL Data Library, June 1997
 A:Description: Sequence and organization of the lactococcal isometric bIL170 phage geno.
 A:Reference number: Z14903
 A:Accession: T03355
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-211 <CRU>
 A:Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AAC27226.1; PID:g3282307
 C:Genetics:
 A:Gene: el2
 C:Superfamily: Lactococcus phage bIL170 gene el2 protein

Query Match 85.0%; Score 34; DB 2; Length 211;
 Best Local Similarity 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSW 6
 |||||
 Db 29 LSWSWA 34

RESULT 11
 E84949
 tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) [imported] - Buchnera sp. (strain A:
 C:Species: Buchnera sp.
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: E84949
 R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
 Nature 407, 81-86, 2000
 A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
 A:Reference number: A84930; MUID:20445173; PMID:10993077
 A:Accession: E84949
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-411 <STO>
 A:Cross-references: GB:AP000398; GSPDB:GN00144
 A:Experimental source: strain APS
 C:Genetics:
 A:Gene: folC; BU167
 C:Superfamily: folylpolyglutamate synthase
 C:Keywords: ligase

Query Match 85.0%; Score 34; DB 2; Length 411;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
:|||||
Db 219 IDMSW 223

RESULT 12

T31511

Hypothetical protein Y116A8C.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000

C:Accession: T31511

R:McMurray, A.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21041

A:Accession: T31511

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-433 <WIL>

A:Cross-references: EMBL:AL117204; PIDN:CAB55145.1; CESP:Y116A8C.9

A:Experimental source: clone Y116A8C

C:Genetics:

A:Gene: CESP:Y116A8C.9

A:Introns: 16/2; 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1

C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.9

Query Match 85.0%; Score 34; DB 2; Length 433;

Best Local Similarity 66.7%; Pred. No. 2.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 6

:|||||

Db 174 VDWTA 179

RESULT 13

T14235

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Synechococcus sp. (strain PCC 70

C:Species: Synechococcus sp.

A:Variety: strain PCC 7002

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002

C:Accession: T14235

R:Klughammer, B.; Sultemeyer, D.; Badger, M.R.; Price, G.D.

submitted to the EMBL Data Library, April 1997

A:Description: Involvement of ndhF3, ndhD3 and ORF427 genes in high affinity CO2 uptake

A:Reference number: Z17936

A:Accession: T14235

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-616 <KLU>

A:Cross-references: EMBL:U97516; NID:G2232044; PID:G2232046; PIDN:AAB62184.1

A:Experimental source: strain PCC 7002

C:Genetics:

A:Note: ndhF3

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match

Best Local Similarity 85.0%; Score 34; DB 2; Length 616;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSW 6

:|||||

Db 115 MDWGWA 120

RESULT 14

A10379

probable potassium efflux system YP03129 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: A10379
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10379

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1139 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:gl5981067; GSPDB:GN00175

C:Genetics:

A:Gene: YP03129

Query Match 85.0%; Score 34; DB 2; Length 1139;

Best Local Similarity 80.0%; Pred. No. 5.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5

:|||||

Db 480 MDMSW 484

RESULT 15

B82531

conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C:Accession: B82531

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: AB2515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82531

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-198 <SIM>

A:Cross-references: GB:AB004072; GB:AB003849; NID:g9107884; PIDN:AAF85463.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

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M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

C:Genetics:

A:Contents: annotation

A:Gene: XF2666

C:Superfamily: conserved hypothetical protein MJ1677

Query Match

Best Local Similarity 82.5%; Score 33; DB 2; Length 198;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6

:|||||

Db 135 DWNWA 139

Search completed: February 18, 2004, 14:38:38

Job time : 8.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDWSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10	US-09-847-940B-5
2	40	100.0	6	11	US-09-847-946A-5
3	40	100.0	6	11	US-09-847-946A-40
4	40	100.0	6	11	US-09-847-946A-62
5	40	100.0	7	11	US-09-847-946A-66
6	40	100.0	8	11	US-09-847-946A-59
7	40	100.0	8	11	US-09-847-946A-67
8	40	100.0	9	11	US-09-847-946A-58
9	40	100.0	9	11	US-09-847-946A-61
10	40	100.0	9	11	US-09-847-946A-64
11	40	100.0	9	11	US-09-847-946A-65
12	40	100.0	10	11	US-09-847-946A-57
13	40	100.0	10	11	US-09-847-946A-60
14	40	100.0	10	11	US-09-847-946A-63
15	36	90.0	6	10	US-09-847-940B-2

16	36	90.0	6	11	US-09-847-946A-2	Sequence 2, Appli
17	36	90.0	6	11	US-09-847-946A-33	Sequence 33, Appl
18	36	90.0	6	11	US-09-847-946A-41	Sequence 41, Appl
19	36	90.0	6	11	US-09-847-946A-73	Sequence 73, Appl
20	36	90.0	7	11	US-09-847-946A-37	Sequence 37, Appl
21	36	90.0	7	11	US-09-847-946A-77	Sequence 77, Appl
22	36	90.0	8	11	US-09-847-946A-30	Sequence 30, Appl
23	36	90.0	8	11	US-09-847-946A-38	Sequence 38, Appl
24	36	90.0	8	11	US-09-847-946A-70	Sequence 70, Appl
25	36	90.0	8	11	US-09-847-946A-78	Sequence 78, Appl
26	36	90.0	9	11	US-09-847-946A-29	Sequence 29, Appl
27	36	90.0	9	11	US-09-847-946A-32	Sequence 32, Appl
28	36	90.0	9	11	US-09-847-946A-35	Sequence 35, Appl
29	36	90.0	9	11	US-09-847-946A-36	Sequence 36, Appl
30	36	90.0	9	11	US-09-847-946A-69	Sequence 69, Appl
31	36	90.0	9	11	US-09-847-946A-72	Sequence 72, Appl
32	36	90.0	9	11	US-09-847-946A-75	Sequence 75, Appl
33	36	90.0	9	11	US-09-847-946A-76	Sequence 76, Appl
34	36	90.0	10	11	US-09-847-946A-31	Sequence 31, Appl
35	36	90.0	10	11	US-09-847-946A-34	Sequence 34, Appl
36	36	90.0	10	11	US-09-847-946A-71	Sequence 71, Appl
37	36	90.0	10	11	US-09-847-946A-74	Sequence 74, Appl
38	36	90.0	11	11	US-09-847-946A-28	Sequence 28, Appl
39	36	90.0	11	11	US-09-847-946A-68	Sequence 68, Appl
40	36	90.0	11	11	US-09-847-946A-132	Sequence 132, App
41	36	90.0	11	11	US-09-847-946A-140	Sequence 140, App
42	36	90.0	12	11	US-09-847-946A-43	Sequence 43, Appl
43	36	90.0	13	11	US-09-847-946A-143	Sequence 143, App
44	36	90.0	13	11	US-09-847-946A-144	Sequence 144, App
45	36	90.0	13	11	US-09-847-946A-145	Sequence 145, App

ALIGNMENTS

RESULT 1

US-09-847-940B-5
; Sequence 5, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 6
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-5

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWA 6
|||
Db 1 LDWSWA 6

RESULT 2

US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-5

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
Db 1 LDWSWA 6

RESULT 3
US-09-847-946A-40
; Sequence 40, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-40

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
Db 1 LDWSWA 6

RESULT 4
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-62

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
Db 1 LDWSWA 6

RESULT 5
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-66

Query Match 100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
Db 1 LDWSWA 6

RESULT 6

US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
DB 3 LDWSWA 8

RESULT 7
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-67

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
DB 1 LDWSWA 6

RESULT 8
US-09-847-946A-58
; Sequence 58, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-58

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
| | | | |
DB 1 LDWSWA 6

RESULT 9
US-09-847-946A-61
; Sequence 61, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-61

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 |||||
 Db 1 LDWSWA 6

RESULT 10

US-09-847-946A-64
 ; Sequence 64, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 64
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-64

Query Match 100.0%; Score 40; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
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 Db 3 LDWSWA 8

RESULT 11

US-09-847-946A-65
 ; Sequence 65, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 65
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-65

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 |||||
 Db 2 LDWSWA 7

RESULT 12

US-09-847-946A-57
 ; Sequence 57, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 57
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-57

Query Match 100.0%; Score 40; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWA 6
 |||||
 Db 2 LDWSWA 7

RESULT 13

US-09-847-946A-60
 ; Sequence 60, Application US/09847946A
 ; Publication No. US20030054999A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Michael J
 ; APPLICANT: Ghosh, Sankar
 ; APPLICANT: Findeis, Mark A
 ; APPLICANT: Phillips, Kathryn
 ; APPLICANT: Hannig, Gerhard
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 ; FILE REFERENCE: PPI-119
 ; CURRENT APPLICATION NUMBER: US/09/847,946A
 ; CURRENT FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,261
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 09/643,260
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 60
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
 ; OTHER INFORMATION: sequence
 US-09-847-946A-60

US-09-847-946A-60

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSA 6
| | | | |
Db 2 LDWSA 7

RESULT 14

US-09-847-946A-63
; Sequence 63, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-63

Query Match

Best Local Similarity 100.0%; Score 40; DB 11; Length 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSA 6
| | | | |
Db 3 LDWSA 8

RESULT 15

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match

90.0%; Score 36; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDWSW 5
| | | | |
Db 1 LDWSW 5

Search completed: February 18, 2004, 15:41:55
Job time : 16.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archesp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	205	16	Q9ACRS streptomyces
2	40	100.0	227	4	Q8IXK8 homo sapien
3	40	100.0	355	11	Q8BIT9 mus musculus
4	40	100.0	452	4	Q96AB7 homo sapien
5	40	100.0	477	11	Q9CVU6 mus musculus
6	40	100.0	484	4	Q9BTU6 homo sapien
7	37	92.5	154	11	Q8BGD2 mus musculus
8	37	92.5	1083	13	Q90WQ8 oncorhynch
9	37	92.5	1083	13	Q8AXU2 oncorhynch
10	37	92.5	1100	13	Q90WQ9 oncorhynch
11	37	92.5	1329	16	Q9CD30 mycobacteri
12	36	90.0	48	16	Q8VKB2 mycobacteri
13	36	90.0	236	3	Q8NJY9 blonectria
14	36	90.0	261	2	Q9AGT7 caldicellul
15	36	90.0	273	16	Q8NS79 corynebacte
16	36	90.0	274	16	Q8G659 bifidobacte

17	36	90.0	310	2	Q9XBS7	Q9XBS7 zymomonas m
18	36	90.0	310	16	Q8FRF1	Q8FRF1 corynebacte
19	36	90.0	358	10	O50002	O50002 prunus arme
20	36	90.0	703	10	Q9FISO	Q9FISO arabidopsis
21	36	90.0	703	10	Q8GYG3	Q8GYG3 arabidopsis
22	36	90.0	740	6	Q9SKV1	Q9SKV1 bos taurus
23	36	90.0	745	11	Q8CBT3	Q8CBT3 mus musculu
24	36	90.0	747	16	O69735	O69735 mycobacteri
25	36	90.0	756	6	Q9SKV0	Q9SKV0 bos taurus
26	36	90.0	803	17	Q97UH8	Q97UH8 sulfolobus
27	36	90.0	889	16	Q9AAZ6	Q9AAZ6 caulobacter
28	36	90.0	996	2	Q9AQH0	Q9AQH0 caldicellul
29	36	90.0	1005	10	Q9XGZ2	Q9XGZ2 arabidopsis
30	36	90.0	1139	16	Q8ZC91	Q8ZC91 streptomyce
31	36	90.0	1345	16	Q9L060	Q9L060 streptomyce
32	36	90.0	1426	2	Q9X3P6	Q9X3P6 caldicellul
33	36	90.0	1751	2	Q9AQG4	Q9AQG4 caldicellul
34	36	90.0	1770	2	Q9X3P5	Q9X3P5 caldicellul
35	36	90.0	5435	2	Q9L4X2	Q9L4X2 streptomyce
36	35	87.5	49	6	Q8SPL6	Q8SPL6 equus cabal
37	35	87.5	161	6	Q8MJT3	Q8MJT3 oryctolagus
38	35	87.5	161	11	Q9Z1P9	Q9Z1P9 rattus norv
39	35	87.5	200	16	Q8NS33	Q8NS33 corynebacte
40	35	87.5	241	16	Q8FR42	Q8FR42 corynebacte
41	35	87.5	323	6	Q9TT79	Q9TT79 ovis aries
42	35	87.5	562	16	Q98AG0	Q98AG0 rhizobium 1
43	35	87.5	565	2	Q9KJ20	Q9KJ20 actinopolys
44	35	87.5	596	5	Q8SSN6	Q8SSN6 dictyosteli
45	35	87.5	616	17	O27025	O27025 methanobact

ALIGNMENTS

RESULT 1

Q9ACRS PRELIMINARY; PRT; 205 AA.
ID Q9ACRS;
AC Q9ACRS;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein SCPI.253.
GN SCPI.253.
OS Streptomyces coelicolor.
OG Plasmid SCPI.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=21996410; PubMed=12000953;
RA Thomson S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Bentley N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36779.1; --
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 100.0%; Score 40; DB 16; Length 205;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

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Db      10 ADMSWL 15
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RESULT 2
Q8IXK8      PRELIMINARY;      PRT;      227 AA.
AC Q8IXK8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to hypothetical protein BC017335.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040173; AAH40173.1; -.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;

Query Match      100.0%; Score 40; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWL 6
|||||
Db      113 ADMSWL 118
|||||
RESULT 3
Q8BIT9      PRELIMINARY;      PRT;      355 AA.
AC Q8BIT9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK087998; BAC40084.1; -.
SQ SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;

Query Match      100.0%; Score 40; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWL 6
|||||
Db      215 ADMSWL 220
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RESULT 4
Q96AB7      PRELIMINARY;      PRT;      452 AA.
AC Q96AB7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isozaki T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017335; AAH17335.1; -.
DR EMBL; AK075115; BAC11411.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25EE38096733 CRC64;

Query Match      100.0%; Score 40; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWL 6
|||||
Db      338 ADMSWL 343
|||||
RESULT 5
Q9CYU6      PRELIMINARY;      PRT;      477 AA.
AC Q9CYU6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 2810443J12RIK protein (Mitochondrial ribosomal protein L41
DE homolog).
GN 2810443J12RIK.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayaishizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK013297; BAB28775.1; -.
 DR EMBL; AK078448; BAC37279.1; -.
 DR MGD; MGI:1914478; 2810443J12Rik.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 3.
 DR SMART; SM00320; WD40; 4.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS00882; WD_REPEATS_2; 1.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 477 AA; 53201 MW; 2655573524A4BA9C CRC64;

Query Match 100.0%; Score 40; DB 11; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 |||||
 DB 337 ADMSWL 342

RESULT 6
 Q9BTV6 PRELIMINARY; PRT; 484 AA.
 ID Q9BTV6;
 AC Q9BTV6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003123; AAH03123.1; -.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 2.
 DR SMART; SM00320; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS00882; WD_REPEATS_2; 1.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 FT NON TER
 SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7358E CRC64;

Query Match 100.0%; Score 40; DB 4; Length 484;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 |||||
 DB 370 ADMSWL 375

RESULT 7

Q8BGD2 PRELIMINARY; PRT; 154 AA.
 ID Q8BGD2;
 AC Q8BGD2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK043157; BAC31480.1; -.
 DR EMBL; AK049078; BAC33535.1; -.
 KW Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 154 AA; 16524 MW; A526724D4074D888 CRC64;

Query Match 92.5%; Score 37; DB 11; Length 154;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
 |||||
 DB 9 ADMSWL 14

RESULT 8
 Q90W08 PRELIMINARY; PRT; 1083 AA.
 ID Q90W08;
 AC Q90W08;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Inducible nitric oxide synthase (EC 1.14.13.39).
 GN INOS
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Gonad;
 RA Wang T., Ward M., Grabowski P.S., Secombe C.J.;
 RT "Molecular cloning, gene organization and expression of rainbow trout
 RT (Oncorhynchus mykiss) inducible nitric oxide synthase (iNOS) gene.";
 RL J. Biochem. 358:747-755(2001).
 DR EMBL; AJ300555; CAC83069.1; -.
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001094; Flavodoxin like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN cyt reductase.
 DR InterPro; IPR004030; NO synthase.
 DR InterPro; IPR001433; Oxid_FAD/NAD(P).
 DR Pfam; PF00667; FAD binding_1; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF02898; NO synthase; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR PROSITE; PS60001; NOS; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 1083 AA; 123060 MW; 53E4DFD2FASAB85D CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1083;
Best Local Similarity 83.3%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 ADMSWL 6
DB 402 ADWAWL 407

RESULT 9

Q8AXU2 PRELIMINARY; PRT; 1083 AA.
AC Q8AXU2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Inducible nitric oxide synthase (EC 1.14.13.39).
GN iNOS.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T., Bols N., Secombes C.J.;
RT "Two Promoters of inducible nitric oxide synthase gene exist in rainbow trout evidenced by studies with RTs-11 and RTG-2 cell lines.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295230; CAC82807.1; -.
KW Oxidoreductase.
SQ SEQUENCE 1083 AA; 123033 MW; B0F95C3F033AF249 CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1083;
Best Local Similarity 83.3%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 ADMSWL 6
DB 402 ADWAWL 407

RESULT 10

Q90WQ9 PRELIMINARY; PRT; 1100 AA.
AC Q90WQ9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Inducible nitric oxide synthase (EC 1.14.13.39).
GN iNOS.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;
RT "Molecular cloning, gene organization and expression of rainbow trout (Oncorhynchus mykiss) inducible nitric oxide synthase (iNOS) gene.";
RL J. Biochem. 358:747-755(2001).
DR EMBL; AJ295231; CAC82808.1; -.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN cyt redctase.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 1.

DR Pfam; PF02898; NO synthase; 1.
DR PRINTS; PRO0369; FLAVODOXIN.
DR PRINTS; PRO0371; FPNCR.
DR PROSITE; PS60001; NOS; 1.
KW Oxidoreductase.
SQ SEQUENCE 1100 AA; 125079 MW; E4763388C97D608F CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1100;
Best Local Similarity 83.3%; Pred. No. 1.1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 ADMSWL 6
DB 419 ADWAWL 424

RESULT 11

Q9CD30 PRELIMINARY; PRT; 1329 AA.
AC Q9CD30;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein ML2535.
GN ML2535.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583926; CAC32066.1; -.
DR Leproma; ML2535; -.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR002543; FtsK SpoIIIE.
DR Pfam; PF01580; FtsK SpoIIIE; 2.
DR SMART; SM00382; AAA_3.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1329 AA; 146129 MW; F8A85758D600E7D8 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 1329;
Best Local Similarity 83.3%; Pred. No. 1.3e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 ADMSWL 6
DB 260 SDMSWL 265

RESULT 12

Q8VKB2 PRELIMINARY; PRT; 48 AA.
AC Q8VKB2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein MT0946.
GN MT0946.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Unayama L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bielei W.;
 RT "whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE006980; AAK45193.1; -
 DR TIGR; MT0946; -
 KW Hypothetical protein.
 SQ SEQUENCE 48 AA; 5265 MW; C0BFA9D6AA2EF8DF CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 48;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 DB 13 AEMSWL 18
 RESULT 13
 Q8NJY9 PRELIMINARY; PRT; 236 AA.
 AC Q8NJY9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Endoglucanase.
 GN CEL12C.
 OS Bionectria ochroleuca.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Bionectriaceae; Bionectria.
 OX NCBI_TaxID=29856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22067395; PubMed=12073090;
 RA Goedgebuur F., Fowler T., Phillips J., van der Kley P.,
 RA van Solingen P., Dankmeyer L., Power S.D.;
 RT "Cloning and relational analysis of 15 novel fungal endoglucanases
 RT from family 12 glycosyl hydrolase.";
 RL Curr. Genet. 41:89-98(2002).
 DR EMBL; AF435065; AAM77708.1; -
 DR InterPro; IPR002594; Glyco_hydro.12.
 DR Pfam; PF01670; Glyco_hydro.12; 1.
 DR ProDom; PD004316; Glyco_hydro.12; 1.
 SQ SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;
 Query Match 90.0%; Score 36; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 DB 63 ADMSW 67
 RESULT 14
 Q9AQG7 PRELIMINARY; PRT; 261 AA.
 AC Q9AQG7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Glycosyl hydrolase 6 (Fragment).
 OS Caldicellulosiruptor sp. Tok7B.1.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;

OC Caldicellulosiruptor.
 OX NCBI_TaxID=80339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tok7B.1;
 RX MEDLINE=20171169; PubMed=10706665;
 RA Gibbs M.D., Reeves R.A., Farrington G.K., Anderson P., Williams D.P.,
 RA Bergquist P.L.;
 RT "Multidomain and multifunctional glycosyl hydrolases from the extreme
 RT thermophile Caldicellulosiruptor isolate Tok7B.1";
 RL Curr. Microbiol. 40:333-340(2000).
 DR EMBL; AF078040; AAK06391.1; -
 DR HSSP; Q06851; INBC.
 DR InterPro; IPR001956; CBD_3.
 DR Pfam; PF00942; CBM_3; 1.
 DR ProDom; PD001947; CBD_3; 1.
 KW Hydrolase.
 FT NON_TER 1 261
 FT SEQUENCE 261 AA; 28759 MW; 4771744A26A6AE04 CRC64;
 Query Match 90.0%; Score 36; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSWL 6
 DB 237 DMSWL 241
 RESULT 15
 Q8NS79 PRELIMINARY; PRT; 273 AA.
 ID Q8NS79;
 AC Q8NS79;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol
 DE monophosphatase family.
 GN CGL0800.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005276; BAB98193.1; -
 DR InterPro; IPR000760; Inositol_P.
 DR Pfam; PF00459; inositol_P; 1.
 KW Complete proteome.
 SQ SEQUENCE 273 AA; 29072 MW; C132E2C67E0BBA4D CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 273;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 DB 225 ADMSWL 230
 Search completed: February 18, 2004, 14:35:38
 Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	470	1 NOS2_ONCMY	Q92091 oncorhynchu
2	36	90.0	470	1 NRAM_IADBU	Q07570 influenza a
3	36	90.0	470	1 NRAM_IADCH	Q07571 influenza a
4	36	90.0	470	1 NRAM_IADH2	Q07572 influenza a
5	36	90.0	470	1 NRAM_IADM2	Q07573 influenza a
6	36	90.0	470	1 NRAM_IADU3	Q07574 influenza a
7	36	90.0	470	1 NRAM_IAGFN	Q07575 influenza a
8	36	90.0	470	1 NRAM_IAGHD	Q07576 influenza a
9	36	90.0	470	1 NRAM_IAHJI	Q07577 influenza a
10	36	90.0	470	1 NRAM_IAMAE	Q07578 influenza a
11	36	90.0	470	1 NRAM_IATKL	Q07579 influenza a
12	36	90.0	745	1 IKKB_HUMAN	Q15111 h inhibitor
13	36	90.0	745	1 IKKA_MOUSE	Q06880 m inhibitor
14	36	90.0	756	1 IKKB_HUMAN	Q14920 homo sapien
15	36	90.0	757	1 IKKB_MOUSE	Q08351 mus musculus
16	36	90.0	757	1 IKCB_RAT	Q09478 rattus norv
17	36	90.0	1039	1 GUNB_CALSA	P10474 c endogluca
18	36	90.0	1275	1 RPBC_MYXXA	Q50864 myxococcus
19	35	87.5	99	1 NOS3_SHEEP	P79289 ovis aries
20	35	87.5	914	1 GUX2_CLOSR	P50900 clostridium
21	35	87.5	1201	1 NOS3_MOUSE	P70313 mus musculus
22	35	87.5	1202	1 NOS3_HUMAN	P29474 homo sapien
23	35	87.5	1204	1 NOS3_BOVIN	P29473 bos taurus
24	35	87.5	1204	1 NOS3_PIG	Q28989 sus scrofa
25	34	85.0	220	1 Y132_METJA	Q57596 methanococc
26	34	85.0	282	1 3MG2_ECOLI	P04395 escherichia
27	34	85.0	410	1 Y801_DEIRA	Q91w68 deinococcus
28	34	85.0	529	1 GUAA_MYCLE	P46810 mycobacteri
29	34	85.0	578	1 YC20_METJA	Q58617 methanococc
30	34	85.0	579	1 YC12_KLEPN	Q48458 klebsiella
31	34	85.0	591	1 NOS2_CANFA	Q62699 canis famil
32	34	85.0	1144	1 NOS2_MOUSE	P29477 mus musculus
33	34	85.0	1147	1 NOS2_RAT	Q06518 rattus norv

ALIGNMENTS

RESULT 1				
NOS2_ONCMY				
ID	NOS2_ONCMY	STANDARD;	PRT;	470 AA.
AC	Q92091;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Nitric oxide synthase, inducible (SC 1.14.13.39) (NOS, type II)			
DE	(Inducible NOS) (iNOS) (Fragment).			
GN	NOS2.			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RN	[1]_TaxID=8022;			
RP	SEQUENCE FROM N.A.			
RA	Grabowski P.S., Laing K.J., Hardie L., Macguigan F., Ralston S.,			
RA	Secombes C.J.;			
RT	"Detection of mRNA for a nitric oxide synthase in macrophages and			
RT	gill of rainbow trout challenged with an attenuated bacterial			
RT	pathogen.";			
RL	(In) Moncada S., Stamler J., Gross S., Higgs E.A. (eds.);			
RL	4th International meeting on the biology of nitric oxide, Amelia			
RL	Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,			
RL	Brookfield (1996).			
CC	-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE			
CC	WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO			
CC	MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.			
CC	-I- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +			
CC	nitric oxide + N NADP(+).			
CC	-I- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES			
CC	TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF			
CC	THE ENZYME (BY SIMILARITY).			
CC	-I- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY			
CC	SIMILARITY).			
CC	-I- SUBUNIT: Homodimer (By similarity).			
CC	-I- SIMILARITY: BSLONGS TO THE NOS FAMILY.			
CC	-I- SIMILARITY: Contains 1 flavodoxin-like domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; X97013; CAA65736.1; -			
CC	HSSP; P29477; iNOS.			
DR	InterPro; IPR003097; FAD binding.			
DR	InterPro; IPR001094; Flavodoxin_like.			
DR	InterPro; IPR001226; Flavodoxin.			
DR	InterPro; IPR004030; NO synthase.			
DR	Pfam; PF00667; FAD binding_1; 1.			
DR	Pfam; PF00258; flavodoxin_1.			

O60591 homo sapien
O54705 cavia porce
P35228 homo sapien
P22533 caldocellum
P22534 caldocellum
P80943 ovis aries
Q29422 ovis aries
O34453 bacillus su
P27250 escherichia
O93883 penicillium
O13911 schizosacch
Q07584 influenza a

DR Pfam; PF02898; NO synthase; 1.
 DR PRINTS; PRO0369; FLAVODOXIN.
 DR PROSITE; PS0902; FLAVODOXIN LIKE; 1.
 DR PROSITE; PS6001; NOS; PARTIAL.
 KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme.
 FT NON_TER 1
 FT DOMAIN 139 159 CALMODULIN-BINDING (POTENTIAL).
 FT FLAVODOXIN-LIKE.
 FT NP_BIND 253 284 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 398 409 FAD (ADP PART) (BY SIMILARITY).
 FT NON_TER 470 470
 SQ SEQUENCE 470 AA; 53329 MW; 40BG717EE500B64D CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 83.3%; Pred.No. 82;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ADMSWL 6
 Db 89 ADMDWL 94
 RESULT 2
 NRAM IADBU
 ID NRAM IADBU STANDARD; PRT; 470 AA.
 AC Q07570;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Duck/Burjatia/652/88).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."
 RL Virology 193:868-876(1993).
 CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL; L06572; AAA43365.1; .
 CC HSSP; P06820; 2BAT.
 CC InterPro; IPR001860; Glyco_hydro_34.
 CC Pfam; PF00064; neur; 1.
 CC ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 273 HEAD OF NEURAMINIDASE.
 FT BY SIMILARITY.
 FT ACT_SITE 273 273 BY SIMILARITY.

FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F6F8AD CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred.No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 Db 453 ADMSW 457
 RESULT 3
 NRAM IADCH
 ID NRAM IADCH STANDARD; PRT; 470 AA.
 AC Q07571;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses."
 RL Virology 193:868-876(1993).
 CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
 CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL; L06573; AAA43367.1; .
 CC HSSP; P06820; 2BAT.
 CC InterPro; IPR001860; Glyco_hydro_34.
 CC Pfam; PF00064; neur; 1.
 CC ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 273 HEAD OF NEURAMINIDASE.
 FT BY SIMILARITY.
 FT ACT_SITE 273 273 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT ACT_SITE 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 169AB89FBE8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 4
NRAM_IADH2 STANDARD; PRT; 470 AA.
AC Q07572;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase [EC 3.2.1.18].
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC EMBL; L06574; AAA43372.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52015 MW; E1C1D3E2C650B93C CRC64;
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Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 5
NRAM_IADM2 STANDARD; PRT; 470 AA.
AC Q07573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase [EC 3.2.1.18].
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
-----
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CC EMBL; L06575; AAA43404.1; -.
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9FE364C1F49 CRC64;
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QY      1 ADWSW 5
Db      453 ADWSW 457

RESULT 6
ID      NRAM IADU3
AC      Q07599;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neuraminidase (EC 3.2.1.18)
GN      NA
OS      Influenza A virus (strain A/Duck/Ukraine/1/63).
OC      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC      Influenza A viruses; Influenzavirus A.
OX      NCBI_TaxID=11374;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93212520; PubMed=8460490;
RA      Saito T., Kawakoka Y., Webster R.G.;
RT      "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT      viruses."
RL      Virology 193:868-876(1993).
CC      -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC      chains of the host cell surface proteins and from the viral
CC      envelope. Such a reaction prevents self-aggregation and facilitate
CC      the mobility of the virus to and from the site of infection.
CC      -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC      alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC      oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC      synthetic substrates.
CC      -!- SUBUNIT: Homotetramer.
CC      -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC      SPIKE ON THE SURFACE OF THE VIRION.
CC      -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; L06576; AAA16234.1; -.
CC      HSSP; P06820; 2BAT.
CC      InterPro; IPR001860; Glyco_hydro_34.
CC      Pfam; PF00064; neur; 1.
CC      ProDom; PD000431; Glyco_hydro_34; 1.
CC      Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC      TRANSMEM 7 37 ANCHOR (BY SIMILARITY).
CC      DOMAIN 38 88 HYPERVARIABLE STALK REGION.
CC      ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
CC      ACT_SITE 275 275 PROBABLE.
CC      CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      453 ADWSW 457

RESULT 7
ID      NRAM IAGFN
AC      Q07574;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neuraminidase (EC 3.2.1.18)
GN      NA
OS      Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC      Influenza A viruses; Influenzavirus A.
OX      NCBI_TaxID=38963;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93212520; PubMed=8460490;
RA      Saito T., Kawakoka Y., Webster R.G.;
RT      "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT      viruses."
RL      Virology 193:868-876(1993).
CC      -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC      chains of the host cell surface proteins and from the viral
CC      envelope. Such a reaction prevents self-aggregation and facilitate
CC      the mobility of the virus to and from the site of infection.
CC      -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC      alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC      oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC      synthetic substrates.
CC      -!- SUBUNIT: Homotetramer.
CC      -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC      SPIKE ON THE SURFACE OF THE VIRION.
CC      -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; L06584; AAA43428.1; -.
CC      HSSP; P06820; 2BAT.
CC      InterPro; IPR001860; Glyco_hydro_34.
CC      Pfam; PF00064; neur; 1.
CC      ProDom; PD000431; Glyco_hydro_34; 1.
CC      Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
CC      TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
CC      DOMAIN 39 88 HYPERVARIABLE STALK REGION.
CC      ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
CC      ACT_SITE 275 275 BY SIMILARITY.
CC      CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;
SQ
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      453 ADWSW 457

RESULT 8
ID      NRAM IAHGD
AC      Q07577;

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DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Herring gull/DE/677/89).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38964;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 viruses";
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL; L06585; AAA43368.1; --
 DR HSPSP; P06820; 2BAT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADWSW 5
 Db 453 ADWSW 457
 RESULT 9
 ID_NRAM_IARJI STANDARD; PRT; 470 AA.
 AC Q07578;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).

GN NA.
 OS Influenza A virus (strain A/Equine/Jillin/1/89).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 viruses";
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
 CC SPIKE ON THE SURFACE OF THE VIRION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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 CC -----
 CC EMBL; L06579; AAA43374.1; --
 DR HSPSP; P06820; 2BAT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADWSW 5
 Db 453 ADWSW 457
 RESULT 10
 ID_NRAM_IAMAE STANDARD; PRT; 470 AA.
 AC Q07583;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.

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OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL; L06586; AAA43369.1; -.
DR HSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 11
NRAM_IATKL STANDARD; PRT; 470 AA.
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;

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RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06588; AAA43410.1; -.
DR HSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; DE573742ABFF1E6B CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 12
IKKA_HUMAN STANDARD; PRT; 745 AA.
AC O1511; O14666; Q13132; Q92467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkkappaB kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;

```


RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
 RL "Identification and characterization of an IkappaB kinase.";
 RN Cell 90:373-383(1997).
 RP [2]
 RX SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE=9739468; PubMed=9252186;
 RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RL "A cytokine-responsive IkappaB kinase that activates the transcription
 RT factor NF-kappaB.";
 RN Nature 388:548-554(1997).
 RP [3]
 RX SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RA TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Marcuro F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RL "IKK-1 and IKK-2: Cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RN Science 278:860-866(1997).
 RP [4]
 RX SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RC MEDLINE=99032998; PubMed=9813230;
 RX Hu M.C.-T., Wang Y.-P.;
 RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RP [5]
 RX SEQUENCE OF 32-745 FROM N.A.
 RP TISSUE=Cervical carcinoma;
 RC MEDLINE=96258427; PubMed=8777433;
 RX Connelly M.A., Marcu K.B.;
 RA "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RP [6]
 RX PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 RP AND SER-180
 RX MEDLINE=98168283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RL "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RT Ser-176.";
 RP Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RP [7]
 RX PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,
 RA Donner D.B.;
 RL "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RP [8]
 RX IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RA "Positive and negative regulation of IkappaB kinase activity through
 RT IkappaB subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RP [9]
 RX IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RP [10]
 RX REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RL "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";

Am. J. Physiol. 278:C451-C462(2000).
 [11]
 RL SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKKBG.
 RN MEDLINE=21968797; PubMed=11971985;
 RX Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 RA O'Malley B.W.;
 RL "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
 RT activity by I kappa B kinase.";
 RN Mol. Cell. Biol. 22:3549-3561(2002).
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -I- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKBG and CREBBP.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- TISSUE SPECIFICITY: Widely expressed.
 CC -I- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.

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 DR EMBL; AF012890; AAC51662.1; -;
 DR EMBL; AF009225; AAC51671.1; -;
 DR EMBL; AF080157; AAD08996.1; -;
 DR EMBL; U22532; AAC50713.1; -;
 DR HSSP; Q63450; IA06.
 DR Genew; HGNC:1974; CHUK.
 DR MIM; 600664; -;
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0008384; P-IkappaB kinase activity; TAS.
 DR GO; GO:0007345; P-embryogenesis and morphogenesis; TAS.
 DR GO; GO:0007252; P-I-kappaB phosphorylation; TAS.
 DR GO; GO:0006955; P-immune response; TAS.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 302 PROTEIN KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 21 29 NEMO-BINDING.
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 ATP (BY SIMILARITY).
 FT MOD_RES 23 23 BY SIMILARITY.
 FT MOD_RES 176 176 PHOSPHORYLATION (BY PRK/AKT1).
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 176 176 S->M: LOSS OF AUTOPHOSPHORYLATION.
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF

FT MUTAGEN 176 176 ACTIVITY.
 FT T->E: FULL ACTIVATION.
 FT T->A: NO CHANGE IN PHOSPHORYLATION.
 FT S->A: NO CHANGE IN PHOSPHORYLATION.
 FT E -> G (IN REF. 2).
 FT L -> R (IN REF. 5).
 FT TS -> AY (IN REF. 5).
 FT P -> A (IN REF. 3 AND 5).
 FT TS -> DL (IN REF. 5).
 FT SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
 DB 739 DWSWL 743

RESULT 13
 ID IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC Q60680; Q9D2X3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1-)
 DE (I-kappa-B kinase alpha) (IKKalpha) (IKK-alpha) (I-kappa-B kinase
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
 GN CHUK OR IKKA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BNLB/c;
 RX MEDLINE=9604444; PubMed=7558004;
 RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RT chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=BNLB/c;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakurai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=20198447; PubMed=10733566;
 RA McKenzie P.R., Connelly M.A., Balzarano D., Mueller J.R.,
 RA Geleziunas R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase kinase-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [8]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
 CC -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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CC      IKAPPAB KINASE SUBFAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U12473; PAC52589.1; --
DR      EMBL; AK018671; BAB31335.1; --
DR      PIR; I49101; I49101.
DR      HSP; Q63450; IAO6.
DR      MGD; MGI:99484; Chuk.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR002290; Ser_Thr_kinase.
DR      InterPro; IPR001245; Tyr_kinase.
DR      Pfam; PF00089; pkinase; 1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;
KW      Phosphorylation; Alternative splicing.
FT      DOMAIN 15 300 PROTEIN_KINASE.
FT      DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT      DOMAIN 738 743 NEMO-BINDING.
FT      NP_BIND 21 29 ATP (BY SIMILARITY).
FT      BINDING 44 44 ATP (BY SIMILARITY).
FT      ACT_SITE 144 144 BY SIMILARITY.
FT      MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)
FT      MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
FT      VARSPLIC 452 471 (BY SIMILARITY).
FT      VARSPLIC 472 745 MSLRYNANLTGMKNLTLS -> IPRKNVKSMEGRNGKGH
FT      VARSPLIC 577 584 /FTID=VSP_004866.
FT      VARSPLIC 585 745 /FTID=VSP_004867.
FT      VARSPLIC 585 745 /FTID=VSP_004868.
FT      VARSPLIC 585 745 /FTID=VSP_004869.
FT      CONFLICT 236 236 K -> E (IN REF. 3).
FT      CONFLICT 400 400 S -> Y (IN REF. 3).
SQ      SEQUENCE 745 AA; 84728 MW; 3FEF5582AFF92233 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWL 6
Db      739 DWSWL 743

RESULT 14
ID      IKKB HUMAN STANDARD; PRT; 756 AA.
AC      O14920; O75327;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE      (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE      2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN      IKKB OR IKKB.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      NCBI_TaxID=9606;

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RN      [1]
RP      SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC      TISSUE=Cervical carcinoma;
RX      MEDLINE=98008813; PubMed=9346484;
RA      Mercuro F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA      Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT      "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT      NF-kappaB activation.";
RL      Science 278:866-866(1997).
RN      [2]
RP      SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX      MEDLINE=98008814; PubMed=9346485;
RA      Woronicz J.D., Gao X., Cao X., Rothe M., Goeddel D.V.;
RT      "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT      IkappaB kinase-alpha and NIK.";
RL      Science 278:866-869(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RX      MEDLINE=99032998; PubMed=9813230;
RA      Hu M.C.-T., Wang Y.-P.;
RT      "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT      embryonic tissues but localized to different human chromosomes.";
RL      Gene 222:31-40(1998).
RN      [4]
RP      SEQUENCE FROM N.A., AND GENE MAPPING.
RX      MEDLINE=98438415; PubMed=9763654;
RA      Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT      "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
RT      9p12-->p11 by in situ hybridization.";
RL      Cytogenet. Cell Genet. 82:32-33(1998).
RN      [5]
RP      SEQUENCE OF 1-256 FROM N.A.
RC      TISSUE=Lung;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Heish F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [6]
RP      IKK PHOSPHORYLATION.
RX      MEDLINE=99038238; PubMed=9819420;
RA      Nemoto S., DiDonato J.A., Lin A.;
RT      "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT      kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL      Mol. Cell. Biol. 18:7336-7343(1998).
RN      [7]
RP      REVIEW.
RX      MEDLINE=20178139; PubMed=10712233;
RA      Jobin C., Sartor R.B.;
RT      "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT      inflammation and protection.";
RL      Am. J. Physiol. 278:C451-C462(2000).
RN      [8]
RP      IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.
RX      MEDLINE=21968797; PubMed=11971985;
RA      Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,

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RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RL activity by I kappa B kinase";
Mol. Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (by similarity).
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
CC and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC -----
CC DR EMBL; AF029684; AAC51860.1; -;
CC DR EMBL; AF080158; AAD08997.1; -;
CC DR EMBL; AF031416; AAC64675.1; -;
CC DR EMBL; BC006231; AAR06231.1; -;
CC DR HSSP; Q63450; 1A06.
CC DR Genew; HGNC:5960; IKKBK.
CC DR MTM; 603258; -.
CC DR GO; GO:0005737; Cytoplasm; NAS.
CC DR GO; GO:0005524; F:ATP binding activity; NAS.
CC DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
CC DR GO; GO:0016563; F:transcriptional activator activity; NAS.
CC DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
CC DR InterPro; IPR000719; Prot kinase.
CC DR InterPro; IPR002290; Ser_Thr_pkinase.
CC DR Pfam; PF00069; pkinase; 1.
CC DR Pfam; PF00240; ubiquitin; 1.
CC DR ProDom; PD000001; Prot kinase; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC KW Phosphorylation.
CC FT DOMAIN 15 300 PROTEIN KINASE.
CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
CC FT DOMAIN 737 742 NEMO-BINDING.
CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
CC FT BINDING 44 44 ATP (BY SIMILARITY).
CC FT ACT_SITE 145 145 BY SIMILARITY.
CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 177 177 PHOSPHORYLATION.
CC FT MOD_RES 181 181 PHOSPHORYLATION.
CC FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
CC EFFECT ON BINDING TO NIK.
CC FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
CC FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
CC FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
CC FT MUTAGEN 181 181 S->E: FULL ACTIVATION.
CC FT CONFLICT 231 255 WSKVKRQKSEVDIVSEEDLVGTVKF -> CVRWMPQTVVHS
CC CNPSTLGGGRWI (IN REF. 5).
CC FT CONFLICT 425 425 Q -> H (IN REF. 1).
CC FT CONFLICT 756 AA; 86563 MW; P9CADF671AE9E14E CRC64;
CC SQ SEQUENCE

Query Match 90.0%; Score 36; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;
QY 2 DMSWL 6
DB 738 DMSWL 742
RESULT 15
IKKB MOUSE
ID IKKB MOUSE STANDARD; PRT; 757 AA.
AC O88351; O9R1J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
GN IKKB OR IKKB (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT "Murine IKB kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of IKB.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=99455228; PubMed=10523828.
RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
RT developmentally regulated protein kinase.";
RL Oncogene 18:5514-5524(1999).
RN [4]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [5]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB

CC and CREBBP (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.

CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout

CC the mouse embryo, at E9.5 day its expression begins to be

CC localized to the brain, neural ganglia, neural tube, and in liver

CC at E12.5 day. At E15.5 day, the expression is further restricted

CC to specific tissues of the embryo.

CC -1- PTM: Phosphorylated by MKK1 and probably also by MAP3K14/NIK.

CC Weakly autophosphorylated.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC IKAPPAB KINASE SUBFAMILY.

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CC or send an email to license@sib-sib.ch).

DR EMBL; AF026524; AAC23557.1; -

DR EMBL; AF088910; AAD52095.1; -

DR HSP; Q63450; IA06.

DR MGD; MGI:1338071; Ikbxb.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_Thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot_kinase; 1.

DR ProSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

DR ProSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR ProSITE; PS00011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;

KW Phosphorylation.

FT	DOMAIN	15	300	PROTEIN KINASE.
FT	DOMAIN	458	479	LEUCINE-ZIPPER (POTENTIAL).
FT	DOMAIN	737	742	NEMO-BINDING
FT	NP_BIND	21	29	ATP (BY SIMILARITY).
FT	BINDING	44	44	ATP (BY SIMILARITY).
FT	ACT_SITE	145	145	BY SIMILARITY.
FT	MOD_RES	23	23	PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	177	177	PHOSPHORYLATION (BY SIMILARITY).
FT	MOD_RES	181	181	PHOSPHORYLATION (BY SIMILARITY).
FT	CONFLICT	56	56	N -> D (IN REF. 2).
FT	CONFLICT	343	343	N -> D (IN REF. 2).
FT	CONFLICT	356	356	K -> E (IN REF. 2).
FT	CONFLICT	390	390	L -> F (IN REF. 2).
FT	CONFLICT	406	406	P -> Q (IN REF. 2).
FT	CONFLICT	573	573	K -> R (IN REF. 2).
FT	CONFLICT	736	757	TLDSWQLQMEDEERCSLEQACD -> VTA (IN REF. 2).

FT SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;

Query Match 90.0%; Score 36; DB 1; Length 757;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6

|||||

Db 738 DWSWL 742

Search completed: February 18, 2004, 14:28:03

Job time : 3.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*
1: piri.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	132	2 S65785	mel-13a protein -
2	37	92.5	132	2 D87226	conserved hypotet
3	36	90.0	122	2 S69909	Ig V-D-J region (M
4	36	90.0	745	1 I49101	conserved helix-lo
5	36	90.0	747	2 D70802	hypothetical prote
6	36	90.0	803	2 F90485	hypothetical prote
7	36	90.0	889	2 E87104	TonB-dependent rec
8	36	90.0	915	2 A43802	cellulase (EC 3.2.
9	36	90.0	1039	2 S02711	cellulase (EC 3.2.
10	36	90.0	1139	2 A10379	probable potassium
11	36	90.0	1275	2 T18556	O-antigen biosynth
12	35	87.5	616	2 C69226	type I restriction
13	35	87.5	1202	2 S71424	nitric-oxide synth
14	35	87.5	1203	1 A47501	nitric-oxide synth
15	35	87.5	1205	1 A38943	nitric-oxide synth
16	35	87.5	1409	2 S74916	alkaline phosphata
17	35	87.5	1879	2 S74915	extracellular nucl
18	34	85.0	214	2 G83692	hypothetical prote
19	34	85.0	220	2 D64316	restriction modifi
20	34	85.0	248	2 T44932	3-oxoacyl-l-acyl-ca
21	34	85.0	276	2 B75337	hypothetical prote
22	34	85.0	282	1 DGEQWA	DNA-3-methyladenin
23	34	85.0	282	2 C90988	3-methyl-adenine D
24	34	85.0	282	2 G85833	3-methyl-adenine D
25	34	85.0	283	2 A86923	probable glycosyl
26	34	85.0	287	2 C90290	hypothetical prote
27	34	85.0	289	2 A10770	DNA-3-methyladenin
28	34	85.0	304	1 B70696	probable rfbE prot
29	34	85.0	368	2 AF1434	AA3-600 quinol oxi

30	34	85.0	368	2 AF1806	AA3-600 quinol oxi
31	34	85.0	410	2 D75475	lycopenase cyclase -
32	34	85.0	529	2 C86958	probable GMP synth
33	34	85.0	549	2 A87347	hypothetical prote
34	34	85.0	578	2 C64452	restriction modifi
35	34	85.0	590	2 S72813	GMP synthase (glut
36	34	85.0	623	2 E75221	type I restriction
37	34	85.0	1144	1 A43271	nitric-oxide synth
38	34	85.0	1147	1 S47647	nitric-oxide synth
39	34	85.0	1147	1 I56575	nitric-oxide synth
40	34	85.0	1147	1 S38253	nitric-oxide synth
41	34	85.0	1147	1 I53165	nitric-oxide synth
42	34	85.0	1147	2 JC5027	nitric-oxide synth
43	34	85.0	1147	2 JC5028	nitric-oxide synth
44	34	85.0	1147	2 JC5029	nitric-oxide synth
45	34	85.0	1147	2 S65440	nitric-oxide synth

ALIGNMENTS

RESULT 1

S65785

mel-13a protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999

C:Accession: S65785

R:Retau, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.

Biochim. Biophys. Acta 1305, 109-112, 1996

A:Title: Cloning and characterization of two transcripts generated from the mel-13 gene

A:Reference number: S65785; MUID:96180310; PMID:8597592

A:Accession: S65785

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <TET>

A:Cross-references: EMBL:U35309

C:Genetics:

A:Gene: mel-13

C:Superfamily: mouse mel-13a protein

C:Keywords: alternative splicing

Query Match 92.5%; Score 37; DB 2; Length 132;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

Db 57 SDMSWL 62

RESULT 2

D87226

conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: D87226

R:Cole, S.T.; Eglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: D87226

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1329 <STO>

A:Cross-references: GB:AL450380; NID:gl3093796; PIDN:CAC32066.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML2535

Query Match 92.5%; Score 37; DB 2; Length 1329;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
:|||||
Db 260 SDMSWL 265

RESULT 3
S69909
IG V-D-J region (MS) - human
C:Species: Homo sapiens (man)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69909
R:Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A:Reference number: S69909; MUID:94335315; PMID:8057663
A:Accession: S69909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SAH>
A:Cross-references: EMBL:Z33399; NID:9871348; PIDN:CAA83850.1; PID:9871349
A:Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 36; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 33 DMSWL 37

RESULT 4
I49101
conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I49101
R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
A:Reference number: I49101; MUID:96044444; PMID:7558004
A:Accession: I49101
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-745 <RES>
A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C:Genetics:

A:Gene: CHUK
C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 739 DMSWL 743

RESULT 5
D70802
hypothetical protein Rv3870 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: D70802
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rogers, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70802
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-747 <COL>
A:Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAA17962.1; PID:g296022
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3870

Query Match 90.0%; Score 36; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 267 DMSWL 271

RESULT 6
F90485
hypothetical protein SSO3039 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: F90485
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: F90485
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-803 <RUB>
A:Cross-references: GB:AE006641; NID:gl3816440; PIDN:AAK43141.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO3039

Query Match 90.0%; Score 36; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
:|||||
Db 540 DMSWL 544

RESULT 7
E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87304
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon-
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87304
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-889 <STO>
A:Cross-references: GB:AE005673; NID:gl3421615; PIDN:AAK22433.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
|||||

Db 618 ADMSW 622

RESULT 8

A43802
cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Caldocellum
N;Alternate names: endo-1,4-beta-glucanase
C;Species: Caldocellum saccharolyticum
C;Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
C;Accession: A43802
R;Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L.
Appl. Environ. Microbiol. 56, 3117-3124, 1990
A;Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile
A;Reference number: A43802; MUID:91136262; PMID:2126700
A;Accession: A43802
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-915 <SAU>
A;Cross-references: EMBL:X13602
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A;Pathway: cellulose degradation
C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;20-320/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 915;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||

Db 469 DMSWL 473

RESULT 9

S02711
cellulase (EC 3.2.1.4) precursor - Caldocellum saccharolyticum
N;Alternate names: endo-1,4-beta-glucanase
N;Contains: cellulase (EC 3.2.1.4); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91)
C;Species: Caldocellum saccharolyticum
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S02711
R;Saul, D.J.; Williams, L.C.; Love, D.R.; Chamley, L.W.; Bergquist, P.L.
Nucleic Acids Res. 17, 439, 1989
A;Title: Nucleotide sequence of a gene from Caldocellum saccharolyticum encoding for ex
A;Reference number: S02711; MUID:89098398; PMID:2789517
A;Accession: S02711
A;Molecule type: DNA
A;Residues: 1-1039 <SAU>
A;Cross-references: EMBL:X13602; NID:g40645; PIDN:CAA13936.1; PID:g40646
C;Genetics:
A;Gene: celB
C;Function:
A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A;Pathway: cellulose degradation
C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1039/Product: cellulase #status predicted <MAT>
F;72-373/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 1039;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||

Db 540 DMSWL 544

RESULT 10

A10379
probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: A10379
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: A10379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1139 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:g15981067; GSPDB:GN00175
C;Genetics:
A;Gene: YPO3129

Query Match 90.0%; Score 36; DB 2; Length 1139;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
|||||

Db 481 DMSWL 485

RESULT 11

T18556
O-antigen biosynthesis protein homolog rfbC - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18556
R;Guo, D.; Bowden, M.G.; Pershad, R.; Kaplan, H.B.
J. Bacteriol. 178, 1631-1639, 1996
A;Title: The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette transport
A;Reference number: Z18970; MUID:96198166; PMID:8626291
A;Accession: T18556
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1275 <GUO>
A;Cross-references: EMBL:U36795; NID:g1235659; PID:g1235662; PIDN:AAB05019.1
C;Genetics:
A;Note: rfbC

Query Match 90.0%; Score 36; DB 2; Length 1275;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWL 6
|||||

Db 348 ADMSWL 353

RESULT 12

C69226
type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicu
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: C69226
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69226
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-616 <MTH>
A:Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85440.1; PID:g262204
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH942
A:Start codon: GTG
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 87.5%; Score 35; DB 2; Length 616;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||:|:
Db 425 ADWAWI 430

RESULT 13
S71424
nitric-oxide synthase (EC 1.14.13.39), endothelial - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 04-Mar-2000
C:Accession: S71424
R:Gnanapandithen, K.; Chen, Z.; Kau, C.L.; Gorczynski, R.M.; Marsden, P.A.
Biochim. Biophys. Acta 1308, 103-106, 1996
A:Title: Cloning and characterization of murine endothelial constitutive nitric oxide synthase
A:Reference number: S71424; MUID:96350460; PMID:8764825
A:Accession: S71424
A:Molecule type: mRNA
A:Residues: 1-1202 <GNA>
A:Cross-references: EMBL:U53142; NID:gl518955; PIDN:AAC52766.1; PID:gl518956
A:Experimental source: fetal cardiac
C:Genetics:
A:Gene: NOS

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase
C:Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN
F:490-509/Region: calmodulin binding #status predicted
F:519-1158/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:521-702/Domain: flavodoxin homology <FLX>
F:647-679/Region: FMN binding #status predicted
F:790-803/Region: FAD-pyrophosphate binding #status predicted
F:934-945/Region: FAD-isoxaloxazine binding #status predicted
F:1009-1027/Region: NADP-ribose binding #status predicted
F:1107-1123/Region: NADP-adenine binding #status predicted
F:127/Modified site: myristylated amino end (Gly) #status predicted
F:2/Modified site: aspartic acid (Asn) #status predicted
F:183/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 2; Length 1202;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||:|:
Db 442 ADWAWI 447

RESULT 14
A47501
nitric-oxide synthase (EC 1.14.13.39), endothelial - human
C:Species: Homo sapiens (man)
C>Date: 02-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 03-Mar-2000
C:Accession: A47501; S24052; A38948; A49813; A42867; S45691; I37361
R:Marsden, P.A.; Heng, H.H.Q.; Scherer, S.W.; Stewart, R.J.; Hall, A.V.; Shi, X.M.; Tsui, J. Biol. Chem. 268, 17478-17488, 1993
A:Title: Structure and chromosomal localization of the human constitutive endothelial nitric oxide synthase
A:Reference number: A47501; MUID:93352539; PMID:7688726
A:Accession: A47501
A:Molecule type: DNA
A:Residues: 1-1203 <MAR1>
A:Cross-references: GB:L10709; NID:g348235; PIDN:AAA36365.1; PID:g348237; GB:L10693; NID:0698; NID:g348224; GB:L10699; NID:g348225; GB:L10700; NID:g348226; GB:L10701; NID:g34822

ID:g348232; GB:L10707; NID:g348233; GB:L10708; NID:g348234
R:Marsden, P.A.; Schapert, K.T.; Chen, H.S.; Flowers, M.; Sundell, C.L.; Wilcox, J.N.; FEBS Lett. 307, 287-293, 1992
A:Title: Molecular cloning and characterization of human endothelial nitric oxide synthase
A:Reference number: S24052; MUID:92354731; PMID:1379542
A:Accession: S24052
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <MAR2>
A:Cross-references: GB:M95296; NID:gl89259; PIDN:AAA36372.1; PID:gl89260
R:Janssens, S.P.; Shimouchi, A.; Quettermous, T.; Bloch, D.B.; Bloch, K.D. submitted to GenBank, September 1992
A:Reference number: A38948
A:Accession: A38948
A:Molecule type: mRNA
A:Residues: 1-1203 <JAN1>
A:Cross-references: GB:M93718; NID:gl89211; PIDN:AAA36364.1; PID:gl89212
A:Note: the sequence in GenBank entry HUMNIOXSYN, release 111.0, has been corrected to R:Janssens, S.P.; Shimouchi, A.; Quettermous, T.; Bloch, D.B.; Bloch, K.D. J. Biol. Chem. 267, 22694b, 1992
A:Reference number: A49813; MUID:93054573; PMID:1385404
A:Contents: erratum
A:Accession: A49813
A:Molecule type: mRNA
A:Residues: 1191-1203 <JAN2>
A:Cross-references: PIDN:AAB23920.1; PID:g258793
A:Note: sequence extracted from NCBI backbone (NCBIP:117314)
R:Janssens, S.P.; Shimouchi, A.; Quettermous, T.; Bloch, D.B.; Bloch, K.D. J. Biol. Chem. 267, 14519-14522, 1992
A:Title: Cloning and expression of a cDNA encoding human endothelium-derived relaxing factor
A:Reference number: A42867; MUID:92340475; PMID:1378832
A:Accession: A42867
A:Molecule type: mRNA
A:Residues: 1-82, 'S', 84-179, 'F', 181-566, 'W', 568-647, 'Q', 649-854, 'V', 856-1008, 'G', 1010-1133, 'PQ', 'QRPYRACHPLPSV' <JAN3>
A:Cross-references: GB:M93718; NID:gl89211
A:Note: this sequence has been revised in reference A49813
R:Garvey, E.P.; Turtle, J.V.; Covington, K.; Merrill, B.M.; Wood, E.R.; Baylis, S.A.; Ch. Arch. Biochem. Biophys. 311, 235-241, 1994
A:Title: Purification and characterization of the constitutive nitric oxide synthase from human endothelial nitric oxide synthase
A:Reference number: S45691; MUID:94263196; PMID:7515611
A:Accession: S45691
A:Molecule type: protein
A:Residues: 'XX', 169-175, 531-536, 'X', 538-540, 835, 'X', 837-843, 'X', 845, 876-877, 'X', 879-881
A:Experimental source: Placenta
R:Nadaud, S.; Bonnardaux, A.; Lathrop, M.; Soubrier, P. Biochem. Biophys. Res. Commun. 198, 1027-1033, 1994
A:Title: Gene structure, polymorphism and mapping of the human endothelial nitric oxide synthase
A:Reference number: I37361; MUID:94161710; PMID:7509596
A:Accession: I37361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-297, 'D', 299-566, 'W', 568-1193, 'E', 1195-1203 <NAD>
A:Cross-references: EMBL:X76303; NID:g461307; PIDN:CAA53950.1; PID:g825652
C:Genetics:
A:Gene: GDB:NOS3
A:Cross-references: GDB:209976; OMIM:163729
A:Map position: 7q36-7q36
A:Introns: 53/2; 90/3; 140/2; 194/3; 225/2; 272/3; 319/2; 377/3; 411/3; 476/3; 501/2; 54/2
C:Function:
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reductase
C:Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN
F:491-509/Region: calmodulin binding #status predicted
F:520-1159/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:522-703/Domain: flavodoxin homology <FLX>
F:648-680/Region: FMN binding #status predicted
F:791-804/Region: FAD-pyrophosphate binding #status predicted
F:935-946/Region: FAD-isoxaloxazine binding #status predicted
F:1010-1028/Region: NADP-ribose binding #status predicted
F:1108-1124/Region: NADP-adenine binding #status predicted
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted

F;184/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1203;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||:
Db 443 ADWAWI 448

RESULT 15

A38943
N;nitric-oxide synthase (EC 1.14.13.39), endothelial - bovine
N;Alternate names: ECNOS; nitric-oxide synthase type III
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Jun-1995 #sequence revision 02-Jun-1995 #text change 03-Mar-2000
C;Accession: A38943; A46033; I45945; A42841; I45946; A38944
R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
submitted to GenBank, July 1992
A;Reference number: A38943
A;Accession: A38943
A;Molecule type: mRNA
A;Residues: 1-1205 <LAMI>
A;Cross-references: GB:M89952; NID:G162976; PIDN:AAA30494.1; PID:G162977
A;Experimental source: aortic endothelial cells
R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 6348-6352, 1992
A;Title: Endothelial nitric oxide synthase: molecular cloning and characterization of a
A;Reference number: A46033; MUID:92335295; PMID:1378626
A;Accession: A46033
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-860, 'I', 862-1205 <LAM2>
A;Cross-references: GB:M89952; NID:G162976
A;Experimental source: endothelial
A;Note: sequence extracted from NCBI backbone (NCBIP:108720)
R;Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; Al
J. Clin. Invest. 90, 2092-2096, 1992
A;Title: Molecular Cloning and Characterization of the constitutive bovine aortic Endoth
A;Reference number: I45945; MUID:93055452; PMID:1385480
A;Accession: I45945
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1205 <NIS>
A;Cross-references: GB:M99057; NID:G163421; PIDN:AAA30667.1; PID:G163422
R;Sessa, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly
J. Biol. Chem. 267, 15274-15276, 1992
A;Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxid
A;Reference number: A42841; MUID:92348367; PMID:1379225
A;Accession: A42841
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-51, 'N', 53-99, 'R', 101-147, 'M', 149-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-3
'K', 517-692, 'G', 694-740, 'A', 742-753, 'N', 755-799, 'N', 801-803, 'SA', 806-856, 'V', 858-906, 'LV
A;Experimental source: aortic endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typog
A;Accession: I45946
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99, 'R', 101-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-454, 'Y', 456-458, 'P', 460
A;Cross-references: GB:M95674; NID:G163426; PIDN:AAA30669.1; PID:G163427
A;Experimental source: aortic endothelial cells
A;Note: submitted to GenBank, August 1992
A;Note: GenBank entry BOVNOS, release 103.0, has a typographical error in the reference
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN
F;493-512/Region: calmodulin binding #status predicted
F;522-1161/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;524-705/Domain: flavodoxin homology <FLX>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F;3/Modified site: aspartic acid (Asn) #status predicted
F;186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1205;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||:
Db 445 ADWAWI 450

Search completed: February 18, 2004, 14:38:36
Job time : 7.5921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10	US-09-847-940B-4
2	40	100.0	6	11	US-09-847-946A-4
3	40	100.0	6	11	US-09-847-946A-39
4	40	100.0	6	11	US-09-847-946A-51
5	40	100.0	7	11	US-09-847-946A-55
6	40	100.0	8	11	US-09-847-946A-48
7	40	100.0	8	11	US-09-847-946A-56
8	40	100.0	9	11	US-09-847-946A-47
9	40	100.0	9	11	US-09-847-946A-50
10	40	100.0	9	11	US-09-847-946A-53
11	40	100.0	9	11	US-09-847-946A-54
12	40	100.0	10	11	US-09-847-946A-49
13	40	100.0	10	11	US-09-847-946A-52
14	40	100.0	11	11	US-09-847-946A-46
15	40	100.0	501	15	US-10-171-311-234

16	38	95.0	312	12	US-10-306-762-23	Sequence 23, Appl
17	38	95.0	605	15	US-10-156-761-9070	Sequence 9070, Ap
18	36	90.0	6	10	US-09-847-940B-2	Sequence 2, Appl
19	36	90.0	6	11	US-09-847-946A-2	Sequence 2, Appl
20	36	90.0	6	11	US-09-847-946A-33	Sequence 33, Appl
21	36	90.0	6	11	US-09-847-946A-41	Sequence 41, Appl
22	36	90.0	6	11	US-09-847-946A-73	Sequence 73, Appl
23	36	90.0	7	11	US-09-847-946A-37	Sequence 37, Appl
24	36	90.0	7	11	US-09-847-946A-77	Sequence 77, Appl
25	36	90.0	8	11	US-09-847-946A-30	Sequence 30, Appl
26	36	90.0	8	11	US-09-847-946A-38	Sequence 38, Appl
27	36	90.0	8	11	US-09-847-946A-70	Sequence 70, Appl
28	36	90.0	8	11	US-09-847-946A-78	Sequence 78, Appl
29	36	90.0	9	11	US-09-847-946A-29	Sequence 29, Appl
30	36	90.0	9	11	US-09-847-946A-32	Sequence 32, Appl
31	36	90.0	9	11	US-09-847-946A-35	Sequence 35, Appl
32	36	90.0	9	11	US-09-847-946A-36	Sequence 36, Appl
33	36	90.0	9	11	US-09-847-946A-59	Sequence 59, Appl
34	36	90.0	9	11	US-09-847-946A-72	Sequence 72, Appl
35	36	90.0	9	11	US-09-847-946A-75	Sequence 75, Appl
36	36	90.0	9	11	US-09-847-946A-76	Sequence 76, Appl
37	36	90.0	10	11	US-09-847-946A-31	Sequence 31, Appl
38	36	90.0	10	11	US-09-847-946A-34	Sequence 34, Appl
39	36	90.0	10	11	US-09-847-946A-71	Sequence 71, Appl
40	36	90.0	10	11	US-09-847-946A-74	Sequence 74, Appl
41	36	90.0	11	11	US-09-847-946A-28	Sequence 28, Appl
42	36	90.0	11	11	US-09-847-946A-58	Sequence 58, Appl
43	36	90.0	11	11	US-09-847-946A-132	Sequence 132, App
44	36	90.0	11	11	US-09-847-946A-140	Sequence 140, App
45	36	90.0	13	11	US-09-847-946A-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6
| | | | |
Db 1 ADMSWL 6

RESULT 2
US-09-847-946A-4
; Sequence 4, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

```
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4
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Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ADWSWL 6
Db 1 ADWSWL 6
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RESULT 3
US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-39
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Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ADWSWL 6
Db 1 ADWSWL 6
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```
RESULT 4
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-51
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Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ADWSWL 6
Db 1 ADWSWL 6
```

```
RESULT 5
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-55
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Query Match 100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 ADWSWL 6
Db 1 ADWSWL 6
```

```
RESULT 6
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US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 3 ADWSWL 8

RESULT 7
US-09-847-946A-56
; Sequence 56, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-56

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 1 ADWSWL 6

RESULT 8
US-09-847-946A-47
; Sequence 47, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
Db 1 ADWSWL 6

RESULT 9
US-09-847-946A-50
; Sequence 50, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||
Db 1 ADWSWL 6

RESULT 10

US-09-847-946A-53
; Sequence 53, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-53

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||
Db 3 ADWSWL 8

RESULT 11

US-09-847-946A-54
; Sequence 54, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-54

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||
Db 2 ADWSWL 7

RESULT 12

US-09-847-946A-49
; Sequence 49, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-49

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
|||||
Db 2 ADWSWL 7

RESULT 13

US-09-847-946A-52
; Sequence 52, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-52

US-09-847-946A-52

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
| | | | |
DB 3 ADWSWL 8

RESULT 14

US-09-847-946A-46
; Sequence 46, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-46

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
| | | | |
DB 3 ADWSWL 8

RESULT 15

US-10-171-311-234
; Sequence 234, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936

; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 234
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-234

Query Match 100.0%; Score 40; DB 15; Length 501;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWL 6
| | | | |
DB 387 ADWSWL 392

Search completed: February 18, 2004, 15:41:55
Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-4
Perfect score: 40
Sequence: 1 ADMSW 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	142	4	US-09-252-991A-31533
2	36	90.0	174	4	US-09-325-932A-163
3	36	90.0	225	4	US-09-325-932A-162
4	36	90.0	378	4	US-09-325-932A-158
5	36	90.0	616	3	US-09-136-574A-47
6	36	90.0	745	2	US-08-887-518-3
7	36	90.0	745	2	US-09-023-321-3
8	36	90.0	745	2	US-08-890-853-4
9	36	90.0	745	2	US-09-032-475-3
10	36	90.0	745	2	US-09-099-125A-4
11	36	90.0	745	2	US-09-099-124A-4
12	36	90.0	745	3	US-09-032-476-4
13	36	90.0	745	3	US-08-890-854-4
14	36	90.0	745	3	US-09-023-324-4
15	36	90.0	745	3	US-09-168-629-2
16	36	90.0	745	3	US-08-910-820-10
17	36	90.0	745	3	US-08-810-131A-2
18	36	90.0	745	4	US-09-109-986-4
19	36	90.0	745	4	US-09-844-908-10
20	36	90.0	745	4	US-09-868-758-3
21	36	90.0	756	2	US-08-887-518-4
22	36	90.0	756	2	US-09-023-321-4
23	36	90.0	756	2	US-08-890-853-2
24	36	90.0	756	2	US-09-032-475-4
25	36	90.0	756	2	US-09-099-125A-2
26	36	90.0	756	2	US-09-099-124A-2
27	36	90.0	756	3	US-09-032-476-2

28	36	90.0	756	3	US-08-890-854-2	Sequence 2, Appli
29	36	90.0	756	3	US-09-023-324-2	Sequence 2, Appli
30	36	90.0	756	3	US-09-168-629-15	Sequence 15, Appli
31	36	90.0	756	3	US-08-910-820-9	Sequence 9, Appli
32	36	90.0	756	4	US-09-109-986-2	Sequence 2, Appli
33	36	90.0	756	4	US-09-844-908-9	Sequence 9, Appli
34	36	90.0	756	4	US-09-868-758-4	Sequence 4, Appli
35	36	90.0	996	4	US-09-417-197-123	Sequence 123, App
36	36	90.0	997	4	US-09-417-197-121	Sequence 121, App
37	36	90.0	1426	3	US-09-136-574A-43	Sequence 43, Appli
38	36	90.0	1751	3	US-09-136-574A-44	Sequence 44, Appli
39	35	87.5	1205	1	US-07-908-245-2	Sequence 2, Appli
40	35	87.5	1205	2	US-08-319-866-10	Sequence 10, Appli
41	35	87.5	1205	3	US-09-123-708-6	Sequence 6, Appli
42	35	87.5	1205	3	US-09-123-624-6	Sequence 6, Appli
43	34	85.0	170	4	US-09-199-637A-339	Sequence 339, App
44	34	85.0	518	4	US-09-065-383-27	Sequence 27, Appli
45	34	85.0	537	4	US-09-655-270A-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match 90.0%; Score 36; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 94 ADMSW 98

RESULT 2
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant level
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

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Query Match          90.0%; Score 36; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 109 ADMSW 113

RESULT 3
US-09-325-932A-162
; Sequence 162, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-162

Query Match          90.0%; Score 36; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 100 ADMSW 104

RESULT 4
US-09-325-932A-158
; Sequence 158, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-158

Query Match          90.0%; Score 36; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 128 ADMSW 132

RESULT 5
US-09-136-574A-47
; Sequence 47, Application US/09136574A
; Patent No. 6294366
; GENERAL INFORMATION:

```

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; APPLICANT: Farrington, Graham K.
; Anderson, Paige
; Gibbs, Moreland
; Bergquist, Peter
; Daniels, Roy
; Morgan, Hugh W.
; Williams, Diane P.
; TITLE OF INVENTION: Compositions and Methods for
; Treating Cellulose Containing Fabrics Using Truncated
; Cellulase Enzyme Compositions
;
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,574A
; FILING DATE: 19-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/932,571
; FILING DATE: September 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: 1997US001/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 616 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-136-574A-47

Query Match          90.0%; Score 36; DB 3; Length 616;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 123 DWSWL 127

RESULT 6
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/887,518
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

RESULT 7
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-023-321-3
Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DMSWL 6
Db 739 DMSWL 743
RESULT 8
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
Db 739 DMSWL 743

RESULT 9
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 739 DWSWL 743

RESULT 10
US-09-099-125A-4
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 739 DWSWL 743

RESULT 11
US-09-099-124A-4
Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
Db 739 DWSWL 743

Db 739 DMSWL 743

RESULT 12

US-09-032-476-4

Sequence 4, Application US/09032476

Patent No. 6235492

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaodan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032,476

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-032-476-4

Query Match 90.0%; Score 36; DB 3; Length 745;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6

Db 739 DMSWL 743

RESULT 13

US-08-890-854-4

Sequence 4, Application US/08890854

Patent No. 6235512

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaodan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,324

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-032-476-4

Query Match 90.0%; Score 36; DB 3; Length 745;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6

Db 739 DMSWL 743

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/890,854

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-890-854-4

Query Match 90.0%; Score 36; DB 3; Length 745;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6

Db 739 DMSWL 743

RESULT 14

US-09-023-324-4

Sequence 4, Application US/09023324

Patent No. 6235513

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaodan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,324

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
|
|
|
|
Db 739 DWSWL 743

RESULT 15
US-09-168-629-2
; Sequence 2, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: DiDonato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2

Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWL 6
|
|
|
|
Db 739 DWSWL 743

Search completed: February 18, 2004, 14:41:46
Job time : 8.06579 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	214	1	RADC RHOCA
2	25	100.0	259	1	ECX2_ARCFU
3	26	100.0	550	1	SYR MYCTU
4	26	100.0	638	1	SCAD HUMAN
5	26	100.0	638	1	SCAD PANTR
6	26	100.0	745	1	METE CORGL
7	26	100.0	855	1	GAFI SCHPO
8	26	100.0	858	1	SYL VIBCH
9	26	100.0	1006	1	MT10 SCHPO
10	26	100.0	1313	1	ACE RAT
11	24	92.3	197	1	YE7A METJA
12	24	92.3	298	1	CDK2_HUMAN
13	24	92.3	298	1	CDK2 RAT
14	24	92.3	346	1	CDK2 MOUSE
15	24	92.3	358	1	ALF ECOLI
16	24	92.3	385	1	ALR_ANASP
17	24	92.3	393	1	DCAM_HORCH
18	24	92.3	404	1	DDO2_ECOLI
19	24	92.3	446	1	DTA2_RALSO
20	24	92.3	506	1	HUTH SALT
21	24	92.3	506	1	HUTH SALT
22	24	92.3	518	1	FLAA_AQUAE
23	24	92.3	933	1	SLAP_CANFE
24	24	92.3	964	1	MSH2_YEAST
25	24	92.3	970	1	SECA_CHLPN
26	24	92.3	3255	1	POLG LMV0
27	24	92.3	3255	1	POLG LMVE
28	24	92.3	145	1	MA29_DERFA
29	23	88.5	161	1	PHAB_SYNTP6
30	23	88.5	193	1	ACDI_XANAC
31	23	88.5	201	1	CTFI_HUMAN
32	23	88.5	242	1	6PGL_PSEFU
33	23	88.5	247	1	6PGL_MYCTU

34	23	88.5	249	1	CYSH_SINY3	P72794 synechocyt
35	23	88.5	249	1	STXA_HUMAN	O60499 homo sapien
36	23	88.5	295	1	KPRS_METWA	Q8pux3 mechanosarc
37	23	88.5	351	1	PTA_RICPR	Q9ze39 rickettsia
38	23	88.5	355	1	LEU3_SPIPL	Q00412 spirulina p
39	23	88.5	366	1	REQ2_XENLA	Q9w636 xenopus lae
40	23	88.5	372	1	MTOX_SALTY	P58524 salmonella
41	23	88.5	372	1	MTOX_SALTY	P58525 salmonella
42	23	88.5	380	1	SCHA_STRHA	Q05361 streptomyce
43	23	88.5	388	1	REO1_XENLA	Q9w638 xenopus lae
44	23	88.5	400	1	DCAM_MAIZE	O24575 zea mays (m
45	23	88.5	411	1	BHB2_MOUSE	O35185 mus musculu

ALIGNMENTS

RESULT 1
RADC RHOCA
ID RADC RHOCA STANDARD; PRT; 214 AA.
AC P72255;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA repair protein radc homolog.
GN RADC.
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OC NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RX MEDLINE=20118379; PubMed=10652786;
RA Katsiou E., Nickel C.M., Garcia A.F., Tadros M.H.;
RT "Molecular analysis and identification of the radC gene from the
phototrophic bacterium Rhodobacter capsulatus B10.";
RL Microbiol. Res. 154:233-239(1999).
CC -!- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
CC -!- INDUCTION: Induced about five-fold after UV-irradiation.
CC -!- SIMILARITY: Belongs to the radC family.

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EMBL; U74017; AAB18255.1; -.
HAMAP; MF_00018; -; 1.
InterPro; IPR001405; RadC.
Pfam; PF04002; RadC; 1.
ProDom; PD007415; RadC; 1.
TIGRFAMs; TIGR00608; radc; 1.
PROSITE; PS01302; RadC; 1.
KW DNA repair.
SQ SEQUENCE 214 AA; 23792 MW; D008997B20C6743D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
|||
Db 154 LDASAL 159

RESULT 2
ECX2_ARCFU STANDARD; PRT; 259 AA.
ID ECX2_ARCFU
AC O29756;

DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable exosome complex exonuclease 2 (EC 3.1.13.-).
 AF0494.
 GN Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Hickey E.K., Peterson J.D.,
 RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Kyrpides N.C.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.J., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -1- FUNCTION: Probably involved in the 3'->5' degradation of a variety
 CC of RNA species (Potential).
 CC -1- SUBUNIT: Component of the archaeal exosome multienzyme
 CC ribonuclease complex (Potential).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE RNASE PH FAMILY.
 CC
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 CC
 CC EMBL; AE001070; AAB90743.1; -.
 CC PIR; F69311; F69311.
 CC TIGR; AF0494; -.
 CC HAMAP; MF_00622; -; 1.
 CC InterPro; IPR001247; 3 Exonuclease.
 CC Pfam; PF01138; RNase PH; 1.
 CC Pfam; PF03725; RNase PH; 1.
 CC Exosome; Hydrolase; Nuclease; Exonuclease; Complete proteome.
 KW SEQUENCE 259 AA; 28646 MW; E8289D46F9DDCB3 CRC64;
 SQ
 Query Match 100.0%; Score 26; DB 1; Length 259;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 DB 149 LDASAL 154
 RESULT 3
 SYR_MYCTU STANDARD; PRT; 550 AA.
 ID SYR_MYCTU
 AC Q10609;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
 GN ARGRS OR RV1292 OR MT1331 OR MTCY373.12.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
 CC diphosphate + L-arginyl-tRNA(Arg).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 CC
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 CC
 CC EMBL; Z73419; CAA97757.1; -.
 CC EMBL; AE007007; AAK45593.1; -.
 CC PIR; H70772; H70772.
 CC TIGR; MT1331; -.
 CC TubercuList; RV1292; -.
 CC HAMAP; MF_00123; -; 1.
 CC InterPro; IPR001278; Arg_tRNA-synt_1c.
 CC InterPro; IPR005148; N-
 CC InterPro; IPR001412; tRNA-synt_1.
 CC Pfam; PF03485; N-Arg; 1.
 CC Pfam; PF00750; tRNA-synt_1d; 1.
 CC PRINTS; PR01038; TRNASYNTHARG.
 CC TIGRFAMs; TIGR00456; argS; 1.
 CC PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 130 140 "HIGH" REGION.
 SQ SEQUENCE 550 AA; 59709 MW; 4F11239A6238124D CRC64;
 Query Match 100.0%; Score 26; DB 1; Length 550;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 DB 23 LDASAL 28
 RESULT 4
 SCAD_HUMAN
 ID SCAD_HUMAN STANDARD; PRT; 638 AA.
 AC P51172;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Amiloride-sensitive sodium channel delta-subunit (Epithelial Na+
 DE channel delta subunit) (Delta ENaC) (Nonvoltage-gated sodium channel
 DE 1 delta subunit) (SCNED) (Delta NaCh)
 GN SCNN1D OR DNACH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96070858; PubMed=7499195;
 RA Waldmann R., Champigny G., Bassilana F., Voilley N., Lazdunski M.;
 RT "Molecular cloning and functional expression of a novel amiloride-
 sensitive Na+ channel.";
 RL J. Biol. Chem. 270:127411-27414 (1995).
 CC -!- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
 CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
 CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
 CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
 CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
 CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
 CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
 CC FAMILY.
 CC
 CC -----
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 CC -----
 CC EMBL; U38254; AAC50283.1; -;
 DR PIR; I39196; I39196.
 DR Genew; HGNC:10601; SCNN1D.
 DR MIM; 601328; -;
 DR GO; GO:0015280; F:amiloride-sensitive sodium channel activity; TAS.
 DR GO; GO:0006814; P:sodium ion transport; TAS.
 DR InterPro; IPR004724; EnaC.
 DR InterPro; IPR001873; Na+channel_ASC.
 DR Pfam; PF00858; ASC; 1.
 DR TIGRFAMs; TIGR00859; ENaC; 1.
 DR PROSITE; PS01206; ASC; 1.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 FT DOMAIN 1 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT DOMAIN 108 530 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 531 551 POTENTIAL.
 FT DOMAIN 552 638 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 638 AA; 70274 MW; 7CD5181F8497F5CF CRC64;
 Query Match 100.0%; Score 26; DB 1; Length 638;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 DB 551 LDASAL 556
 RESULT 5
 SCAD_PANTR STANDARD; PRT; 638 AA.
 ID SCAD_PANTR
 AC O46547;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Amiloride-sensitive sodium channel delta-subunit (Epithelial Na+
 DE channel delta subunit) (Delta ENaC) (Nonvoltage-gated sodium channel
 DE 1 delta subunit) (SCNED) (Delta NaCh)
 GN SCNN1D OR DNACH.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Testis;
 RA Al-Khalili O.K., Eaton D.C.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL
 CC INHIBITED BY THE DIURETIC AMILORIDE. MEDIATE THE ELECTRODIFFUSION
 CC OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
 CC THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
 CC REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
 CC ALSO PLAYS A ROLE IN TASTE PERCEPTION (By similarity).
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
 CC SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
 CC FAMILY.
 CC
 CC -----
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 CC -----
 CC EMBL; AF038165; AAB92659.1; -;
 DR InterPro; IPR004724; EnaC.
 DR InterPro; IPR001873; Na+channel_ASC.
 DR Pfam; PF00858; ASC; 1.
 DR PRINTS; PR01078; AMINACHANNEL.
 DR TIGRFAMs; TIGR00859; ENaC; 1.
 DR PROSITE; PS01206; ASC; 1.
 KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 FT DOMAIN 1 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT DOMAIN 108 530 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 531 551 POTENTIAL.
 FT DOMAIN 552 638 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 638 AA; 70187 MW; 321E9597D6A78D38 CRC64;
 Query Match 100.0%; Score 26; DB 1; Length 638;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 DB 551 LDASAL 556
 RESULT 6
 METE CORGL STANDARD; PRT; 745 AA.
 ID METE CORGL
 AC Q8NEB3;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 5-methyltetrahydroxytryptophan--homocysteine methyltransferase
 DE (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)

(Cobalamin-independent methionine synthase).
 DE METE OR CG1139.
 GN Corynebacterium glutamicum (Brevibacterium flavum).
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Catalyzes the transfer of a methyl group from 5-methyltetrahydrofolate to homocysteine resulting in methionine formation (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
 CC -!- COFACTOR: Zinc; binds one ion per subunit (By similarity).
 CC -!- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
 CC -!- SIMILARITY: Belongs to the vitamin-B12 independent methionine synthase family.
 CC -----
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 CC -----
 DR EMBL; AF005277; BAB98532.1; -;
 DR HAMAP; MF_00172; -; 1;
 DR InterPro; IPR002629; Methionine_synth.
 DR InterPro; IPR006276; Met_synth_B12ind.
 DR Pfam; PF01717; Methionine_synth; 1.
 DR ProDom; PD004692; Methionine_synth; 2.
 DR TIGRFAMs; TIGR01371; met_synth_B12ind; 1.
 DR Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
 KW Complete proteome.
 FT METAL 628 628 ZINC (BY SIMILARITY).
 FT METAL 630 630 ZINC (BY SIMILARITY).
 FT METAL 713 713 ZINC (BY SIMILARITY).
 SQ SEQUENCE 745 AA; 81312 MW; 856E05DE7398ED1F CRC64;
 Query Match 100.0%; Score 26; DB 1; Length 745;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 Db 140 LDASAL 145
 RESULT 7
 ID GAF1 SCHPO STANDARD; PRT; 855 AA.
 AC Q10280; O94482; Q9USK9;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription factor gaf1 (Gaf-1).
 OS GAF1 OR SPC11902.01 OR SPC1417.01C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jørgensen K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymouprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.K., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RN Nature 415:871-880(2002).
 CC [2]
 CC SEQUENCE OF 566-855 FROM N.A.
 CC MEDLINE=9382525; PubMed=9714831;
 CC Hoe K.-L., Won M.S., Chung K.-S., Park S.-K., Kim D.-U., Jang Y.-J., Yoo O.-J., Yoo H.-S.;
 CC "Molecular cloning of gaf1, a Schizosaccharomyces pombe GATA factor, which can function as a transcriptional activator.";
 CC Gene 215:319-328(1998)
 CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: Contains 1 GATA-type zinc finger.
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 CC -----
 DR EMBL; AL035076; CA22647.1; -;
 DR EMBL; AL049521; CAB40003.1; -;
 DR EMBL; L31601; AAC35593.1; -;
 DR PIR; T41336; T41336.
 DR HSP; P17429; 4GAT.
 DR TRANSFAC; T02831; -;
 DR GeneDB_Spombe; SPC11902.01; -;
 DR InterPro; IPR000679; Znf_GATA.
 DR Pfam; PF00320; GATA; 1.
 DR PRINTS; PR00619; GATAZNFINGER.
 DR SMART; SM00401; Znf_GATA; 1.
 DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
 DR PROSITE; PS01114; GATA_ZN_FINGER_2; 1.
 KW Transcription regulation; Activator; DNA-binding; Zinc-finger; Nuclear protein.
 FT ZN FING 635
 SQ SEQUENCE 855 AA; 91776 MW; 3D932F83D2DB6774 CRC64;
 Query Match 100.0%; Score 26; DB 1; Length 855;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDASAL 6
 Db 211 LDASAL 216
 RESULT 8
 SYL_VIBCH

ID SYL VIBCH STANDARD; PRT; 858 AA.
AC Q9KTE6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
GS LEUS OR VC0956.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Emdonlaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nieman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae";
RL Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
diphosphate + L-leucyl-tRNA(Leu).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL: AE004177; AAF94118.1; ALT_INIT.
CC TIGR: VC0956; -.
CC HAMAP: MF_00049; -.
CC InterPro: IPR002302; Leu-tRNA-synt1a.
CC InterPro: IPR002300; tRNA-synt_1a.
CC InterPro: IPR001412; tRNA-synt_1.
CC Pfam: PF00133; tRNA-synt_1; 1.
CC PRINTS: PR00985; TRNASYNTHILEU.
CC TIGRfams: TIGR00396; leuS_bact; 1.
CC PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 42 52 "HIGH" REGION.
FT SITE 618 622 "KMSKS" REGION.
FT BINDING 621 621 ATP (BY SIMILARITY).
SQ SEQUENCE 858 AA; 96621 MW; A4D59A2E1C9F1292 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 858;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDASAL 6
Db 688 LDASAL 693
RESULT 9
MT10 SCHPO STANDARD; PRT; 1006 AA.
ID MT10 SCHPO
AC Q09878;
DT 01-FEB-1996 (Rel. 33, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable sulfite reductase [NADPH] flavoprotein component
(BC 1.8.1.2).

GN SPC584.01C.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walen S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF
SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED
FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE (BY SIMILARITY).
CC
CC -1- CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O = sulfite + 3
NADPH.
CC
CC -1- COFACTOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
ONE FAD PER CHAIN (BY SIMILARITY).
CC
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CC
CC EMBL: AL032824; CAA21818.2; -.
CC FIR: T41439; T41439.
CC HSSP: P00388; 1AMO.
CC GeneDB SPombe: SPC584.01c; -.
CC InterPro: IPR003097; FAD_binding.
CC InterPro: IPR001709; FPN_Cyt_redctse.
CC InterPro: IPR001433; Oxred_FAD/NAD(P).
CC Pfam: PF00667; FAD_binding_1; 1.
CC Pfam: PF00175; NAD_binding_1; 1.
CC PRINTS: PR00371; FPNCR.
CC Oxidoreductase; Flavoprotein; NADP; FAD; FMN; Electron transport;
KW Cysteine biosynthesis.
FT NP BIND 658 669 FAD (ADP PART) (BY SIMILARITY).
FT NP BIND 788 798 FAD (FLAVIN PART) (BY SIMILARITY).
SQ SEQUENCE 1006 AA; 111352 MW; 2EA2086D69561D33 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 1006;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDASAL 6

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CC -----
 DR EMBL; U67588; AAB99480.1; -
 DR PIR; A64484; A64484.
 DR TIGR; MJ1474; -

DR HAMAP; MF 00265; -; 1.
 DR InterPro; IPR002851; DUF133.
 DR InterPro; IPR002716; PIN.
 DR InterPro; IPR006596; PINC.
 DR Pfam; PF01850; PIN; 1.
 DR ProDom; PD013236; DUF133; 1.
 DR SMART; SM00670; PINC; 1.

KW Hypothetical protein; Complete proteome.
 FT DOMAIN 181 197
 FT LYS-RICH.

SQ SEQUENCE 197 AA; 22781 MW; 70075BBG26934F58 CRC64;
 Query Match 92.3%; Score 24; DB 1; Length 197;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 DB 36 LDASAI 41

RESULT 12
 CDK2_HUMAN
 ID CDK2_HUMAN STANDARD; PRT; 298 AA.
 AC P24941;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cell division protein kinase 2 (EC 2.7.1.-) (p33 protein kinase).
 GN CDK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91330891; PubMed=1714386;
 RA Elledge S.J., Spottswood M.R.;
 RT "A new human p34 protein kinase, CDK2, identified by complementation
 RT of a cdc28 mutation in *Saccharomyces cerevisiae*, is a homolog of
 RT *Xenopus* Egl.";
 RL EMBO J. 10:2653-2659(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91367262; PubMed=1653904;
 RA Tsai L.-H., Harlow E., Meyerson M.;
 RT "Isolation of the human cdk2 gene that encodes the cyclin A- and
 RT adenovirus E1A-associated p33 kinase.";
 RL Nature 353:174-177(1991).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92020980; PubMed=1717994;
 RA Ninomiya-Tsuji J., Nomoto S., Yasuda H., Reed S.I., Matsumoto K.;
 RT "Cloning of a human cDNA encoding a CDC2-related kinase by
 RT complementation of a budding yeast *cdc28* mutation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9006-9010(1991).
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schachwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Placenta;

RX MEDLINE=22388257; PubMed=12477932;
 RA Scrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.P., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN PHOSPHORYLATION SITES.
 RX MEDLINE=93010995; PubMed=1396589;
 RA Gu Y., Rosenblatt J., O'Morgan D.O.;
 RT "Cell cycle regulation of CDK2 activity by phosphorylation of Thr160
 RT and Tyr15.";
 RL EMBO J. 11:3995-4005(1992).
 RN [7]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=93288132; PubMed=8510751;
 RA de Bondt H.L., Rosenblatt J., Jancarik J., Jones H.D.,
 RA Morgan D.O., Kim S.-H.;
 RT "Crystal structure of cyclin-dependent kinase 2.";
 RL Nature 363:595-602(1993).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CYCLIN A.
 RX MEDLINE=95356811; PubMed=7630397;
 RA Jeffery P.D., Russo A.A., Polyak K., Gibbs E., Hurwitz J.,
 RA Massague J., Pavletich N.P.;
 RT "Mechanism of CDK activation revealed by the structure of a
 RT cyclinA-CDK2 complex.";
 RL Nature 376:313-320(1995).
 RN [9]
 RN X-RAY CRYSTALLOGRAPHY (2.33 ANGSTROMS) OF COMPLEX WITH L868276.
 RX MEDLINE=96181476; PubMed=8610110;
 RA de Azevedo W.F. Jr., Muleer-Dieckmann H.-J., Schulze-Gahmen U.,
 RA Worland P.J., Sausville E., Kim S.-H.;
 RT "Structural basis for specificity and potency of a flavonoid
 RT inhibitor of human CDK2, a cell cycle kinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:2735-2740(1996).
 RN [10]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CG2A AND KIP1.
 RX MEDLINE=96300318; PubMed=8684460;
 RA Russo A.A., Jeffery P.D., Patten A.K., Massague J., Pavletich N.P.;
 RT "Crystal structure of the p27Kip1 cyclin-dependent-kinase inhibitor
 RT bound to the cyclin A-CDK2 complex.";
 RL Nature 382:325-331(1996).
 RN [11]
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CG2A.
 RX MEDLINE=96313126; PubMed=8756328;
 RA Russo A.A., Jeffery P.D., Pavletich N.P.;
 RT "Structural basis of cyclin-dependent kinase activation by
 RT phosphorylation.";
 RL Nat. Struct. Biol. 3:696-700(1996).
 RN [12]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97075215; PubMed=8917641;
 RA Schulze-Gahmen U., de Bondt H.L., Kim S.-H.;
 RT "High-resolution crystal structures of human cyclin-dependent kinase
 RT 2 with and without ATP: bound waters and natural ligand as guides for
 RT inhibitor design.";
 RL J. Med. Chem. 39:4540-4546(1996).

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DR PDB; 1H1S; 19-SEP-02.
DR PDB; 1H24; 01-FEB-03.
DR PDB; 1H25; 01-FEB-03.
DR PDB; 1H26; 01-FEB-03.
DR PDB; 1H28; 01-FEB-03.
DR PDB; 1JSV; 29-AUG-01.
DR PDB; 1JVP; 21-DEC-01.
DR PDB; 1KE5; 14-MAY-02.
DR PDB; 1KE6; 14-MAY-02.
DR PDB; 1KE7; 14-MAY-02.
DR PDB; 1KE8; 14-MAY-02.
DR PDB; 1KE9; 14-MAY-02.

Query Match          92.3%; Score 24; DB 1; Length 298;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 91 MDASAL 96

RESULT 13
CDK2 RAT
ID CDK2 RAT STANDARD; PRT; 298 AA.
AC Q63699; Q09136;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell division protein kinase 2 (EC 2.7.1.1.-).
GN CDK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=95166553; PubMed=7862443;
RA Kotani S., Endo T., Kitagawa M., Higashi H., Onaya T.;
RT "A variant form of cyclin-dependent kinase 2 (Cdk2) in a malignantly
transformed rat thyroid (FRTL-Tc) cell line.";
RL Oncogene 10:663-669(1995).
RN [2]
RS SEQUENCE OF 19-124 FROM N.A.
RX MEDLINE=96113578; PubMed=8673024;
RA Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;
RT "Synergistic gene expressions of cyclin E, cdk2, cdk5 and E2F-1
during the prolactin-induced G1/S transition in rat Nb2 pre-T
lymphoma cells.";
RL Biochem. Mol. Biol. Int. 37:393-399(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
CC INTERACTS WITH CYCLIN A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
CC DURING S PHASE AND G2.
CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=CDK2-alpha;
CC IsoId=Q63699-1; Sequence=Displayed;
CC Name=CDK2-beta;
CC IsoId=Q63699-2; Sequence=Not described;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDK2/CDKX SUBFAMILY.
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CC EMBL; D28753; BAA05947.1; --
CC EMBL; D63162; BAA09638.1; --
CC HSSP; P24941; 1AQL
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR002290; Ser_Chk_pkinase.
CC DR Pfam; PF00069; pkinase; 1.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SM00220; S_TKC; 1.
CC DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC DR Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
CC KW Cell division; Mitosis; Phosphorylation; Alternative splicing.
CC FT DOMAIN 4 286 PROTEIN KINASE.
CC FT NP_BIND 10 18 ATP (BY SIMILARITY).
CC FT BINDING 33 33 ATP (BY SIMILARITY).
CC FT ACT_SITE 127 127 BY SIMILARITY.
CC FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
CC FT CONFLICT 79 79 V -> C (IN REF. 2).
CC FT CONFLICT 99 99 L -> I (IN REF. 2).
CC FT CONFLICT 124 124 L -> C (IN REF. 2).
CC SQ SEQUENCE 298 AA; 33887 MW; C8CB3ADCE9B57F88 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 298;
Best Local Similarity 83.3%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 LDASAL 6
DB 91 MDASAL 96

RESULT 14
CDK2 MOUSE
ID CDK2 MOUSE STANDARD; PRT; 346 AA.
AC P97377; O55105;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Exon-intron organization of the murine cyclin-dependent kinase-2
DE Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
GN CDK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM CDK2-ALPHA).
RC STRAIN=C57BL/6;
RA Jun D., Lee Y.H., Park H.K., Kim Y.H.;
RT "Exon-intron organization of the murine cyclin-dependent kinase-2
RT genes Cdk2-alpha and Cdk2-beta.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RA Ellenrieder C., Bartosch B., Lee G.Y., Murphy M., Sweeney C.,
RA Hergersberg M., Hunt T., Carrington M., Jaussi R.;
RT "The 39 kDa form of CDK2 arises through alternative splicing, is
RT expressed in many but not all mammals, and is an active kinase.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
CC DURING S PHASE AND G2.
CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=CDK2-beta;
CC IsoId=P97377-1; Sequence=Displayed;
CC Name=CDK2-alpha;

```

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CC IsoId=P97377-2; Sequence=VSP_004800;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CDKX SUBFAMILY.
CC -----
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CC EMBL; AJ223732; CAAL1533.1; --
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CC DR Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
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CC FT NP_BIND 10 18 ATP (BY SIMILARITY).
CC FT BINDING 33 33 ATP (BY SIMILARITY).
CC FT ACT_SITE 127 127 BY SIMILARITY.
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CC FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
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QY 1 LDASAL 6
DB 91 MDASAL 96

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DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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GN Escherichia coli,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334, 623;
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RT "Identification, molecular cloning and sequence analysis of a gene
RT cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
RT phosphoglycerate kinase and a putative second glyceraldehyde 3-
RT phosphate dehydrogenase of Escherichia coli.";
RL Mol. Microbiol. 3:723-732(1989).

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RN [2] SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.
 RP SPECIES=E.coli;
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 RA "Cloning, sequence analysis and over-expression of the gene for the
 RT class II fructose 1,6-bisphosphate aldolase of *Escherichia coli*."
 RL Biochem. J. 257:529-534(1989).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533(2001).
 RN [5]
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 RX MEDLINE=21156231; PubMed=1158796;
 RA Hayaishi T., Makino K., Onihisi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [6]
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 RC SPECIES=E.coli; STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of *Escherichia coli* K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [7]
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 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RX MEDLINE=98263247; PubMed=9600841;
 RA Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M.,
 RA Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
 RA Williams K.L., Hochstrasser D.F.;
 RT "Protein identification with N and C-terminal sequence tags in
 proteome projects.";
 RL J. Mol. Biol. 278:599-608(1998).
 RN [8]
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 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
 through comparison with genomes of *Escherichia coli* K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN [9]
 RN ZINC-LIGANDS, AND MUTAGENESIS.

RC SPECIES=E.coli;
 RX MEDLINE=93170474; PubMed=8436219;
 RA Berry A., Marshall K.E.;
 RT "Identification of zinc-binding ligands in the class II fructose-1,6-
 bisphosphate aldolase of *Escherichia coli*.";
 RL FEBS Lett. 318:11-16(1993).
 RN [10]
 RN X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS).
 RC SPECIES=E.coli;
 RX MEDLINE=96433074; PubMed=8836102;
 RA Blom N.S., Tetreault S., Coulombe R., Sygusch J.;
 RT "Novel active site in *Escherichia coli* fructose 1,6-bisphosphate
 aldolase.";
 RL Nat. Struct. Biol. 3:856-862(1996).
 RN [11]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC SPECIES=E.coli;
 RX MEDLINE=97094986; PubMed=8939754;
 RA Cooper S.J., Leonard G.A., McSweeney S.M., Thompson A.W.,
 RA Naismith J.H., Qamar S., Plater A., Berry A., Hunter W.N.;
 RT "The crystal structure of a class II fructose-1,6-bisphosphate
 aldolase shows a novel binuclear metal-binding active site embedded
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 RL Structure 4:1303-1315(1996).
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 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RC SPECIES=E.coli;
 RX MEDLINE=99182425; PubMed=10080900;
 RA Hall D.R., Leonard G.A., Reed C.D., Watt C.I., Berry A., Hunter W.N.;
 RT "The crystal structure of *Escherichia coli* class II fructose-1,
 6-bisphosphate aldolase in complex with phosphoglycolohydroxamate
 reveals details of mechanism and specificity.";
 RL J. Mol. Biol. 287:393-394(1999).
 CC -!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone,
 phosphate + D-glyceraldehyde 3-phosphate.
 CC -!- COFACTOR: ZINC.
 CC -!- PATHWAY: Glycolysis; sixth step.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Belongs to class II fructose-bisphosphate aldolase
 family.
 CC -----
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 DR EMBL; U28377; AAA69092.1; -;
 DR EMBL; AE000376; AAC75962.1; -;
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 DR PIR; D91103; D91103.
 DR PIR; S02177; ADEC2A.
 DR PDB; 1DOS; 07-JUL-97.
 DR PDB; 1ZEN; 07-JUL-97.
 DR PDB; 1B57; 07-JAN-00.
 DR SWISS-2DPAGE; P11604; COLI.
 DR EcoGene; EG10282; fbaA.
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 DR ProDom; PD002376; K_bp_aldolase; 1.
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FT MUTAGEN 110 110 H->A: LOSS OF ACTIVITY.
FT MUTAGEN 111 111 C->A: PARTIAL LOSS OF ACTIVITY.
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Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
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Db 190 MDASAL 195

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
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Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	26	100.0	28	11	US-09-847-940B-19
5	26	100.0	191	15	US-10-156-761-8434
6	26	100.0	191	15	US-10-156-761-13332
7	26	100.0	191	15	US-10-156-761-13333
8	26	100.0	191	15	US-10-156-761-14915
9	26	100.0	240	10	US-09-738-626-4338
10	26	100.0	374	12	US-10-104-047-3578
11	26	100.0	600	11	US-09-746-660A-106
12	26	100.0	638	10	US-09-983-204-18
13	26	100.0	638	14	US-10-133-157-8
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18	100.0	745	11	US-09-746-660A-104	Sequence 104, App
19	100.0	1006	12	US-10-369-493-22729	Sequence 22729, A
20	92.3	14	14	US-10-038-612-107	Sequence 107, App
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22	92.3	21	14	US-10-038-612-106	Sequence 106, App
23	92.3	40	15	US-10-044-967-18	Sequence 18, Appl
24	92.3	157	16	US-10-080-170-565	Sequence 565, App
25	92.3	191	15	US-10-156-761-11481	Sequence 11481, A
26	92.3	259	12	US-10-369-493-9612	Sequence 9612, Ap
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29	92.3	298	12	US-10-174-794-13	Sequence 13, Appl
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31	92.3	298	12	US-10-295-681-29	Sequence 29, Appl
32	92.3	298	12	US-10-295-681-31	Sequence 31, Appl
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35	92.3	304	10	US-09-976-059-3	Sequence 3, Appl1
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37	92.3	346	12	US-10-295-681-45	Sequence 45, Appl
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43	92.3	405	12	US-10-338-915-6	Sequence 6, Appl1
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ALIGNMENTS

RESULT 1
US-09-847-940B-3
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; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ. ID NOS: 27
; SOFTWARE: PatentIn, Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-3

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Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LDASAL 6

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; Sequence 3, Application US/09847946A
; Publication NO. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
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Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
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Db 20 LDASAL 25
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RESULT 4
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; Sequence 19, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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RESULT 5
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; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-8434

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; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13332
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13332

Query Match 100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 41 LDASAL 46

RESULT 7
US-10-156-761-13333
; Sequence 13333, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 13333
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13333

Query Match 100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 41 LDASAL 46

RESULT 8
US-10-156-761-14915
; Sequence 14915, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14915
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14915

Query Match 100.0%; Score 26; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 41 LDASAL 46

RESULT 9
US-09-738-626-4338
; Sequence 4338, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOIKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4338
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4338

Query Match 100.0%; Score 26; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 70 LDASAL 75

RESULT 10
US-10-104-047-3578
; Sequence 3578, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
 ; FILE REFERENCE: H1-A0105
 ; CURRENT APPLICATION NUMBER: US/10/104,047
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE:
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3578
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-104-047-3578

Query Match 100.0%; Score 26; DB 12; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 |||||
 Db 287 LDASAL 292

RESULT 11
 US-09-746-660A-106
 ; Sequence 106, Application US/09746660A
 ; Publication No. US20030049804A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; APPLICANT: Kim, Jun-Won
 ; APPLICANT: Lee, Heung-Schick
 ; APPLICANT: Hwang, Byung-Joon
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; FILE REFERENCE: BGI-121CP2
 ; CURRENT APPLICATION NUMBER: US/09/746,660A
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 09/606740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 09/603124
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: PatentIn Vers. 2.0
 ; SEQ ID NO 106
 ; LENGTH: 600
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 ; US-09-746-660A-106

Query Match 100.0%; Score 26; DB 11; Length 600;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 |||||
 Db 140 LDASAL 145

RESULT 12

US-09-983-204-18
 ; Sequence 18, Application US/09983204
 ; Patent No. US20020173000A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RENARD, STEPHANE
 ; APPLICANT: BESNARD, FRANCOIS
 ; APPLICANT: GRAHAM, DAVID
 ; TITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
 ; FILE REFERENCE: 07586.0010
 ; CURRENT APPLICATION NUMBER: US/09/983,204
 ; CURRENT FILING DATE: 2001-10-23
 ; PRIOR APPLICATION NUMBER: 09/424,666
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: PCT/EP98/02884
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 97401196.7
 ; PRIOR FILING DATE: 1997-05-30
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 638
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: HNACHD
 ; US-09-983-204-18

Query Match 100.0%; Score 26; DB 10; Length 638;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 |||||
 Db 551 LDASAL 556

RESULT 13
 US-10-133-157-8
 ; Sequence 8, Application US/10133157
 ; Publication No. US20020184054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CALLAMARAS, NICHOLAS
 ; APPLICANT: CHANG, HONG
 ; TITLE OF INVENTION: HIGH THROUGHPUT CELL-BASED ASSAY FOR MONITORING SODIUM
 ; TITLE OF INVENTION: CHANNEL ACTIVITY AND DISCOVERY OF SALTY TASTE
 ; TITLE OF INVENTION: MODULATING COMPOUNDS
 ; FILE REFERENCE: 078003-0280790
 ; CURRENT APPLICATION NUMBER: US/10/133,157
 ; CURRENT FILING DATE: 2002-04-26
 ; PRIOR APPLICATION NUMBER: 60/287,413
 ; PRIOR FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 638
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-133-157-8

Query Match 100.0%; Score 26; DB 14; Length 638;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
 |||||
 Db 551 LDASAL 556

RESULT 14
 US-09-738-626-6815
 ; Sequence 6815, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIALI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, NASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6815
LENGTH: 659
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6815

Query Match 100.0%; Score 26; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 132 LDASAL 137

RESULT 15
US-10-104-047-3501
Sequence 3501, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3501
LENGTH: 704
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3501

Query Match 100.0%; Score 26; DB 12; Length 704;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 617 LDASAL 622

Search completed: February 18, 2004, 15:41:55
Job time : 17.7529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	293	4	US-09-252-991A-17296
2	26	100.0	1313	3	US-08-989-299-9
3	24	92.3	20	3	US-09-140-149-9
4	24	92.3	20	4	US-09-615-917-9
5	24	92.3	40	4	US-08-480-993-18
6	24	92.3	83	1	US-08-370-225-16
7	24	92.3	83	1	US-08-461-859-16
8	24	92.3	83	5	PCT-US93-10069-16
9	24	92.3	165	4	US-09-252-991A-23877
10	24	92.3	257	4	US-09-328-352-4324
11	24	92.3	274	1	US-08-318-947A-20
12	24	92.3	274	2	US-08-785-303-20
13	24	92.3	289	4	US-09-107-532A-4402
14	24	92.3	298	2	US-08-874-347-25
15	24	92.3	298	2	US-08-969-106-2
16	24	92.3	298	3	US-09-093-522-25
17	24	92.3	298	4	US-09-457-040B-29
18	24	92.3	298	4	US-09-411-628-13
19	24	92.3	298	4	US-09-338-125-2
20	24	92.3	298	4	US-09-266-225D-14
21	24	92.3	359	4	US-09-098-219B-2
22	24	92.3	405	1	US-08-370-193A-9
23	24	92.3	544	4	US-08-417-197-113
24	24	92.3	544	4	US-09-417-197-115
25	24	92.3	723	4	US-09-434-408-2
26	24	92.3	970	4	US-09-198-452A-906
27	24	92.3	1042	4	US-09-512-250C-32

28	24	92.3	2618	3	US-09-413-814-28	Sequence 28, Appl
29	23	88.5	44	3	US-08-905-223-345	Sequence 345, App
30	23	88.5	65	1	US-08-227-536-6	Sequence 6, Appli
31	23	88.5	65	5	PCT-US95-04682-6	Sequence 6, Appli
32	23	88.5	159	4	US-09-252-991A-24779	Sequence 24779, A
33	23	88.5	201	1	US-08-444-083-8	Sequence 8, Appli
34	23	88.5	201	1	US-08-286-304-8	Sequence 8, Appli
35	23	88.5	201	1	US-08-442-745-8	Sequence 8, Appli
36	23	88.5	201	1	US-08-443-129-8	Sequence 8, Appli
37	23	88.5	201	1	US-08-443-952-8	Sequence 8, Appli
38	23	88.5	201	1	US-08-443-130-8	Sequence 8, Appli
39	23	88.5	201	1	US-08-792-019B-11	Sequence 11, Appl
40	23	88.5	201	3	US-09-106-182-4	Sequence 4, Appli
41	23	88.5	201	3	US-08-988-819-11	Sequence 11, Appl
42	23	88.5	201	3	US-08-898-911-8	Sequence 8, Appli
43	23	88.5	201	3	US-09-016-534-11	Sequence 11, Appl
44	23	88.5	201	4	US-09-848-183-3	Sequence 3, Appli
45	23	88.5	201	5	PCT-US95-04467-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-17296
; Sequence 17296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17296
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17296

Query Match 100.0%; Score 26; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
Db 91 LDASAL 96

RESULT 2
US-08-989-299-9
; Sequence 9, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E. Beth
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-299-9

Query Match 100.0%; Score 26; DB 3; Length 1313;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 600 LDASAL 605
|||||

RESULT 3

US-09-140-149-9
Sequence 9, Application US/09140149
Patent No. 6117680
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of
FILE REFERENCE: 363C
CURRENT APPLICATION NUMBER: US/09/140,149
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 08/918,401
EARLIER FILING DATE: 1997-08-26
EARLIER APPLICATION NUMBER: 08/920,610
EARLIER FILING DATE: 1997-08-27
EARLIER APPLICATION NUMBER: 09/126,009
EARLIER FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: PCT/US97/15219
EARLIER FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-140-149-9

Query Match 92.3%; Score 24; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 11 MDASAL 16
|||||

RESULT 4

US-09-615-917-9
Sequence 9, Application US/09615917
Patent No. 6479653
GENERAL INFORMATION:
APPLICANT: Natesan, Sridaran
TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of
FILE REFERENCE: 363C continuation
CURRENT APPLICATION NUMBER: US/09/615,917
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 08/918,401
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 08/920,610
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 09/126,009
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 09/140,149
PRIOR FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-615-917-9

Query Match 92.3%; Score 24; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 11 MDASAL 16
|||||

RESULT 5

US-09-480-993-18
Sequence 18, Application US/09480993
Patent No. 6383790
GENERAL INFORMATION:
APPLICANT: Shokat, Kevan M.
TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation
FILE REFERENCE: 51538-5001-US
CURRENT APPLICATION NUMBER: US/09/480,993
CURRENT FILING DATE: 2000-01-11
EARLIER APPLICATION NUMBER: US 60/115,340
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Cdk2, cyclin-dependent kinase
US-09-480-993-18

Query Match 92.3%; Score 24; DB 4; Length 40;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 33 MDASAL 38
|||||

RESULT 6

US-08-370-225-16

; Sequence 16, Application US/08370225
; Patent No. 5580736

; GENERAL INFORMATION:

; APPLICANT: Brent, Roger

; APPLICANT: Gyuris, Jeno

; APPLICANT: Golemish, Erica

; TITLE OF INVENTION: Interaction Trap System for Isolating

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/370,225

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,038

; FILING DATE: 10/30/92

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00786/143001

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 83

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-370-225-16

Query Match

Best Local Similarity 92.3%; Score 24; DB 1; Length 83;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6

Db 18 MDASAL 23

RESULT 7

US-08-461-859-16

; Sequence 16, Application US/08461859

; Patent No. 5786169

; GENERAL INFORMATION:

; APPLICANT: Brent, Roger

; APPLICANT: Gyuris, Jeno

; APPLICANT: Golemish, Erica

; TITLE OF INVENTION: Interaction Trap System for Isolating

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,859

; FILING DATE: June 5, 1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/370,225

; FILING DATE: January 9, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,038

; FILING DATE: October 30, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Lech, Karen P.

; REGISTRATION NUMBER: 35,238

; REFERENCE/DOCKET NUMBER: 00786/143002

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 83

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-461-859-16

Query Match

Best Local Similarity 92.3%; Score 24; DB 1; Length 83;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6

Db 18 MDASAL 23

RESULT 8

PCT-US93-10069-16

; Sequence 16, Application PC/TUS9310069

; GENERAL INFORMATION:

; APPLICANT: Brent, Roger

; APPLICANT: Gyuris, Jeno

; APPLICANT: Golemish, Erica

; TITLE OF INVENTION: Interaction Trap System for Isolating

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/10069

; FILING DATE: 20-OCT-1993

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/969,038

; FILING DATE: 10/30/92

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00786/143001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

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; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 83
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; PCT-US93-10069-16

Query Match          92.3%; Score 24; DB 5; Length 83;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
DB      18 MDASAL 23

RESULT 9
US-09-252-991A-23877
; Sequence 23877, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23877
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23877

Query Match          92.3%; Score 24; DB 4; Length 165;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
DB      150 IDASAL 155

RESULT 10
US-09-328-352-4324
; Sequence 4324, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4324
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-4324

Query Match          92.3%; Score 24; DB 4; Length 257;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
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DB      5 IDASAL 10

RESULT 11
US-08-318-947A-20
; Sequence 20, Application US/08318947A
; Patent No. 5798245
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,947A
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,530
; FILING DATE: 07-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mack, Susan J.
; REGISTRATION NUMBER: 30,951
; REFERENCE/DOCKET NUMBER: A6462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-2920
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 274 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-318-947A-20

Query Match          92.3%; Score 24; DB 1; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
DB      91 MDASAL 96

RESULT 12
US-08-795-303-20
; Sequence 20, Application US/08795303
; Patent No. 5948656
; GENERAL INFORMATION:
; APPLICANT: Anderson, Paul J.
; APPLICANT: Tian, Qingsheng
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, NW Suite 800
; CITY: Washington
; STATE: DC
```

COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 04-FEB-1997
APPLICATION NUMBER: US/08/795,303
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/318,947
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: A6462
TELEPHONE: (202)293-7060
TELEFAX: (202)293-2920
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-303-20

Query Match 92.3%; Score 24; DB 2; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
DB 91 MDASAL 96

RESULT 13
US-09-107-532A-4402
; Sequence 4402, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4402:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...289
SEQUENCE DESCRIPTION: SEQ ID NO: 4402:
US-09-107-532A-4402

Query Match 92.3%; Score 24; DB 4; Length 289;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
:|||||
DB 96 IDASAL 101

RESULT 14
US-08-874-347-25
; Sequence 25, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; TITLE OF INVENTION: CARINII
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,347
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-874-347-25

Query Match 92.3%; Score 24; DB 2; Length 298;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 91 MDASAL 96

RESULT 15
US-08-969-106-2
; Sequence 2, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-969-106-2

Query Match 92.3%; Score 24; DB 2; Length 298;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 91 MDASAL 96

Search completed: February 18, 2004, 14:41:45
Job time : 7.06579 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds
(without alignments)
75.239 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10	US-09-847-940B-2
2	40	100.0	6	11	US-09-847-946A-2
3	40	100.0	6	11	US-09-847-946A-33
4	40	100.0	7	11	US-09-847-946A-37
5	40	100.0	8	11	US-09-847-946A-30
6	40	100.0	8	11	US-09-847-946A-38
7	40	100.0	9	11	US-09-847-946A-29
8	40	100.0	9	11	US-09-847-946A-32
9	40	100.0	9	11	US-09-847-946A-35
10	40	100.0	9	11	US-09-847-946A-36
11	40	100.0	10	11	US-09-847-946A-31
12	40	100.0	10	11	US-09-847-946A-34
13	40	100.0	11	11	US-09-847-946A-28
14	40	100.0	11	11	US-09-847-946A-132
15	40	100.0	11	11	US-09-847-946A-140

16	40	100.0	13	11	US-09-847-946A-143	Sequence 143, App
17	40	100.0	13	11	US-09-847-946A-144	Sequence 144, App
18	40	100.0	13	11	US-09-847-946A-145	Sequence 145, App
19	40	100.0	13	11	US-09-847-946A-148	Sequence 148, App
20	40	100.0	17	11	US-09-847-946A-141	Sequence 141, App
21	40	100.0	17	11	US-09-847-946A-142	Sequence 142, App
22	40	100.0	17	11	US-09-847-946A-146	Sequence 146, App
23	40	100.0	17	11	US-09-847-946A-147	Sequence 147, App
24	40	100.0	18	11	US-09-847-946A-131	Sequence 131, App
25	40	100.0	18	11	US-09-847-946A-135	Sequence 135, App
26	40	100.0	18	11	US-09-847-946A-136	Sequence 136, App
27	40	100.0	22	11	US-09-847-946A-133	Sequence 133, App
28	40	100.0	22	11	US-09-847-946A-134	Sequence 134, App
29	40	100.0	22	11	US-09-847-946A-137	Sequence 137, App
30	40	100.0	22	11	US-09-847-946A-138	Sequence 138, App
31	40	100.0	22	11	US-09-847-946A-139	Sequence 139, App
32	40	100.0	28	10	US-09-847-940B-18	Sequence 18, Appl
33	40	100.0	28	10	US-09-847-946A-18	Sequence 18, Appl
34	40	100.0	222	10	US-09-771-161A-141	Sequence 141, Appl
35	40	100.0	745	9	US-09-796-872-2	Sequence 2, Appl
36	40	100.0	745	10	US-09-844-908-10	Sequence 10, Appl
37	40	100.0	745	10	US-09-844-988-10	Sequence 10, Appl
38	40	100.0	745	12	US-10-408-636-3	Sequence 3, Appl
39	40	100.0	745	12	US-10-394-322A-32	Sequence 32, Appl
40	40	100.0	745	15	US-10-243-408-4	Sequence 4, Appl
41	40	100.0	745	15	US-10-059-585-35	Sequence 35, Appl
42	40	100.0	745	15	US-10-338-462-10	Sequence 10, Appl
43	40	100.0	756	9	US-09-796-872-15	Sequence 15, Appl
44	40	100.0	756	10	US-09-771-161A-232	Sequence 232, App
45	40	100.0	756	10	US-09-844-908-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 76+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
| | | | |
Db 1 LDWSWL 6

RESULT 2

US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 1 LDWSWL 6

RESULT 3
US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-33

Query Match 100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 1 LDWSWL 6

RESULT 4
US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1

; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-37

Query Match 100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 1 LDWSWL 6

RESULT 5
US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-30

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 3 LDWSWL 8

RESULT 6

US-09-847-946A-38
; Sequence 38, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-38

Query Match 100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
| | | | |
Db 1 LDWSWL 6

RESULT 7
US-09-847-946A-29
; Sequence 29, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-29

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
| | | | |
Db 1 LDWSWL 6

RESULT 8
US-09-847-946A-32
; Sequence 32, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-32

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
| | | | |
Db 1 LDWSWL 6

RESULT 9
US-09-847-946A-35
; Sequence 35, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-35

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
|||||
Db 3 LDWSWL 8

RESULT 10
US-09-847-946A-36
; Sequence 36, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-36

Query Match 100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05; Length 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
|||||
Db 2 LDWSWL 7

RESULT 11
US-09-847-946A-31
; Sequence 31, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-31

Query Match 100.0%; Score 40; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
|||||
Db 2 LDWSWL 7

RESULT 12
US-09-847-946A-34
; Sequence 34, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-34

Query Match 100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
|||||
Db 3 LDWSWL 8

RESULT 13
US-09-847-946A-28
; Sequence 28, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-28

US-09-847-946A-28

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
| | | | |
Db 3 LDWSWL 8

RESULT 14

US-09-847-946A-132
; Sequence 132, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-132

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
| | | | |
Db 3 LDWSWL 8

RESULT 15

US-09-847-946A-140
; Sequence 140, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-140

Query Match 100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
| | | | |
Db 3 LDWSWL 8

Search completed: February 18, 2004, 15:41:54
Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
(without alignments)
35.929 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	745	2	US-08-887-518-3
2	40	100.0	745	2	US-09-023-321-3
3	40	100.0	745	2	US-08-890-853-4
4	40	100.0	745	2	US-09-032-475-3
5	40	100.0	745	2	US-09-099-125A-4
6	40	100.0	745	2	US-09-099-124A-4
7	40	100.0	745	3	US-09-032-476-4
8	40	100.0	745	3	US-08-890-854-4
9	40	100.0	745	3	US-09-032-324-4
10	40	100.0	745	3	US-09-168-629-2
11	40	100.0	745	3	US-08-910-820-10
12	40	100.0	745	3	US-08-810-131A-2
13	40	100.0	745	3	US-09-109-986-4
14	40	100.0	745	4	US-09-844-908-10
15	40	100.0	745	4	US-09-868-758-3
16	40	100.0	756	2	US-08-887-518-4
17	40	100.0	756	2	US-09-023-321-4
18	40	100.0	756	2	US-08-890-853-2
19	40	100.0	756	2	US-09-032-475-4
20	40	100.0	756	2	US-09-099-125A-2
21	40	100.0	756	2	US-09-099-124A-2
22	40	100.0	756	3	US-09-032-476-2
23	40	100.0	756	3	US-08-890-854-2
24	40	100.0	756	3	US-09-023-324-2
25	40	100.0	756	3	US-09-168-629-15
26	40	100.0	756	3	US-08-910-820-9
27	40	100.0	756	4	US-09-109-986-2

28	40	100.0	756	4	US-09-844-908-9	Sequence 9, Appli
29	40	100.0	756	4	US-09-868-758-4	Sequence 4, Appli
30	40	100.0	996	4	US-09-417-197-123	Sequence 123, App
31	40	100.0	997	4	US-09-417-197-121	Sequence 121, App
32	36	90.0	100	1	US-08-241-853-28	Sequence 28, Appl
33	36	90.0	100	1	US-08-241-853-29	Sequence 29, Appl
34	36	90.0	100	2	US-08-850-917-28	Sequence 28, Appl
35	36	90.0	100	2	US-08-850-917-29	Sequence 29, Appl
36	36	90.0	242	4	US-09-345-236B-3	Sequence 3, Appli
37	36	90.0	334	4	US-09-252-991A-22395	Sequence 22395, A
38	36	90.0	454	4	US-09-252-991A-28780	Sequence 28780, A
39	36	90.0	616	3	US-09-136-574A-47	Sequence 47, Appl
40	36	90.0	982	2	US-08-673-789-4	Sequence 4, Appli
41	36	90.0	983	1	US-08-162-809-16	Sequence 16, Appl
42	36	90.0	983	1	US-08-167-919A-10	Sequence 10, Appl
43	36	90.0	983	2	US-08-449-645A-21	Sequence 21, Appl
44	36	90.0	983	2	US-08-702-367A-21	Sequence 21, Appl
45	36	90.0	983	3	US-08-715-106-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-887-518-3
; Sequence 3, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-887-518-3

Query Match 100.0%; Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LWSWL 6
Db 738 LWSWL 743

```
RESULT 2
US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-3
Query Match 100.0%; Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

RESULT 3
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4
Query Match 100.0%; Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

RESULT 4
US-09-032-475-3
; Sequence 3, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-3
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Query Match 100.0%; Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
DB 738 LDWSWL 743

RESULT 5
US-09-099-125A-4
; Sequence 4, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-125A-4

Query Match 100.0%; Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
DB 738 LDWSWL 743

RESULT 6
US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-4

Query Match 100.0%; Score 40; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
DB 738 LDWSWL 743

RESULT 7
US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R. gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-4

Query Match 100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

RESULT 8
US-08-890-854-4
Sequence 4, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-4

Query Match 100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

RESULT 9
US-09-023-324-4
Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-4

Query Match 100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

RESULT 10
US-09-168-629-2
Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: PUD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 745

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-168-629-2

Query Match 100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6

Db 738 LDWSWL 743

RESULT 11

US-08-910-820-10

; Sequence 10, Application US/08910820

; Patent No. 6258579

; GENERAL INFORMATION:

; APPLICANT: Mercurio, Frank

; APPLICANT: Zhu, Hengyi

; APPLICANT: Barbosa, Miguel

; APPLICANT: Li, Gian

; APPLICANT: Murray, Brian W.

; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE

; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED AND BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/910,820

; FILING DATE: 12-AUG-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 860098.413C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 745 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-910-820-10

Query Match 100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6

Db 738 LDWSWL 743

RESULT 12

US-08-810-131A-2

; Sequence 2, Application US/08810131A

; Patent No. 6268194

; GENERAL INFORMATION:

; APPLICANT: Karin, Michael

; APPLICANT: DiDonato, Joseph A.

; APPLICANT: Rothwarf, David M.

; APPLICANT: Hayakawa, Makio

; APPLICANT: Zandi, Ebrahim

; TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/810,131A

; FILING DATE: 25-FEB-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-UD 2408

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 745 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-810-131A-2

Query Match 100.0%; Score 40; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6

Db 738 LDWSWL 743

RESULT 13

US-09-109-986-4

; Sequence 4, Application US/09109986

; Patent No. 6479266

; GENERAL INFORMATION:

; APPLICANT: Rothe, Mike

; APPLICANT: Cao, Zhaodan

; APPLICANT: R gnier, Catherine

; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/109,986

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-109-986-4

Query Match 100.0%; Score 40; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

RESULT 15
US-09-868-758-3
; Sequence 3, Application US/09868758
; Patent No. 6576439
; GENERAL INFORMATION:
; APPLICANT: Glaxo Wellcome KK
; APPLICANT: Takemoto, Yoshihiro
; APPLICANT: Sakai, Yutaka
; APPLICANT: Hashimoto, Yasuhiro
; TITLE OF INVENTION: IKK3
; FILE REFERENCE: 9950986P
; CURRENT APPLICATION NUMBER: US/09/868,758
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: GB 9828704.8
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-868-758-3

Query Match 100.0%; Score 40; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:45
Job time : 8.06579 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	745	1 I49101	conserved helix-lo
2	38	95.0	1139	2 AI0379	probable potassium
3	37	92.5	322	2 AI3395	NADH2 dehydrogenas
4	36	90.0	122	2 S69909	Ig V-D-J region (M
5	36	90.0	132	2 S65785	mel-13a protein -
6	36	90.0	277	1 JC5900	bo-type ubiquinol
7	36	90.0	296	2 A84985	cytochrome o ubiqu
8	36	90.0	307	1 A36885	bo-type ubiquinol
9	36	90.0	318	2 AD0384	cytochrome o ubiqu
10	36	90.0	331	2 D83480	cytochrome o ubiqu
11	36	90.0	344	2 AG3489	cytochrome o ubiqu
12	36	90.0	353	2 A87469	ubiquinol oxidase
13	36	90.0	362	2 S23471	uroporphyrinogen d
14	36	90.0	386	2 C96006	probable cytochrom
15	36	90.0	409	2 T47298	probable replicati
16	36	90.0	747	2 D70802	hypothetical prote
17	36	90.0	803	2 F90485	hypothetical prote
18	36	90.0	915	2 A43802	cellulase (EC 3.2.
19	36	90.0	983	2 B45583	receptor tyrosine k
20	36	90.0	983	2 A38224	protein-tyrosine k
21	36	90.0	983	2 A45583	receptor tyrosine
22	36	90.0	1039	2 S02711	cellulase (EC 3.2.
23	36	90.0	1329	2 D87226	conserved hypothet
24	35	87.5	162	2 C70829	hypothetical prote
25	35	87.5	348	2 AE2733	NADH ubiquinone ox
26	35	87.5	348	2 G97514	NADH dehydrogenase
27	35	87.5	443	2 AE0309	probable sugar tra
28	34	85.0	82	2 C69013	hypothetical prote
29	34	85.0	116	2 T03472	conserved hypothet

30	34	85.0	214	2 G83692	hypothetical prote
31	34	85.0	282	1 DGEOMA	DNA-3-methyladenin
32	34	85.0	282	2 E90988	3-methyl-adenine D
33	34	85.0	282	2 G85833	3-methyl-adenine D
34	34	85.0	289	2 AI0770	DNA-3-methyladenin
35	34	85.0	299	2 B83243	hypothetical prote
36	34	85.0	332	2 AH2593	cytochrome o ubiqu
37	34	85.0	377	2 B97376	cytochrome ba(3) (
38	34	85.0	394	2 C85064	hypothetical prote
39	34	85.0	411	2 E84949	tetrahydrofolylpol
40	34	85.0	414	2 B82408	hypothetical prote
41	34	85.0	418	2 D85064	hypothetical prote
42	34	85.0	420	2 A54759	cytochrome ba(3) c
43	34	85.0	501	2 S45914	probable glucan 1,
44	34	85.0	764	2 AD3144	formate dehydrogen
45	34	85.0	764	2 H98143	cbhbc protein (U60

ALIGNMENTS

RESULT 1

I49101
conserved helix-loop-helix ubiquitous kinase (SC 2.7.1.1.-) CHUK - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I49101
R;Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
A;Reference number: I49101, MUID:96044444; PMID:7558004
A;Accession: I49101
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-745 <RES>
A;Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C;Genetics:
A;Gene: CHUK
C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homol

C;Keywords: ATP; phosphotransferase
F;13-283/Domain: protein kinase homology <KIN>
Query Match 100.0%; Score 40; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6

|||||
Db 738 LDWSWL 743

RESULT 2

AI0379
probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AI0379
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AI0379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1139 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:g15981067; GSPDB:GN00175
C;Genetics:
A;Gene: YPO3129

Query Match 95.0%; Score 38; DB 2; Length 1139;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
:|||||

Db 480 MDWSWL 485

RESULT 3
AI3395
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) [imported] - Brucella melitensis (strain 1
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C;Accession: AI3395
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3395
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE008917; PIDN:AAL52332.1; PID:gl7983126; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1151
A;Map position: I
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: oxidoreductase

Query Match 92.5%; Score 37; DB 2; Length 322;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
:|||||

Db 174 LDWNWL 179

RESULT 4
IG V-D-J region (MS) - human
S69909
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69909
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A;Reference number: S69909; MUID:94335315; PMID:8057663
A;Accession: S69909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: EMBL:Z33399; NID:g871348; PIDN:CAA83850.1; PID:g871349
A;Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 36; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
:|||||

Db 33 DWSWL 37

RESULT 5
S65785
mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S65785

R;Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A;Reference number: S65785; MUID:96180310; PMID:8597592
A;Accession: S65785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TET>
A;Cross-references: EMBL:U35309
C;Genetics:
A;Gene: mel-13
C;Superfamily: mouse mel-13a protein
C;Keywords: alternative splicing

Query Match 90.0%; Score 36; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWL 6
:|||||

Db 58 DWSWL 62

RESULT 6
JCS900
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum
C;Species: Bradyrhizobium japonicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JCS900
R;Surpin, M.A.; Luebben, M.; Maier, R.J.
Gene 183, 201-206, 1996
A;Title: The Bradyrhizobium japonicum coxXYZ gene cluster encodes a bb3-type ubiquinol
A;Reference number: JCS900; MUID:97149299; PMID:8996107
A;Accession: JCS900
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-277 <SUR>
C;Genetics:
A;Gene: coxW
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res

Query Match 90.0%; Score 36; DB 1; Length 277;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
:|||||

Db 108 LDWKWL 113

RESULT 7
AB4985
cytochrome o ubiquinol oxidase subunit II [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2001
C;Accession: AB4985
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. t
A;Reference number: AB4930; MUID:20445173; PMID:10993077
A;Accession: AB4985
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: cyoA; BU472
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 296;

Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
||| ||
Db 125 LDWKWL 130

RESULT 8
A36885
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti
N;Alternate names: Cytochrome al chain II
C;Species: Acetobacter aceti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A36885
R;Fukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, Y.; Horinouchi
J.; Bacteriol. 175, 4307-4314, 1993
A;Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A
A;Reference number: A36885; MUID:93322308; PMID:8392509
A;Accession: A36885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <FUK>
A;Cross-references: GB:D13185; NID:G409064; PIDN:BAA02480.1; PID:G433186
A;Experimental source: isolate 1023
C;Genetics:
A;Gene: cyaB
C;Complex: heterotetramer; chains I, II, III and IV
C;Function:
A;Description: terminal oxidase for ethanol oxidation
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>
F;48-64/Domain: transmembrane #status predicted <TM1>
F;89-105/Domain: transmembrane #status predicted <TM2>

Query Match 90.0%; Score 36; DB 1; Length 307;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
||| ||
Db 135 LDWKWL 140

RESULT 9
AD0384
cytochrome O ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Yersinia pestis (stra
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD0384
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0384
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92399.1; PID:G15981102; GSPDB:GN00175
C;Genetics:
A;Gene: cyaA
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp

Query Match 90.0%; Score 36; DB 2; Length 318;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6

Db 135 LDWKWL 140
||| ||
RESULT 10
D83480
cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (a
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83480
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <STO>
A;Cross-references: GB:AE004561; GB:AE004091; NID:G9947253; PIDN:AAG04706.1; GSPDB:GN00
A;Experimental source: strain PA01
C;Genetics:
A;Gene: cyoA; PA1317
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 331;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
||| ||
Db 133 LDWKWL 138

RESULT 11
AG3489
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002
C;Accession: AG3489
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL53082.1; PID:G17983945; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME11901
A;Map position: 1
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp

Query Match 90.0%; Score 36; DB 2; Length 344;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
||| ||
Db 141 LDWKWL 146

RESULT 12
AB7469
ubiquinol oxidase subunit II [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001

C;Accession: A87469
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Winn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <STO>
A;Cross-references: GB:AE005673; NID:gl3423199; PIDN:AAK23749.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1773
A;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 353;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
||| ||
Db 146 LDWKWL 151

RESULT 13
S23471
uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: protein YD9609.03; protein YDR047w
C;Species: *Saccharomyces cerevisiae*
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 22-Jun-1999
C;Accession: S23471; S33965; S54033; S20190; S27348; S31312
R;Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rycka, J.; Harrison, L.; Kushner, J.; La
Eur. J. Biochem. 205, 1011-1016, 1992
A;Title: Uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence
A;Reference number: S23471; MUID:92249304; PMID:1576986
A;Accession: S23471
A;Molecule type: DNA
A;Residues: 1-362 <GAR>
A;Cross-references: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
R;Diflumeri, C.; Larocque, R.; Keng, T.
Yeast 9, 613-623, 1993
A;Title: Molecular analysis of HEM6 (HEM12) in *Saccharomyces cerevisiae*, the gene for ur
A;Reference number: S33965; MUID:93348774; PMID:8346678
A;Accession: S33965
A;Molecule type: DNA
A;Residues: 1-362 <DIF>
A;Cross-references: EMBL:Z19089; NID:g4775; PIDN:CAA79514.1; PID:g4776
R;Hunt, S.; Bowman, S.; Harris, D.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54031
A;Accession: S54031
A;Molecule type: DNA
A;Residues: 1-362 <HUN>
A;Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAA89078.1; PID:g798900; MIPS:YDR047w
C;Genetics:
A;Gene: HEM12; HEM6; POP3
A;Cross-references: MIPS:YDR047w; SGD:S0002454
A;Map position: 4R
C;Superfamily: uroporphyrinogen decarboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 279 LDWSW 283

RESULT 14

C96006
probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] - Sinc
C;Species: *Sinorhizobium meliloti*
C;Date: 24-Aug-2001 #sequence revision 24-Aug-2001 #text change 30-Sep-2001
C;Accession: C96006
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrwester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C96006
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:gl5141202; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Pederspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: cyoA; Smb21487
A;Genome: plasmid
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp

Query Match 90.0%; Score 36; DB 2; Length 386;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
||| ||
Db 141 LDWKWL 146

RESULT 15
T47298
probable replication protein - *Arabidopsis thaliana*
N;Alternate names: protein T14K23.110
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 20-Apr-2000
C;Accession: T47298
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24458
A;Accession: T47298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <NYA>
A;Cross-references: EMBL:AL132909
A;Experimental source: cultivar Columbia; BAC clone T14K23
C;Genetics:
A;Map position: 3
A;Introns: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3
A;Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
|||||
Db 190 LDWSW 194

Search completed: February 18, 2004, 14:38:33
Job time : 7.5921 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds
(without alignments)
79.423 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	745	1 IKKA HUMAN	O15111 h inhibitor
2	40	100.0	745	1 IKKA MOUSE	Q06680 m inhibitor
3	40	100.0	756	1 IKKB HUMAN	O14920 homo sapien
4	40	100.0	757	1 IKKB MOUSE	O88351 mus musculus
5	40	100.0	757	1 IKKB RAT	Q9QY78 rattus norv
6	36	90.0	296	1 CYOA_BUCAL	P57544 buchnera ap
7	36	90.0	307	1 QOX2 ACEAC	P50653 acetobacter
8	36	90.0	314	1 CYOA_PSEPU	Q9WWR1 pseudomonas
9	36	90.0	362	1 DCUP YEAST	P32347 saccharomyc
10	36	90.0	983	1 EPAS3_CHICK	P29318 gallus gall
11	36	90.0	983	1 EPAS3_HUMAN	P29320 homo sapien
12	36	90.0	983	1 EPAS3_MOUSE	P29319 mus musculus
13	36	90.0	984	1 EPAS3 RAT	O08680 rattus norv
14	36	90.0	1039	1 GUNB CALSA	P10474 c endogluca
15	35	87.5	290	1 CYOA_BUCAL	O8K993 buchnera ap
16	34	85.0	282	1 3MG2_ECOLI	P04395 escherichia
17	34	85.0	411	1 FOLC_BUCAL	P57265 buchnera ap
18	34	85.0	501	1 YBQ6_YEAST	P38081 saccharomyc
19	34	85.0	1331	1 MANB CALSA	P22533 caldocellum
20	34	85.0	1742	1 GUNA CALSA	P22534 caldocellum
21	33	82.5	336	1 NOSO BACSU	O34453 bacillus su
22	33	82.5	411	1 CYB_CHRVI	O31215 chromatium
23	33	82.5	453	1 NRAM_IAWIL	P03470 influenza a
24	33	82.5	454	1 NRAM_IAPUE	P03468 influenza a
25	33	82.5	524	1 CP72 CATRO	Q05047 catharanthu
26	33	82.5	552	1 NU5M RHISA	Q9ZYM7 rhipicephal
27	33	82.5	579	1 YC12_KLRPN	Q48458 klebsiella
28	33	82.5	656	1 VEXE_SALTI	P43112 salmonella
29	33	82.5	840	1 VPHI_YEAST	P32563 saccharomyc
30	32	80.0	191	1 GDIR_CABEL	Q20496 caenorhabdi
31	32	80.0	210	1 KTHY SCHPO	P36590 schizosacch
32	32	80.0	272	1 CY1_RHORU	P23135 rhodospiril
33	32	80.0	281	1 Y373_MYCPN	P75227 mycoplasma

RESULT 1

ID	IKKA_HUMAN	STANDARD;	PRT;	745 AA.
AC	O15111; O14666; Q13132; Q92467;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1.-)			
DE	(I kappa-B kinase alpha) (IKKKA) (IKK-alpha) (IKKAPAB kinase)			
DE	(I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous			
DE	kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).			
GN	CHUK OR IKKA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RP	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.			
RC	TISSUE=T-cell;			
RX	MEDLINE=97386461; PubMed=9244310;			
RA	Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;			
RT	"Identification and characterization of an IkappaB kinase.";			
RL	Cell 90:373-383(1997).			
RN	[2]			
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RP	MEDLINE=97394468; PubMed=9252186;			
RA	Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;			
RT	"A cytokine-responsive IkappaB kinase that activates the transcription			
RT	factor NF-kappaB.";			
RL	Nature 388:548-554(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND			
RP	SER-176.			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=98008813; PubMed=9346484;			
RA	Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,			
RA	Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;			
RT	"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for			
RT	NF-kappaB activation.";			
RL	Science 278:860-866(1997).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Heart;			
RX	MEDLINE=99032998; PubMed=9813230;			
RC	Hu M.C.-T., Wang Y.-P.;			
RA	"IkappaB kinase-alpha and -beta genes are coexpressed in adult and			
RT	embryonic tissues but localized to different human chromosomes.";			
RL	Gene 222:31-40(1998).			
RN	[5]			
RP	SEQUENCE OF 32-745 FROM N.A.			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=96258427; PubMed=8777433;			
RA	Connelly M.A., Marcu K.B.;			
RT	"CHUK, a new member of the helix-loop-helix and leucine zipper			
RT	families of interacting proteins, contains a serine-threonine kinase			
RT	catalytic domain.";			

P34889 caenorhabdi
O93883 penicillium
P24218 escherichia
P36646 escherichia
Q92091 oncorhynchu
Q07570 influenza a
Q07571 influenza a
Q07572 influenza a
Q07573 influenza a
Q07599 influenza a
Q07574 influenza a
Q07577 influenza a

Cell. Mol. Biol. Res. 41:537-549(1995).
[6]
RN PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
RP AND SER-180.
RX MEDLINE=98188283; PubMed=9520446;
RA Ling L., Cao Z., Goeddel D.V.;
RN "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
RT Ser-176.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
RN [7]
RN PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX MEDLINE=99413720; PubMed=10485710;
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
RN Donner D.B.;
RT "NF-kappaB activation by tumour necrosis factor requires the Akt
RT serine-threonine kinase.";
RL Nature 401:82-85(1999).
RN [8]
RN IKK- α -IKK β BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RN "Positive and negative regulation of IkappaB kinase activity through
RT IkappaB subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [9]
RN IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RN "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [10]
RN REVIEW
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RN "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
RN [11]
RN SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKK β AND IKK γ .
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RN O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC when dephosphorylated.
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
CC a complex composed of NCOA2, NCOA3, IKK β , IKK γ and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF012890; AAC51662.1; -.
DR EMBL; AF009225; AAC51671.1; -.
DR EMBL; AF080157; AAD08996.1; -.
DR EMBL; U22512; AAC50713.1; -.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:1974; CHUK.
DR MIM; 600664; -.
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0008384; P:IkappaB kinase activity; TAS.
DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR000719; Prot.Kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PD00109; TYRKINASE.
DR ProDom; PD000001; Prot.Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 302 PROTEIN KINASE.
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 738 743 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 144 144 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).
FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14).
FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
FT MUTAGEN 176 176 K->M: LOSS OF AUTOPHOSPHORYLATION.
FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
FT ACTIVITY.
FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
FT CONFLICT 543 543 E -> G (IN REF. 2).
FT CONFLICT 604 604 L -> R (IN REF. 5).
FT CONFLICT 679 680 TS -> AV (IN REF. 5).
FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
FT CONFLICT 686 687 TS -> DL (IN REF. 5).
SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;
Query Match 100.0%; Score 40; DB 1; Length 745;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDWSWL 6
Db 738 LDWSWL 743
RESULT 2
ID IKKA_MOUSE STANDARD; PRT; 745 AA.
AC Q60680; Q9D2X3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=BALB/c;
 RC MEDLINE=9604444; PubMed=7558004;
 RA Mock B.A., Connolly M.A., McBride O.W., Korak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 chromosome 10 and mouse chromosome 19.";
 RL Genomics 27:348-351(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=BALB/c;
 RC MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RP STRAIN=CS7BL/6J; TISSUE=Colon;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., De Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayaishizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RC MEDLINE=20198447; PubMed=10733566;
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,
 RA Galeziunas R., Marcu K.B.;
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
 RT IKKbeta have different activation requirements.";
 RL Mol. Cell. Biol. 20:2635-2649(2000).
 RN [5]
 RP PHOSPHORYLATION BY MAP3K14/NIK.
 RC MEDLINE=9918238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [6]
 RP IKKA-IKKB BINDING.
 RC MEDLINE=99212141; PubMed=10195894;
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of IkappaB kinase activity through
 RT IKKbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [7]
 RP IKK PHOSPHORYLATION.
 RC MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).

[8]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated
 CC when dephosphorylated.
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKKG and CREBBP (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q60680-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta LH;
 CC IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
 CC Name=3; Synonyms=Delta H;
 CC IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
 CC -1- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
 CC 3 are expressed predominantly in brain and T-lymphocytes.
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
 CC E11, E15 and E17 days. In the limb development, its expression
 CC predominates in the limb buds at E12.5 day.
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; U12473; AAC52589.1; -;
 DR EMBL; AK018671; BAB31335.1; -;
 DR PIR; I49101; I49101.
 DR HSSP; Q63450; IAO6.
 DR MGD; MGI:99484; Chuk.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Alternative splicing.
 FT DOMAIN 15 300 PROTEIN_KINASE.
 FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 738 743 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1)
 FT MOD_RES 176 176 PHOSPHORYLATION (BY MAP3K14)
 FT (BY SIMILARITY).
 FT (BY SIMILARITY).

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FT VARSPLIC 452 471 MSLRLRYNANLTKMKNLTLS -> IFRKNVKSMEGRKRGH
FT SLF (in isoform 2).
FT /FTId=VSP 004866.
FT VARSPLIC 472 745 Missing (in isoform 2).
FT /FTId=VSP 004867.
FT VARSPLIC 577 584 DHLYSDST -> GKTIQSQY (in isoform 3).
FT /FTId=VSP 004868.
FT VARSPLIC 585 745 Missing (in isoform 3).
FT /FTId=VSP 004869.
FT CONFLICT 236 236 K -> E (IN REF. 3).
FT CONFLICT 400 400 S -> Y (IN REF. 3).
SQ SEQUENCE 745 AA; 84728 MW; 3FEF582AF9F2233 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 32; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDMSWL 6
Db 738 LDMSWL 743

RESULT 3
IKKB_HUMAN
ID IKKB_HUMAN STANDARD; PRT; 756 AA.
AC Q14920; O75327;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKK2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercuro F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
RT 8p12-->p11 by in situ hybridization.";
RL Cytogenet. Cell Genet. 82:32-33(1998).
RN [5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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```

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., DiDonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [7]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462(2000).
RN [8]
RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKBG.
RX MEDLINE=21968797; PubMed=11971985;
RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561(2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (By similarity).
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
CC complex. Phosphorylated IKB-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
CC and CREBBP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -!- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; AF029684; AAC51860.1; -
CC EMBL; AF080158; AAD08997.1; -
CC EMBL; AF031416; AAC64675.1; -
CC EMBL; BC006231; AAH06231.1; -

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DR HSSP; Q63450; 1A06.
DR Genew; HGNC:5960; IKKBK.
DR MIM; 603258; -.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0005524; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00240; Ubiquitin; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW Transferase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 K-S-A: LOSS OF KINASE ACTIVITY AND NO
FT MUTAGEN 44 44 EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S-S-A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S-S-B: FULL ACTIVATION.
FT MUTAGEN 181 181 S-S-A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S-S-B: FULL ACTIVATION.
FT CONFLICT 231 255 WHSKVRQKSEVDIVSDNGTKVF -> CVRMPGTVANS
FT CONFLICT 425 425 CNFTLGGGRWV (IN REF. 5).
FT CONFLICT 425 425 Q -> H (IN REF. 1).
FT CONFLICT 756 756 F9CADF671AE9E14E CRC64;
SQ QUERY MATCH 100.0%; Score 40; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDMSWL 6
| | | | |
DB 737 LDMSWL 742

RESULT 4
IKKB MOUSE STANDARD; PRT; 757 AA.
AC Q88351; Q9R1J6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
DE IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishina S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]

SEQUENCE FROM N.A.
Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
constitutively phosphorylates serine residues of IKK-;
Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[3]
DEVELOPMENTAL STAGE.
MEDLINE=99455228; PubMed=10523828;
Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., stress response signaling
RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
RT developmentally regulated protein kinase."
Oncogene 18:5514-5524(1999).
[4]
IKK PHOSPHORYLATION.
MEDLINE=99038238; PubMed=9819420;
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase 1 and NF-kappaB-inducing kinase."
Mol. Cell. Biol. 18:7336-7343(1998).
[5]
REVIEW
MEDLINE=20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection."
An. J. Physiol. 278:C451-C462(2000).
CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-AUPHA-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
CC and CREBBP (By similarity).
CC -I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC -I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
CC the mouse embryo, at E9.5 day its expression begins to be
CC localized to the brain, neural ganglia, neural tube, and in liver
CC at E12.5 day. At E15.5 day, the expression is further restricted
CC to specific tissues of the embryo.
CC -I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
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EMBL; AF026524; AAC23557.1; -.
EMBL; AF088910; AAD52095.1; -.
HSSP; Q63450; 1A06.
MGD; MGI:1338071; Ikbbk.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_kinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
KW Transferase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.

```

FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDSWLQWDEERCLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 DB 737 LDWSWL 742
 RESULT 5
 IKKB_RAT
 ID IKKB_RAT STANDARD; PRT; 757 AA.
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 CC the dissociation of the inhibitor/NF-kappa-B complex and
 CC ultimately the degradation of the inhibitor. Also phosphorylates
 CC NCOA3.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-P50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
 CC and CREBBP (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF115282; AAF21978.1; -;
 DR HSP; Q63450; IAO6.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFFE46A7DF91F9C CRC64;
 Query Match 100.0%; Score 40; DB 1; Length 757;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 DB 737 LDWSWL 742
 RESULT 6
 CYOA_BUCAI
 ID CYOA_BUCAI STANDARD; PRT; 296 AA.
 AC P57544;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 DE subunit 2).
 DE CYOA OR BU472.
 GN Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -!- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE

CC GROWN AT HIGH AERATION (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.

CC BUT LACK HEME-BINDING DOMAIN.

CC -----

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CC -----

CC EMBL; AP001119; BAB13169.1; ..

CC HSP; P18400; 1CYW.

CC InterPro; IPR001505; Copper_CUA.

CC InterPro; IPR008333; CytoA_II.

CC InterPro; IPR002429; Cyt_C_ox_2.

CC InterPro; IPR000437; ProK_Lipoprot.

CC Pfam; PF00116; COX2; 1.

CC ProDom; PD000131; Copper_CUA; 1.

CC TIGRFAMs; TIGR01433; CytoA_1.

CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.

CC Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;

CC Signal; Lipoprotein; Complete proteome.

CC SIGNAL 1 15 POTENTIAL.

CC CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.

CC LFIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).

CC DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 34 54 POTENTIAL.

CC DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 79 99 POTENTIAL.

CC DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).

CC SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FFBAC CRC64;

CC

Query Match 90.0%; Score 36; DB 1; Length 296;

Best Local Similarity 83.3%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6

DB 125 LDMKWL 130

RESULT 7

COX2_ACEAC

ID COX2_ACEAC STANDARD; PRT; 307 AA.

AC P50653;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome

DE A1 subunit 2) (Oxidase BA(3) subunit 2).

GN CYAB.

OS Acetobacter aceti.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;

OC Acetobacteraceae; Acetobacter.

OX NCBI_TaxID=435;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1023;

RC MEDLINE=93322308; PubMed=8392509;

RA Fukaya M., Tayana K., Tamaki T., Ebisuya H., Okumura H.,

RA Kawamura Y., Horinouchi S., Beppu T.;

RT "Characterization of a cytochrome a1 that functions as a ubiquinol

RT oxidase in Acetobacter aceti.";

RL J. Bacteriol. 175:4307-4314(1993).

CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.

CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.

CC BUT LACK HEME-BINDING DOMAIN.

CC -----

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CC -----

CC EMBL; D13185; BAA02480.1; ..

CC PIR; A36885; A36885.

CC HSP; P18400; 1CYW.

CC InterPro; IPR001505; Copper_CUA.

CC InterPro; IPR008333; CytoA_II.

CC InterPro; IPR002429; Cyt_C_ox_2.

CC Pfam; PF00116; COX2; 1.

CC PRINTS; PR01166; CYCOXIDASEII.

CC ProDom; PD000131; Copper_CUA; 1.

CC TIGRFAMs; TIGR01433; CytoA_1.

CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

CC Oxidoreductase; Transmembrane; Respiratory chain; Signal;

CC Lipoprotein.

CC SIGNAL 1 23 POTENTIAL.

CC CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.

CC LFIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).

CC TRANSMEM 46 66 POTENTIAL.

CC TRANSMEM 87 107 POTENTIAL.

CC SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;

CC

Query Match 90.0%; Score 36; DB 1; Length 307;

Best Local Similarity 83.3%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6

DB 135 LDMKWL 140

RESULT 8

CYOA_PSEPU

ID CYOA_PSEPU STANDARD; PRT; 314 AA.

AC Q9WRI;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O

DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase

DE subunit 2).

GN CYOA.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IH-2000.

RC MEDLINE=99085656; PubMed=9868765;

RA Hirayama H., Takami H., Inoue A., Horikoshi K.;

RT "Isolation and characterization of toluene-sensitive mutants from

RT Pseudomonas putida IH-2000.";

RL FEMS Microbiol. Lett. 169:219-225(1998).

CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT

CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE

CC GROWN AT HIGH AERATION (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.

CC BUT LACK HEME-BINDING DOMAIN.

CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; ABO16787; BAA76356.1; -;
 DR HSSP; P18400; 1CYW.
 DR InterPro; IPR001505; Copper CuA.
 DR InterPro; IPR006333; CytoA II.
 DR InterPro; IPR002429; Cyt_C_ox_2.
 DR Pfam; PF00116; COX2; 1.
 DR ProDom; PD000131; Copper CuA; 1.
 DR TIGRFAMs; TIGR01433; CytoA; 1.
 DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
 KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
 FW Inner membrane; Signal; lipoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 314 UBIQUINOL OXIDASE POLYPEPTIDE II.
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 43 63 POTENTIAL.
 FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 107 POTENTIAL.
 FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).
 SQ SEQUENCE 314 AA; 34702 MW; 96EB04FC3AA77F07 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 314;
 Best Local Similarity 83.3%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 |||||
 DB 133 LDWKWL 138

RESULT 9

ID DCUP YEAST STANDARD; PRT; 362 AA.
 AC P32347;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
 OS HEM12 OR HEM6 OR POP3 OR YD9609.03.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92249304; PubMed=1576986;
 RA Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,
 RA Kushner J., Labbe P.;
 RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12
 RT gene sequence and evidence for two conserved glycines essential for
 RT enzymatic activity.";
 RL Eur. J. Biochem. 205:1011-1016(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93348774; PubMed=8346678;
 RA Dflumeri C., Larocque R., Keng T.;
 RT "Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the
 RT gene for uroporphyrinogen decarboxylase.";
 RL Yeast 9:613-623(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP MUTANTS.
 RX MEDLINE=93111946; PubMed=1471989;
 RA Chelstowska A., Zoadek T., Garey J.R., Kushner J., Rytka J.,
 RA Labbe-Bois R.;

RT "Identification of amino acid changes affecting yeast
 RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
 RT mutant alleles";
 RL Biochem. J. 288:753-757(1992).
 CC -!- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
 CC CO(2).
 CC -!- PATHWAY: Porphyrin and heme biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
 CC -----

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X63721; CAA45253.1; -;
 DR EMBL; Z19089; CAA79514.1; -;
 DR EMBL; Z49209; CAA89078.1; -;
 DR PIR; S23471; S23471.
 DR HSSP; P06132; LURO.
 DR GO; S0002454; HEM12.
 DR GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.
 DR GO; GO:0006783; P:heme biosynthesis; IMP.
 DR InterPro; IPR006361; HemE.
 DR InterPro; IPR000257; Uro_decarbxylys.
 DR Pfam; PF01208; URO-D; 1.
 DR ProDom; PD003225; Uro decarbxylys; 1.
 DR TIGRFAMs; TIGR01464; HemE; 1.
 DR PROSITE; PS00906; UROD_1; 1.
 DR PROSITE; PS00907; UROD_2; 1.
 KW Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
 FT VARIANT 59 S -> F (IN HEM12-6 AND HEM12-12).
 FT VARIANT 62 T -> I (IN HEM12-14).
 FT VARIANT 107 L -> S (IN HEM12-3 AND HEM12-13).
 FT VARIANT 215 S -> N (IN HEM12-2 AND HEM12-11).
 FT MUTAGEN 33 G->D: INACTIVATION.
 FT MUTAGEN 300 G->D: INACTIVATION.
 SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48B62BC277 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 362;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSW 5
 |||||
 DB 279 LDWSW 283

RESULT 10

ID EPA3 CHICK STANDARD; PRT; 983 AA.
 AC P29318;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (CEK4).
 GN EPHA3 OR ETK1 OR CEK4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92031278; PubMed=1657122;
 RA Sajjadi F.G., Pasquale E.B., Subramani S.;
 RT "Identification of a new eph-related receptor tyrosine kinase gene
 RT from mouse and chicken that is developmentally regulated and encodes
 RT at least two forms of the receptor.";

RL New Biol. 3:769-778(1991).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M68514; AAA48666.1; -.
 CC PIR; B45583; B45583.
 CC HSSP; P00523; 2PTK.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR001090; Ephrin_receptor.
 CC InterPro; IPR003961; FNIII.
 CC InterPro; IPR003962; FNIII subd.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR001660; SAM.
 CC InterPro; IPR001245; Tyr_kinase.
 CC InterPro; IPR001426; Ykase_receptorV.
 CC Pfam; PF01404; EPH_lbd; 1.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00536; SAM; 1.
 CC PRINTS; PR00014; FNTYPEIII.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD001495; Ephrin_receptor; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00615; EPH_lbd; 1.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00454; SAM; 1.
 CC SMART; SM00219; TyzKc; 1.
 CC PROSITE; PS01186; EGF_2; UNKNOWN 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 CC PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 CC PROSITE; PS50105; SAM_DOMAIN; 1.
 CC Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 983
 FT DOMAIN 20 540
 FT TRANSMEM 541 564
 FT DOMAIN 565 983
 FT DOMAIN 188 321
 FT DOMAIN 322 431
 FT DOMAIN 432 529
 FT DOMAIN 621 882
 FT DOMAIN 911 975
 FT SITE 981 983
 FT NP_BIND 627 635
 FT BINDING 653 653
 FT ACT_SITE 746 746
 FT MOD_RES 596 596
 FT MOD_RES 602 602
 FT MOD_RES 779 779

FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 983 AA; 109910 MW; E8895F0BDF77651E CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 |||||
 DB 342 LDWSW 346
 RESULT 11
 ID EPA3_HUMAN STANDARD; PRT; 983 AA.
 AC P29320; Q9H2V3; Q9H2V4;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor ETK1) (HEK) (HEK4).
 GN EPHA3 OR ETK1 OR ETK OR HEK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92179233; PubMed=1311845;
 RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
 RT kinase expressed by human lymphoid tumor cell lines.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Melanoma;
 RA Chiari R., Hames G., Stroobant V., Maille B., Texier C., Mach B.,
 RA Boon T., Coulie P.G.;
 RT "Identification of a tumor specific shared antigen derived from an
 RT Eph-receptor and presented to CD4 T cells on HLA class II
 RT molecules".
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
 RX MEDLINE=92147681; PubMed=1737782;
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
 RA Welch K., Loudovaris M., Rockman S., Busmanis I.;
 RT "Isolation and characterization of a novel receptor-type protein
 RT tyrosine kinase (hek) from a human pre-B cell line.";
 RL J. Biol. Chem. 267:3262-3267(1992).
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
 CC FUNCTION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
 CC SECRETED (ISOFORM 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P29320-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P29320-2; Sequence=VSP_002995, VSP_002996;
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 CC RECEPTOR SUBFAMILY.
 CC -----

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EMBL; M83941; AAS58633.1; --
EMBL; AF213459; AAG43576.1; --
EMBL; AF213460; AAG43577.1; --
EMBL; A28003; CAA01906.1; --
PIR; A38224; A38224.
HSP; P00523; 2PTK.
Genew; HGNC:3387; EPHA3.
MIM; 179611; --
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006209; EGF like.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FN_III_subd.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_kinase.
InterPro; IPR001426; YKase_receptorV.
Pfam; PF01404; EPH_lbd; 1.
Pfam; PF00041; fn3; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
ProDom; PD001495; Ephrin_receptor; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00615; EPH_lbd; 1.
SMART; SM00650; FN3; 2.
SMART; SM00454; SAM; 1.
SMART; SM00219; TyKc; 1.
PROSITE; PS01186; EGF_2; UNKNOWN 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS0105; SAM_DOMAIN; 1.
Transferase; tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 983
FT DOMAIN 21 541
FT TRANSMEM 542 565
FT DOMAIN 566 983
FT DOMAIN 189 322
FT DOMAIN 323 432
FT DOMAIN 433 530
FT DOMAIN 621 882
FT DOMAIN 911 975
FT SITE 981 983
FT NP_BIND 627 635
FT BINDING 653 653
FT ACT_SITE 746 746
FT MOD_RES 596 596
FT MOD_RES 602 602
FT MOD_RES 779 779
FT CARBOHYD 232 232
FT CARBOHYD 337 337
FT CARBOHYD 391 391
FT CARBOHYD 404 404
FT CARBOHYD 493 493
FT VARSPPLIC 532 539
FT VARSPPLIC 540 983
Missing (in isoform 2).

FT CONFLICT 507 507 /FTId=VSP_002996.
FT CONFLICT 724 724 F -> L (IN REF. 1; CAA01906).
FT CONFLICT 911 911 V -> L (IN REF. 1; CAA01906).
FT CONFLICT 924 924 S -> T (IN REF. 2).
FT CONFLICT 924 924 R -> W (IN REF. 2).
SQ SEQUENCE 983 AA; 110086 MW; B8D900F80FF5121 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 983;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 1 LDMSW 5
DB 343 LDMSW 347
RESULT 12
EPA3 MOUSE
ID EPA3 MOUSE STANDARD; PRT; 983 AA.
AC P29319.
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor ETK1) (MEK4).
GN EPHA3 OR ETK1 OR MEK4 OR TYRO4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=ICR X Swiss Webster; TISSUE=Embryo;
RA MEDLINE=92031278; PubMed=1657122;
RX Sajjadi F.G., Pasquale E.B., Subramani S.;
RT "Identification of a new eph-related receptor tyrosine kinase gene
RT from mouse and chicken that is developmentally regulated and encodes
RT at least two forms of the receptor."
RL New Biol. 3:769-778(1991).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
CC EPHRIN-A2, -A3, -A4 AND -A5.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM
CC IS SECRETED.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P29319-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P29319-2; Sequence=VSP_002997;
CC -!- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
CC BRAIN, ALSO DETECTED IN TESTIS.
CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC
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DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; EPH_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00105; SAM_DOMAIN; 1.
 DR Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 541 564 POTENTIAL.
 FT DOMAIN 188 321 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 322 431 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 432 529 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 621 882 PROTEIN KINASE.
 FT DOMAIN 911 975 SAM.
 FT SITE 981 983 PD2-BINDING MOTIF (POTENTIAL).
 FT NP_BIND 627 635 ATP (BY SIMILARITY).
 FT BINDING 653 653 ATP (BY SIMILARITY).
 FT ACT_SITE 746 746 BY SIMILARITY.
 FT MOD_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 530 983 Missing (in isoform Short).
 FT /FTId=VSP_002997.
 SO SEQUENCE 983 AA; 109955 MW; BE44A65508107A2 CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 983;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDWSW 5
 Db 342 LDWSW 346
 RESULT 13
 ID EPA3_RAT STANDARD; PRT; 984 AA.
 AC O08680;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor REK4) (TYRO-4).
 GN EPHA3 OR REK4 OR TYRO4.

OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98120505; PubMed=9458884;
 RA Li Y.Y., McTiernan C.P., Feldman A.M.;
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene
 z-Epha3 in neonatal rat cardiomyocytes.";
 RL Am. J. Physiol. 274:H331-H341(1998).
 CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
 EPHRIN-A2, -A3, -A4 AND -A5.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, AND LUNG.
 CC -!- INDUCTION: DOWN-REGULATED BY IL1-BETA IN NEONATAL CARDIAC
 MYOCYTES.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 RECEPTOR SUBFAMILY.

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 or send an email to license@isb-sib.ch).

 DR EMBL; U69278; AAC06273.1; --
 DR HSSP; P00523; 2PTK.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; EPH_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00105; SAM_DOMAIN; 1.
 DR Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 984 EPHRIN TYPE-A RECEPTOR 3.
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 542 565 POTENTIAL.
 FT DOMAIN 566 984 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 189 322 CYS-RICH.
 FT DOMAIN 328 431 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 436 528 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 622 883 PROTEIN KINASE.

FT DOMAIN 912 976 SAM.
 FT SITE 982 984 PDZ-BINDING MOTIF (POTENTIAL).
 FT NP BIND 628 636 ATP (BY SIMILARITY).
 FT BINDING 654 654 ATP (BY SIMILARITY).
 FT ACT_SITE 747 747 BY SIMILARITY.
 FT MOD_RES 597 597 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 603 603 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 780 780 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 984;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSW 5
 DB 343 LDWSW 347
 RESULT 14
 ID GUNB_CALSA STANDARD; PRT; 1039 AA.
 AC F10474;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase/exoglucanase B precursor [Includes: Endoglucanase
 (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 (Cellobiohydrolase); Exoglucanase (EC 3.2.1.1.91) (Exocellobiohydrolase)
 (1,4-beta-cellobiohydrolase)].
 DE CELB.
 GN Caldocellum saccharolyticum (Caldocellulosiraptor saccharolyticus).
 OS Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
 OC Caldicellulosiraptor.
 OX NCBI_TaxID=44001;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89098398; PubMed=2789517;
 RA Saul D.J., Williams L.C., Love D.R., Chamley I.W., Bergquist P.I.;
 RT "Nucleotide sequence of a gene from Caldocellum saccharolyticum
 encoding for exoglucanase and endocellulase activity.";
 RL Nucleic Acids Res. 17:439-439(1989).
 CC -!- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL
 (1,4-BETA-GLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS
 AN ENDOGLUCANASE.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 in cellulose and cellotetraose, releasing cellobiose from the non-
 reducing ends of the chains.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
 F (FAMILY 10 OF GLYCOSYL HYDROLASES).
 CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
 A (FAMILY 5 OF GLYCOSYL HYDROLASES).
 CC
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 CC
 CC EMBL; X13602; CAA31936.1; --
 DR PIR; S02711; S02711.
 DR HSSP; Q06851; INBC.
 DR InterPro; IPR001956; CBD_3.
 DR InterPro; IPR001000; Glyco_hydro_10.

DR InterPro; IPR001547; Glyco_hydro_5.
 DR Pfam; PF00942; CBM_3; 1.
 DR Pfam; PF00150; cellulase; 1.
 DR Pfam; PF00331; Glyco_hydro_10; 1.
 DR PRINTS; PR00134; GLHYDRLASE10.
 DR ProDom; PD001947; CBD_3; 1.
 DR SMART; SM00633; Glyco_10; 1.
 DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Repeat;
 Multifunctional enzyme; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 1039 ENDOGLUCANASE/EXOGLUCANASE B.
 FT DOMAIN 376 416 THR/PRO-RICH, TANDEM REPEATS OF T-P.
 FT DOMAIN 417 570 CELLULOSE-BINDING (BY SIMILARITY).
 FT DOMAIN 571 618 THR/PRO-RICH, TANDEM REPEATS OF T-P.
 FT ACT_SITE 177 177 PROTON DONOR (POTENTIAL).
 FT ACT_SITE 285 285 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 792 792 BY SIMILARITY.
 SQ SEQUENCE 1039 AA; 117641 MW; OE0378171594DDAE CRC64;
 Query Match 90.0%; Score 36; DB 1; Length 1039;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWL 6
 DB 540 DWSWL 544
 RESULT 15
 ID CYOA_BUCAP STANDARD; PRT; 290 AA.
 AC Q8K953;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
 subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 subunit 2).
 DE subunit 2).
 GN CYOA OR BUSG456.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RL Science 296:2376-2379(2002).
 CC -!- FUNCTION: Cytochrome O terminal oxidase complex is the component
 of the aerobic respiratory chain that predominates when cells are
 grown at high aeration (By similarity).
 CC -!- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE014121; AAM67999.1; --
 DR InterPro; IPR001505; Copper_Cua.
 DR InterPro; IPR006333; Cyoa_II.
 DR InterPro; IPR002429; Cyt_cox_2.
 DR InterPro; IPR000437; Prok_Lipoprot.

DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CUA; 1.
DR TIGRFAMs; TIGR01433; CyoA; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Signal; Lipoprotein; Complete proteome.
FT SIGNAL 1 24
FT CHAIN 25 290
FT LIPID 25 25
FT DOMAIN 25 42
FT TRANSMEM 43 63
FT DOMAIN 64 87
FT TRANSMEM 88 108
FT DOMAIN 109 290
SQ SEQUENCE 290 AA; 33730 MW; 3D80A02A84732963 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 290;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDKSWL 6
Db 134 LDWRWL 139

Search completed: February 18, 2004, 14:28:01
Job time : 5.55263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_nhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	740	6 Q95KV1	Q95kv1 bos taurus
2	40	100.0	745	11 Q8CBT3	Q8cbt3 mus musculus
3	40	100.0	756	6 Q95KV0	Q95kv0 bos taurus
4	38	95.0	1139	16 Q8ZC91	Q8zcg1 versinia pe
5	37	92.5	173	16 Q8ESU2	Q8esu2 streptococ
6	37	92.5	173	16 Q8E065	Q8e065 streptococ
7	37	92.5	310	2 Q9XB57	Q9xb57 zymomonas m
8	37	92.5	322	16 Q8Y9K7	Q8y9k7 brucella me
9	37	92.5	347	16 Q98XR3	Q98xr3 rhizobium l
10	37	92.5	347	16 Q8G1B0	Q8g1b0 brucella eu
11	37	92.5	361	16 Q8P955	Q8p955 xanthomonas
12	37	92.5	645	2 Q9X6C6	Q9x6c6 thermus bro
13	36	90.0	85	16 Q8FBL8	Q8fbl8 escherichia
14	36	90.0	205	16 Q9ACR5	Q9acr5 streptomyce
15	36	90.0	227	4 Q81XK8	Q81xk8 homo sapien
16	36	90.0	242	12 Q919K8	Q919k8 culex nigri

17	36	90.0	261	2 Q9AQG7	Q9aqg7 caldicellul
18	36	90.0	282	16 Q8D354	Q8d354 wigglewort
19	36	90.0	288	2 Q8VTT4	Q8vtt4 pseudomonas
20	36	90.0	308	2 Q8KZS2	Q8kzs2 acetobacter
21	36	90.0	313	2 Q8VUQ6	Q8vuq6 pseudomonas
22	36	90.0	318	16 Q8ZC58	Q8zcs8 versinia pe
23	36	90.0	329	16 Q8XVB4	Q8xvb4 raietonia s
24	36	90.0	331	16 Q91427	Q91427 pseudomonas
25	36	90.0	341	16 Q8G3A8	Q8g3a8 brucella eu
26	36	90.0	344	16 Q8VEH7	Q8veh7 brucella me
27	36	90.0	353	16 Q9A7F0	Q9a7f0 caulobacter
28	36	90.0	355	11 Q8BIT9	Q8bit9 mus musculus
29	36	90.0	386	16 Q92U27	Q92u27 rhizobium m
30	36	90.0	393	16 Q987Z1	Q987z1 rhizobium l
31	36	90.0	409	10 Q9M3F6	Q9m3f6 arabidopsis
32	36	90.0	452	4 Q96AB7	Q96ab7 homo sapien
33	36	90.0	477	11 Q9CYU6	Q9cyu6 mus musculus
34	36	90.0	484	4 Q9BTV6	Q9btv6 homo sapien
35	36	90.0	538	11 Q8C9K6	Q8c9k6 mus musculus
36	36	90.0	703	10 Q9FIS0	Q9fis0 arabidopsis
37	36	90.0	703	10 Q8GYG3	Q8gyg3 arabidopsis
38	36	90.0	747	16 Q89735	Q89735 mycobacteri
39	36	90.0	803	17 Q97UH8	Q97uh8 sulfolobus
40	36	90.0	984	11 Q8C3U1	Q8c3u1 mus musculus
41	36	90.0	984	11 Q8BRB1	Q8brb1 mus musculus
42	36	90.0	996	2 Q9AQH0	Q9aqh0 caldicellul
43	36	90.0	1329	16 Q9CD30	Q9cd30 mycobacteri
44	36	90.0	1426	2 Q9X3P6	Q9x3p6 caldicellul
45	36	90.0	1751	2 Q9AQG4	Q9aqg4 caldicellul

ALIGNMENTS

RESULT 1

Q95KV1 ID Q95KV1 PRELIMINARY; PRT; 740 AA.
AC Q95KV1; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE IKB kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;
RT Identification and characterisation of the bovine Ikb kinases (IKBs)
RL alpha, beta and gamma.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AJ414555; CAC93686.1; -;
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F4D176 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 740;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6

|||||

Db 733 LDWSWL 738

RESULT 2

Q8CBT3 PRELIMINARY; PRT; 745 AA.
 AC Q8CBT3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved helix-loop-helix ubiquitous kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR ENBL; AK035326; BAC29034.1; --
 SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 745;

Best Local Similarity 100.0%; Pred. No. 2.1e-02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6

Db 738 LDWSWL 743

RESULT 3

Q95KV0 PRELIMINARY; PRT; 756 AA.
 AC Q95KV0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ikb kinase-beta.
 GN BIK3BETA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;
 RA "Identification and characterisation of the bovine Ikb kinases (IKGs)
 alpha, beta and gamma."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR ENBL; AJ414556; CAC93687.1; --
 DR InterPro; IPR00719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR001245; Tyr pkinase.
 DR Pfam; PF00069; pkinase; I
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A17655 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 756;

Best Local Similarity 100.0%; Pred. No. 2.2e-02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6

Db 737 LDWSWL 742

RESULT 4

Q8ZC91 PRELIMINARY; PRT; 1139 AA.
 AC Q8ZC91;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative potassium efflux system (Putative alpha helix protein).
 GN YPO3129 OR AEPa OR Y1054.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611 (2002).
 DR ENBL; AJ414155; CAC92364.1; --
 DR ENBL; AE013709; AAM84635.1; --
 DR InterPro; IPR006685; MSion_channel.
 DR InterPro; IPR006686; MS_channel_dom.
 DR Pfam; PF00924; MS_channel; 1.
 DR PROSITE; PS01246; UPF0003; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1139 AA; 128409 MW; 7B54108BFC39A6B1 CRC64;

Query Match 95.0%; Score 38; DB 16; Length 1139;

Best Local Similarity 83.3%; Pred. No. 6.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6

Db 480 MDWSWL 485

RESULT 5

Q8ESU2 PRELIMINARY; PRT; 173 AA.
 AC Q8ESU2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN GBS0887.
 OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495;


```

RN  SEQUENCE FROM N.A.
RP  STRAIN=NEM316 / Serotype III;
RX  MEDLINE=22242508; PubMed=12354221;
RA  Glaser P., Rusniok C., Buchrieser C., Chevallier F., Frangeul L.,
RA  Meadek T., Zouine M., Couve E., Lailoui L., Foyart C., Trieu-Cuot P.,
RA  Kunst F.;
RT  "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT  invasive neonatal disease.";
RL  Mol. Microbiol. 45:1499-1513 (2002).
DR  EMBL; AL766847; CAD46531.1; -.
DR  Sagarist; gbs0887; -.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 173 AA; 20135 MW; F5F3404F0224CD1 CRC64;

Query Match          92.5%; Score 37; DB 16; Length 173;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LDWSWL 6
Db  125 LDWAWL 130
|||||

RESULT 6
Q8E065 PRELIMINARY; PRT; 173 AA.
AC  Q8E065;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Acetyltransferase, GNAT family.
GN  SAG0870.
OS  Streptococcus agalactiae (serotype V).
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC  Streptococcus.
OX  NCBI_TaxID=216466;
RN  1
RP  SEQUENCE FROM N.A.
RC  STRAIN=2603 V/R / Serotype V;
RX  MEDLINE=22222988; PubMed=12200547;
RA  Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA  Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA  Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA  DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA  Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA  Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA  Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA  Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA  Fraser C.M.;
RT  "Complete genome sequence and comparative genomic analysis of an
RT  emerging human pathogen, serotype V Streptococcus agalactiae.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR  EMBL; AE014231; AM99756.1; -.
DR  TIGR; SAG0870; -.
KW  Transferase; Complete proteome.
SQ  SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;

Query Match          92.5%; Score 37; DB 16; Length 173;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LDWSWL 6
Db  125 LDWAWL 130
|||||

RESULT 7
Q9XBS7 PRELIMINARY; PRT; 310 AA.
ID  Q9XBS7
AC  Q9XBS7;
DT  01-NOV-1999 (TrEMBLrel. 12, Created)
DT  01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

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DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Putative carboxymethylglutaminase.
GN  DLH.
OS  Zymomonas mobilis.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC  Sphingomonadaceae; Zymomonas.
OX  NCBI_TaxID=542;
RN  1
RP  SEQUENCE FROM N.A.
RC  STRAIN=ZM4;
RA  Um H.W., Kang H.S.;
RT  "The sequence analysis of 42D7 fosmid clone of Zymomonas mobilis
RT  ZM4.";
RL  Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF157493; RAD42398.1; -.
DR  InterPro; IPR002925; DLH.
DR  InterPro; IPR000379; Ser_estrs_site.
DR  Pfam; PF01738; DLH; 1.
SQ  SEQUENCE 310 AA; 34092 MW; 34AC821E1F91259D CRC64;

Query Match          92.5%; Score 37; DB 2; Length 310;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LDWSWL 6
Db  153 VDSWL 158
|||||

RESULT 8
Q8YK7 PRELIMINARY; PRT; 322 AA.
ID  Q8YK7;
AC  Q8YK7;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  NADH-quinone oxidoreductase chain H (BC 1.6.5.3).
GN  BME1151.
OS  Brucella melitensis.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC  Brucellaceae; Brucella.
OX  NCBI_TaxID=29459;
RN  1
RP  SEQUENCE FROM N.A.
RC  STRAIN=16M / ATCC 23456 / Biotype 1;
RX  MEDLINE=20020109; PubMed=11756888;
RA  DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA  Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA  Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA  Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA  Haselkorn R., Kypides N., Overbeek R.;
RT  "The genome sequence of the facultative intracellular pathogen
RT  Brucella melitensis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
DR  EMBL; AE009554; AAL52332.1; -.
DR  InterPro; IPR001694; Resp_NADH_dhl.
DR  Pfam; PF00146; NADHdh; 1.
DR  PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW  Oxidoreductase; Complete proteome.
SQ  SEQUENCE 322 AA; 35966 MW; D5B5B123AB2C13E7 CRC64;

Query Match          92.5%; Score 37; DB 16; Length 322;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 LDWSWL 6
Db  174 LDWNL 179
|||||

RESULT 9
Q98K3 PRELIMINARY; PRT; 347 AA.
ID  Q98K3

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AC Q98KR3;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NADH-ubiquinone dehydrogenase chain 8.
 GN MLL1361.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338 (2000).
 DR EMBL; AF002997; BAB48751.1; -;
 DR InterPro; IPR001694; Resp_NADH_dh1.
 DR Pfam; PF00146; NADHdh; 1.
 DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
 KW Ubiquinone; Complete proteome.
 SQ SEQUENCE 347 AA; 38370 MW; 1092F351BD97EC57 CRC64;
 Query Match 92.5%; Score 37; DB 16; Length 347;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 Db 199 LDWNWL 204
 |||:|
 RESULT 10
 Q8GIB0 PRELIMINARY; PRT; 347 AA.
 AC Q8GIB0;
 DT 01-WAR-2003 (TrEMBLrel. 23, Created)
 DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE NADH dehydrogenase I, H subunit.
 GN NUOH OR BR0809.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read I.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
 DR EMBL; AE014385; AAN29738.1; -;
 DR TIGR; BR0809; -;
 KW Complete proteome.
 SQ SEQUENCE 347 AA; 38428 MW; DA7F7471FD34D127 CRC64;
 Query Match 92.5%; Score 37; DB 16; Length 347;
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSWL 6
 Db 199 LDWNWL 204
 |||:|
 RESULT 11
 Q8P955 PRELIMINARY; PRT; 361 AA.
 AC Q8P955;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Exopolysaccharide biosynthesis protein.
 GN XCC2011.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Camnava F., Cardoso J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Fortmighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463 (2002).
 DR EMBL; AE012305; AAM41300.1; -;
 DR InterPro; IPR002656; Acyl_transf_3.
 DR Pfam; PF01757; Acyl_transf_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;
 Query Match 92.5%; Score 37; DB 16; Length 361;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDWSWL 6
 Db 117 LDWSWL 122
 |||:|
 RESULT 12
 Q9X6C6 PRELIMINARY; PRT; 645 AA.
 AC Q9X6C6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Beta-galactosidase.
 GN BGAT.
 OS Thermus brockianus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=56956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IT1360;
 RX MEDLINE=99402735; PubMed=10473401;
 RA Fridjonsson O., Watzlack H., Gehweiler A., Rohrhirsch T., Mattes R.;

RT "Cloning of the gene encoding a novel thermostable alpha-galactosidase
 from *Thermus brockianus* IRI360.";
 RL Appl. Environ. Microbiol. 65:3955-3963(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=ITI360;
 RX MEDLINE=20203878; PubMed=10741834;
 RA Fridjonsson O., Watzlawick H., Mattes R.;
 RT "The structure of the alpha-galactosidase gene loci in *Thermus*
 brockianus IRI360 and *Thermus thermophilus* TH125.";
 RL Extremophiles 4:23-33(2000).
 DR EMBL; AF1355398; AA03667.1; -;
 DR InterPro; IPR001554; Glyco_hydro_14.
 DR InterPro; IPR003476; Glyco_hydro_42.
 DR Pfam; PF01373; Glyco_hydro_14; 1.
 DR Pfam; PF02449; Glyco_hydro_42; 1.
 SQ SEQUENCE 645 AA; 73420 MW; C79A9E1C0020EC40 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 645;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
 Db 48 LDMAWL 53

RESULT 13
 Q8FBL8 PRELIMINARY; PRT; 85 AA.
 ID Q8FBL8
 AC Q8FBL8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN C4754.

OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=20388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rossch P.,
 RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016769; AA083187.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 85 AA; 9675 MW; 47DADB502F570A8B CRC64;

Query Match 90.0%; Score 36; DB 16; Length 85;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6
 Db 19 IDMSWL 24

RESULT 14
 Q9ACR5 PRELIMINARY; PRT; 205 AA.
 ID Q9ACR5
 AC Q9ACR5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein SCP1.253.
 GN SCP1.253.

OS Streptomyces coelicolor.
 OG Plasmid SCPI.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Batenan A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete *Streptomyces*
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL590464; CAC36779.1; -;
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 Db 11 DMSWL 15

RESULT 15
 Q8IXK8 PRELIMINARY; PRT; 227 AA.
 ID Q8IXK8
 AC Q8IXK8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to hypothetical protein BC017335.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040173; AA040173.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6
 Db 114 DMSWL 118

Search completed: February 18, 2004, 14:35:34
 Job time : 19.3684 secs

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